



## Full wwPDB EM Validation Report ⓘ

Dec 18, 2023 – 06:41 PM EST

PDB ID : 1O1F  
EMDB ID : EMD-1001  
Title : MOLECULAR MODELS OF AVERAGED RIGOR CROSSBRIDGES FROM  
TOMOGRAMS OF INSECT FLIGHT MUSCLE  
Authors : Chen, L.F.; Winkler, H.; Reedy, M.K.; Reedy, M.C.; Taylor, K.A.  
Deposited on : 2002-11-15  
Resolution : 70.00 Å (reported)  
Based on initial models : 1ATN, 2MYS

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev70  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

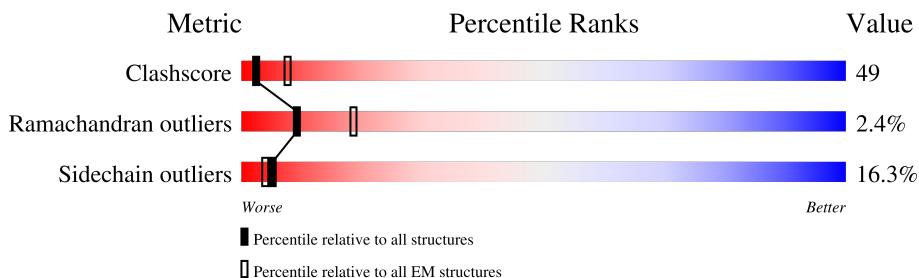
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 70.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	840	100% 26% 50% 20% .
1	D	840	99% 26% 51% 20% .
1	G	840	100% 25% 51% 20% .
1	J	840	99% 25% 51% 20% .
2	B	145	100% 66% 26% 6% .
2	E	145	100% 63% 28% 6% .
2	H	145	100% 63% 28% 6% .
2	K	145	100% 65% 26% 6% .

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Mol	Chain	Length	Quality of chain		
3	C	147	100%	61%	37%
3	F	147	90%	61%	38%
3	I	147	100%	61%	37%
3	L	147	73%	61%	37%
4	0	375	99%	65%	27%
4	1	375	99%	64%	27%
4	2	375	99%	63%	28%
4	3	375	99%	63%	29%
4	4	375	95%	58%	32%
4	5	375	99%	58%	32%
4	6	375	98%	56%	33%
4	7	375	99%	56%	34%
4	8	375	93%	60%	30%
4	V	375	99%	61%	30%
4	W	375	99%	63%	28%
4	X	375	99%	63%	28%
4	Y	375	99%	64%	28%
4	Z	375	99%	64%	28%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
1	MLY	A	505	-	-	X	-
1	MLY	A	553	-	-	X	-
1	MLY	A	764	-	-	X	-
1	MLY	A	768	-	-	X	-
1	MLY	A	839	-	-	X	-
1	MLY	D	553	-	-	X	-
1	MLY	D	782	-	-	X	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
1	MLY	D	839	-	-	X	-
1	MLY	G	553	-	-	X	-
1	MLY	G	764	-	-	X	-
1	MLY	G	768	-	-	X	-
1	MLY	G	84	-	-	X	-
1	MLY	J	553	-	-	X	-
1	MLY	J	764	-	-	X	-
1	MLY	J	768	-	-	X	-
1	MLY	J	84	-	-	X	-

## 2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 76872 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called SKELETAL MUSCLE MYOSIN II.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	840	Total 6797	C 4382	N 1135	O 1243	S 37	0	0
1	D	840	Total 6797	C 4382	N 1135	O 1243	S 37	0	0
1	G	840	Total 6797	C 4382	N 1135	O 1243	S 37	0	0
1	J	840	Total 6797	C 4382	N 1135	O 1243	S 37	0	0

- Molecule 2 is a protein called SKELETAL MUSCLE MYOSIN II REGULATORY LIGHT CHAIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	145	Total 1127	C 717	N 177	O 227	S 6	0	0
2	E	145	Total 1127	C 717	N 177	O 227	S 6	0	0
2	H	145	Total 1127	C 717	N 177	O 227	S 6	0	0
2	K	145	Total 1127	C 717	N 177	O 227	S 6	0	0

- Molecule 3 is a protein called SKELETAL MUSCLE MYOSIN II ESSENTIAL LIGHT CHAIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	147	Total 1123	C 698	N 188	O 230	S 7	0	0
3	F	147	Total 1123	C 698	N 188	O 230	S 7	0	0
3	I	147	Total 1123	C 698	N 188	O 230	S 7	0	0
3	L	147	Total 1123	C 698	N 188	O 230	S 7	0	0

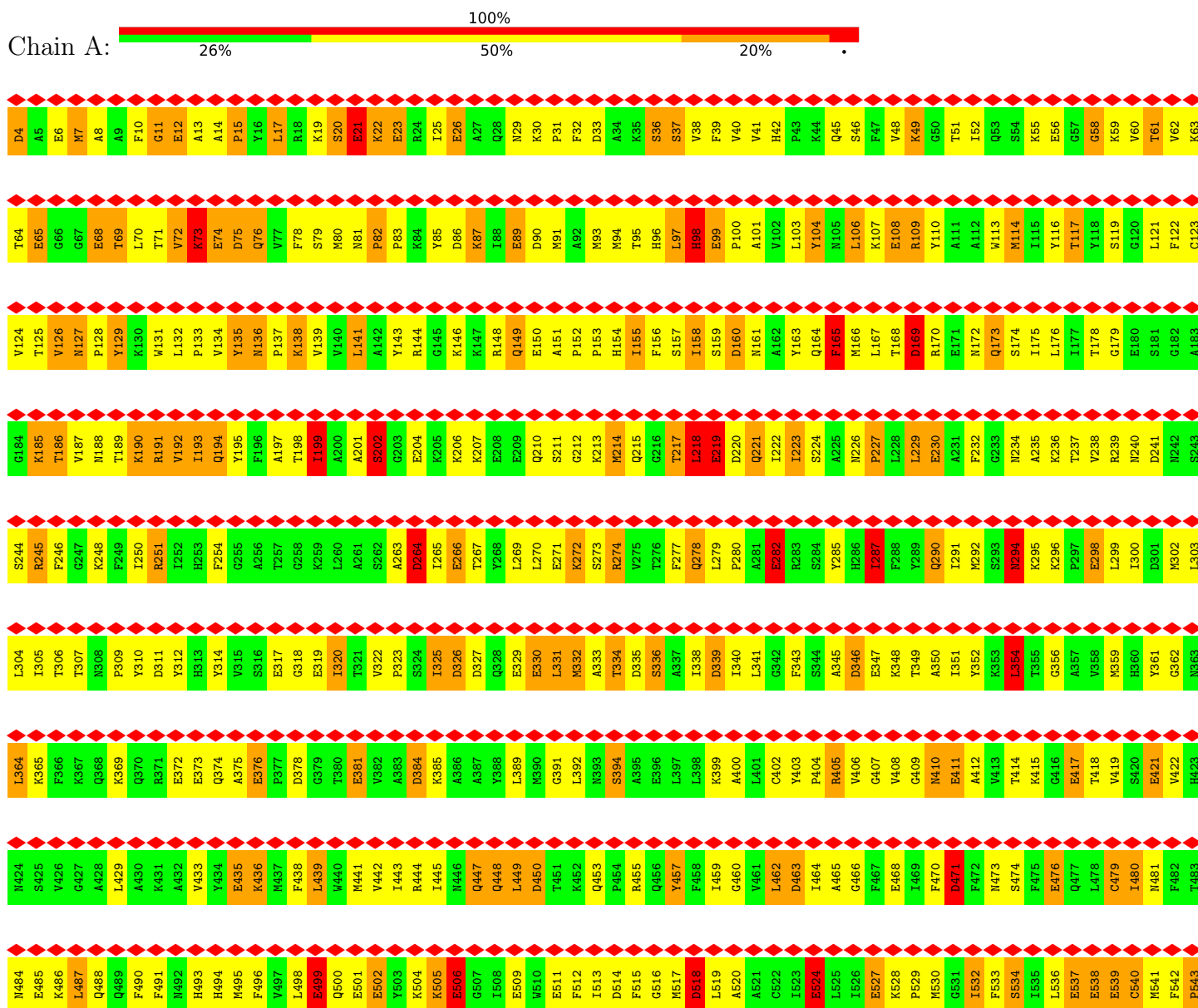
- Molecule 4 is a protein called SKELETAL MUSCLE ACTIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	0	372	Total	C	N	O	S	0	0
			2906	1836	489	561	20		
4	1	372	Total	C	N	O	S	0	0
			2906	1836	489	561	20		
4	2	372	Total	C	N	O	S	0	0
			2906	1836	489	561	20		
4	3	372	Total	C	N	O	S	0	0
			2906	1836	489	561	20		
4	4	372	Total	C	N	O	S	0	0
			2906	1836	489	561	20		
4	5	372	Total	C	N	O	S	0	0
			2906	1836	489	561	20		
4	6	372	Total	C	N	O	S	0	0
			2906	1836	489	561	20		
4	7	372	Total	C	N	O	S	0	0
			2906	1836	489	561	20		
4	8	372	Total	C	N	O	S	0	0
			2906	1836	489	561	20		
4	V	372	Total	C	N	O	S	0	0
			2906	1836	489	561	20		
4	W	372	Total	C	N	O	S	0	0
			2906	1836	489	561	20		
4	X	372	Total	C	N	O	S	0	0
			2906	1836	489	561	20		
4	Y	372	Total	C	N	O	S	0	0
			2906	1836	489	561	20		
4	Z	372	Total	C	N	O	S	0	0
			2906	1836	489	561	20		

### 3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: SKELETAL MUSCLE MYOSIN II



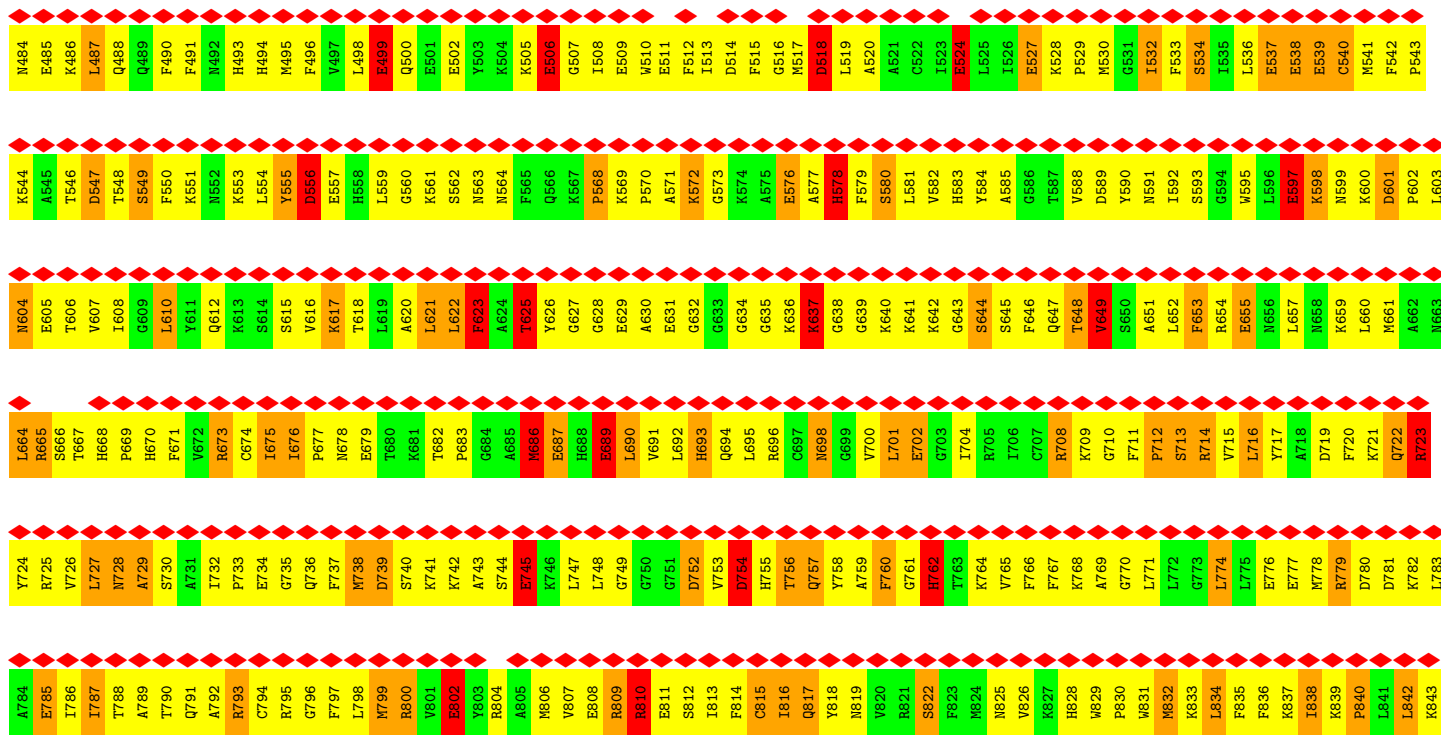
K544	K545	T546	D647	S649	F550	K651	N652	K653	L654	Y655	D656	H658	L659	G660	K661	S662	N663	N664	F665	Q666	K667	P668	K669	P570	A571	K572	G573	K574	A575	E576	A577	H578	F579	S580	L581	V582	H583	Y584	A585	G586	T587	V588	D589	Y590	N591	L592	H593	S593	G594	V595	L596	K598	N599	K600	D601	P602	L603			
N604	E605	T606	V607	L608	G609	L610	Y611	Q612	K613	L614	S615	V616	K617	T618	L619	A620	L621	L622	F623	A624	T625	Y626	G627	G628	P629	A630	E631	G632	G633	G634	G635	K636	K637	G638	G639	K640	K641	K642	G643	S644	A645	F646	Q647	T648	V649	S650	A651	L652	F653	S653	L654	A655	N656	L657	N658	K659	L660	D661	A662	N663
L664	R665	S666	T667	H668	P669	H670	F671	V672	R673	C674	I675	I676	P677	N678	L679	T680	K681	T682	P683	G684	T685	M686	H687	H688	R689	L690	V691	L692	G693	Q694	L695	R696	N698	G699	V700	L701	E702	G703	I704	I706	C707	R708	K709	G710	F711	P712	L713	R714	V715	L716	N717	L718	N719	L720	F721	Q722	R723			
Y724	R725	V726	L727	A728	N729	S730	A731	I732	P733	E734	G735	Q736	F737	M738	D739	S740	K741	K742	A743	S744	E745	K746	L747	L748	G749	G750	G751	D752	V753	D754	H755	T756	T757	Y758	A759	F760	G761	H762	T763	K764	V765	F766	F767	K768	A769	G770	L771	L772	G773	L774	L775	E776	F777	M778	R779	D780	D781	K782	L783	
A784	E785	I786	I787	T788	A789	T790	Q791	A792	R793	C794	R795	G796	F797	L798	M799	R800	V801	E802	Y803	R804	A805	M806	V807	E808	R809	R810	E811	S812	I813	F814	C815	I816	Q817	Y818	N819	V820	S822	F823	M824	N825	V826	K827	H828	N829	P830	M831	M832	L833	L834	F835	F836	I838	K839	P840	L841	L842	K843			

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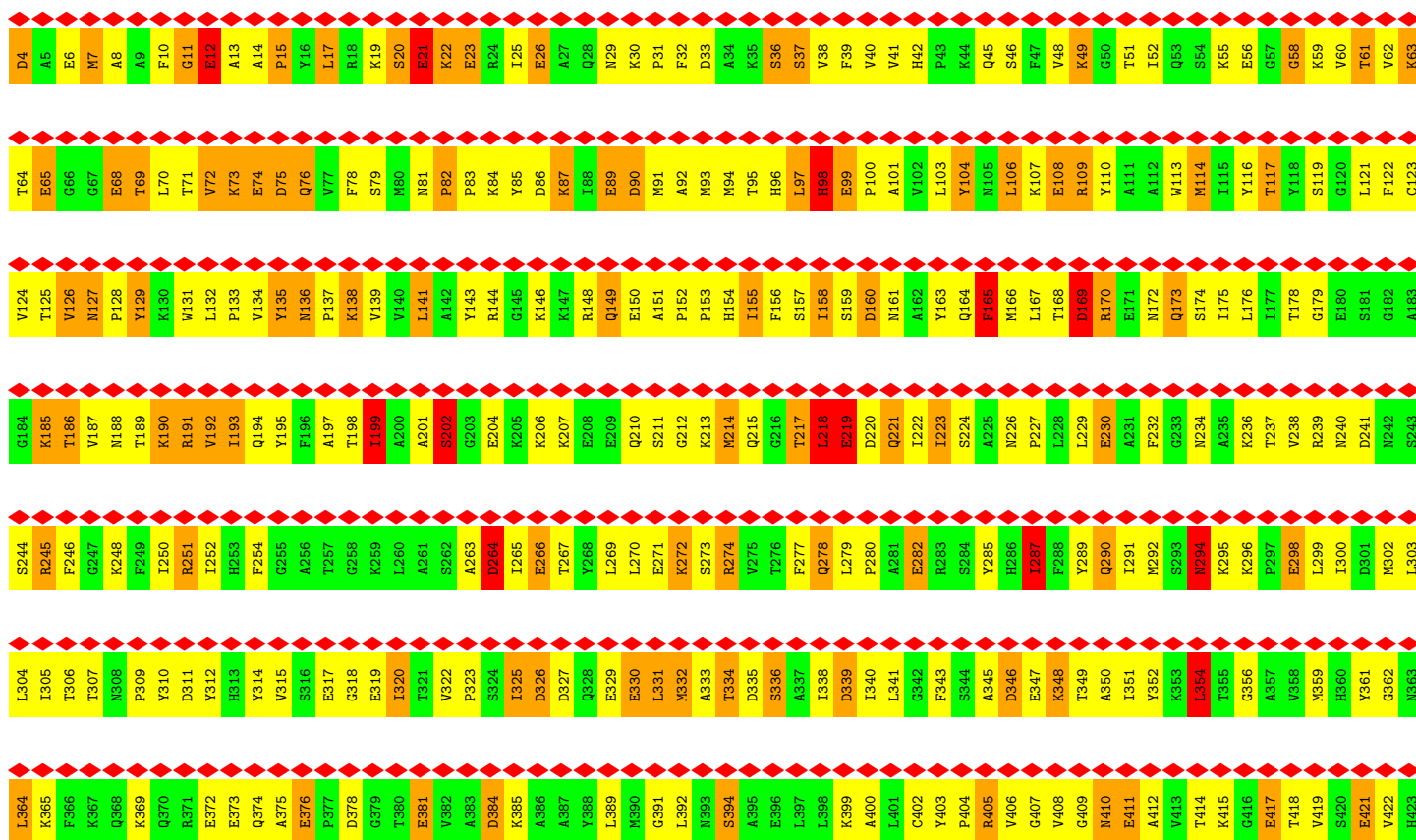


D4	A5	E6	M7	A8	A9	F10	G11	E12	A13	A14	P15	Y16	L17	R18	K19	S20	E21	K22	E23	R24	I25	E26	Q27	Q28	N29	K30	P31	D32	F33	M34	K35	S36	S37	V38	F39	V40	H42	P43	K44	N45	S46	F47	V48	K49	G50	T51	I52	M53	Q53	S54	K55	E56	G57	G58	K59	V60	T61	V62	K63	
T64	E65	G66	G67	E68	T69	L70	T71	V72	K73	E74	D75	Q76	V77	F78	S79	M80	N81	P82	P83	K84	Y85	D86	K87	I88	E89	D90	M91	A92	M93	M94	T95	H96	L97	H88	E99	P100	A101	V102	L103	Y104	N105	L106	K107	E108	R109	Y110	A111	A112	M113	M114	I115	Y116	Y118	S119	G120	L121	F122	C123		
V124	T125	V126	N127	P128	Y129	K130	V131	L132	P133	V134	Y135	N136	P137	K138	V139	V140	L141	A142	Y143	R144	G145	K146	K147	L148	Q149	E150	A151	P152	G153	H154	I155	F156	S157	L158	S159	D160	N161	A162	Y163	Q164	F165	M166	M167	P168	D169	R170	E171	N172	L173	Q173	S174	L175	L176	L177	T178	G179	E180	L181	G182	A183
G184	K185	T186	V187	N188	L189	K190	R191	V192	L193	Q194	Y195	F196	T197	L198	N199	A200	A201	S202	G203	E204	K205	K206	K207	E208	E209	Q210	S211	G212	K213	M214	Q215	G216	L218	E219	D220	Q221	I222	L223	S224	A225	M226	P227	L228	L229	E230	A231	F232	G233	G234	A235	K236	V238	R239	M240	D241	M242	S243			
S244	R245	F246	G247	R248	F249	I250	R251	L252	H253	F254	G255	A256	T257	G258	K259	L260	A261	S262	A263	D264	E265	E266	T267	Y268	L269	L270	E271	K272	S273	R274	V275	T276	F277	Q278	L279	P280	A281	E282	R283	S284	Y285	H286	L287	F288	Y289	Q290	L291	M292	S293	M294	K295	K296	E298	L299	I300	M302	L303			
L304	L305	T306	T307	N308	P309	Y310	D311	Y312	H313	Y314	V315	S316	E317	G318	E319	I320	T321	V322	P323	S324	D325	D326	D327	Q328	E329	E330	L331	M332	A333	T334	D335	S336	L338	D339	L340	L341	G342	F343	P344	S345	A346	D346	E347	K348	T349	A350	L351	Y352	L353	L354	T355	G356	V358	N359	H360	Y361	G362	N363		
L364	K365	F366	K367	Q368	K369	Q370	R371	E372	E373	Q374	A375	E376	P377	D378	G379	T380	E381	V382	A383	D384	K385	A386	A387	Y388	L389	R390	G391	L392	N393	S394	A395	E396	L397	L398	K399	A400	C402	Y403	P404	A405	V406	A407	V408	A409	N410	E411	A412	V413	T414	K415	G416	E417	T418	V419	S420	A421	V422	H423		
N424	S425	V426	G427	K428	L429	A430	K431	A432	V433	Y434	E435	K436	H437	F438	L439	W440	M441	V442	L443	R444	L445	N446	Q447	L448	L449	D450	T451	K452	Q453	F454	R455	Q456	F457	L458	L459	G460	V461	L462	D463	L464	A465	G466	F467	E468	L469	F470	D471	F472	N473	S474	F475	E476	Q477	L478	C479	L480	N481	F482	T483	

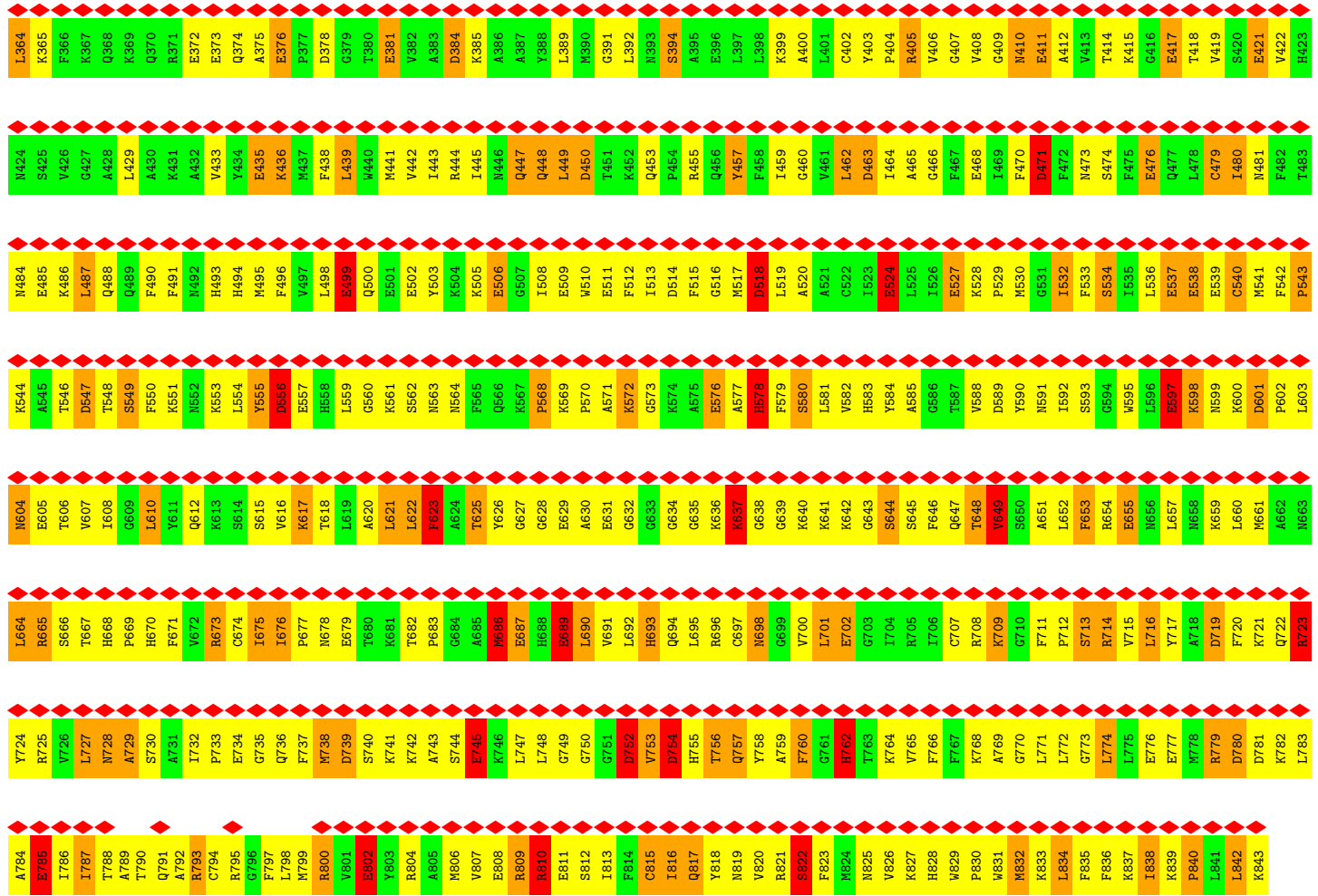




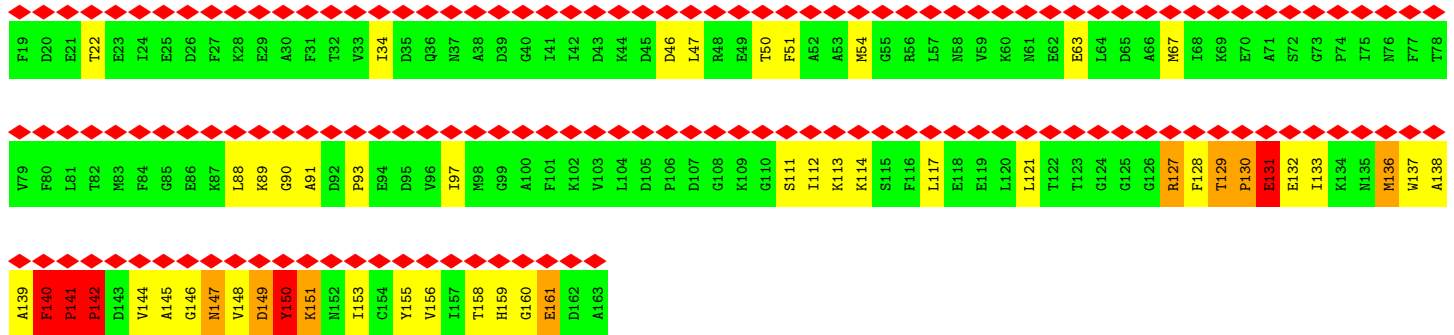
• Molecule 1: SKELETAL MUSCLE MYOSIN II



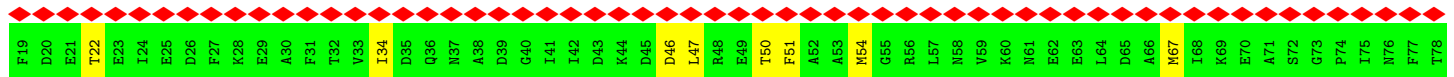


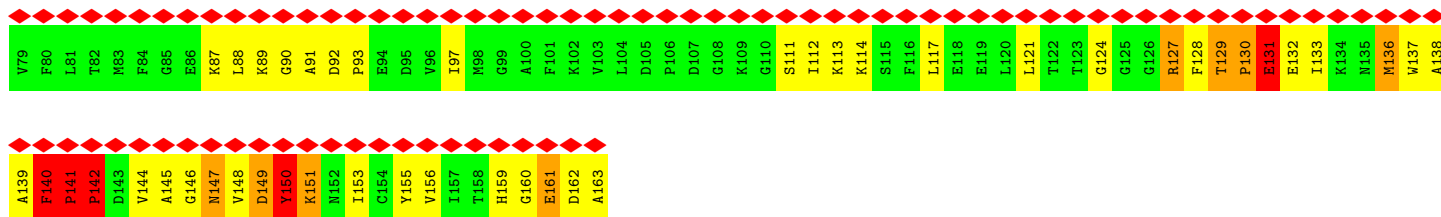


• Molecule 2: SKELETAL MUSCLE MYOSIN II REGULATORY LIGHT CHAIN

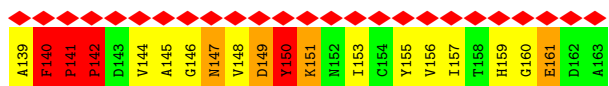
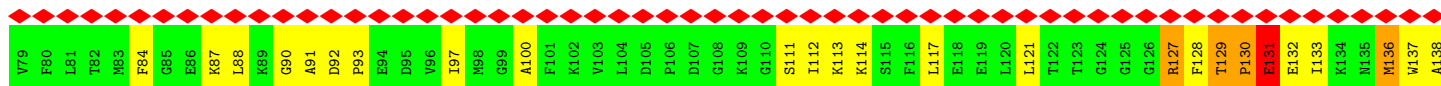
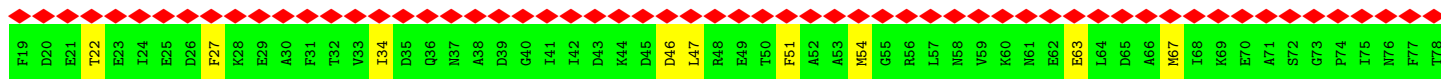


• Molecule 2: SKELETAL MUSCLE MYOSIN II REGULATORY LIGHT CHAIN

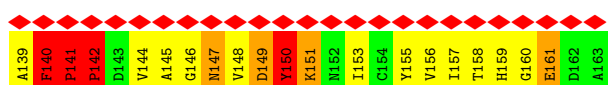
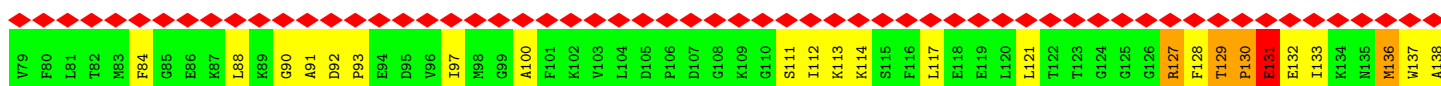




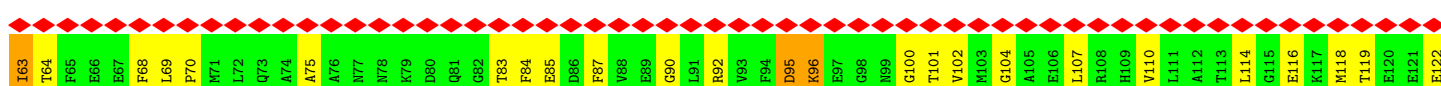
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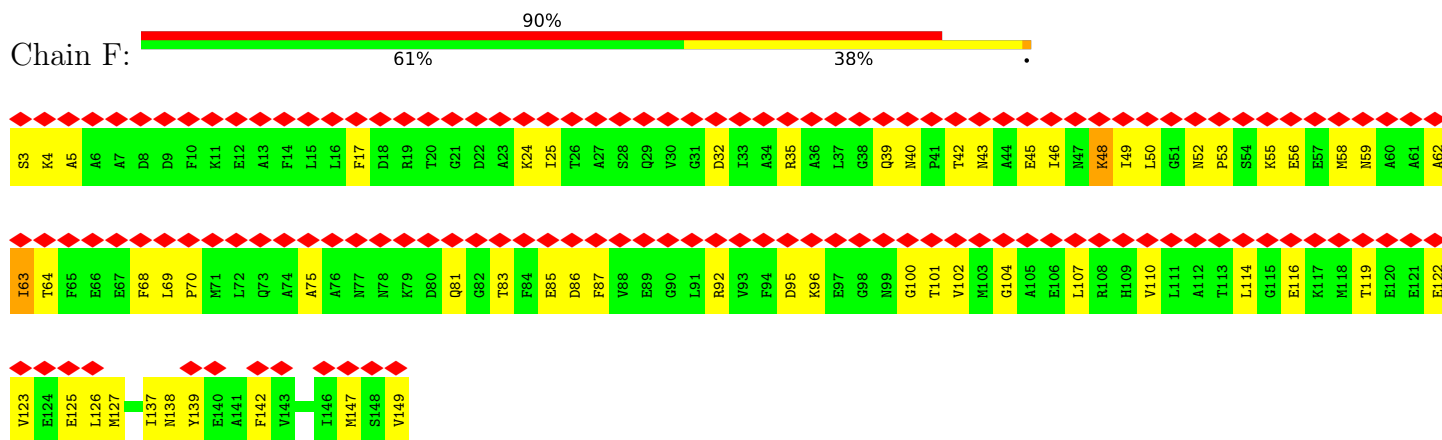
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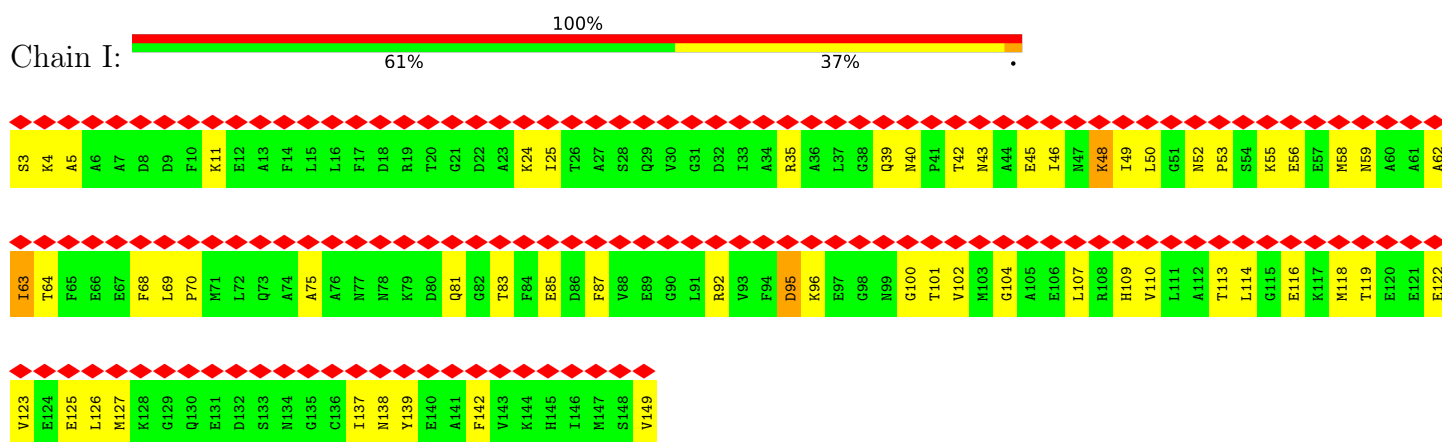
• Molecule 3: SKELETAL MUSCLE MYOSIN II ESSENTIAL LIGHT CHAIN



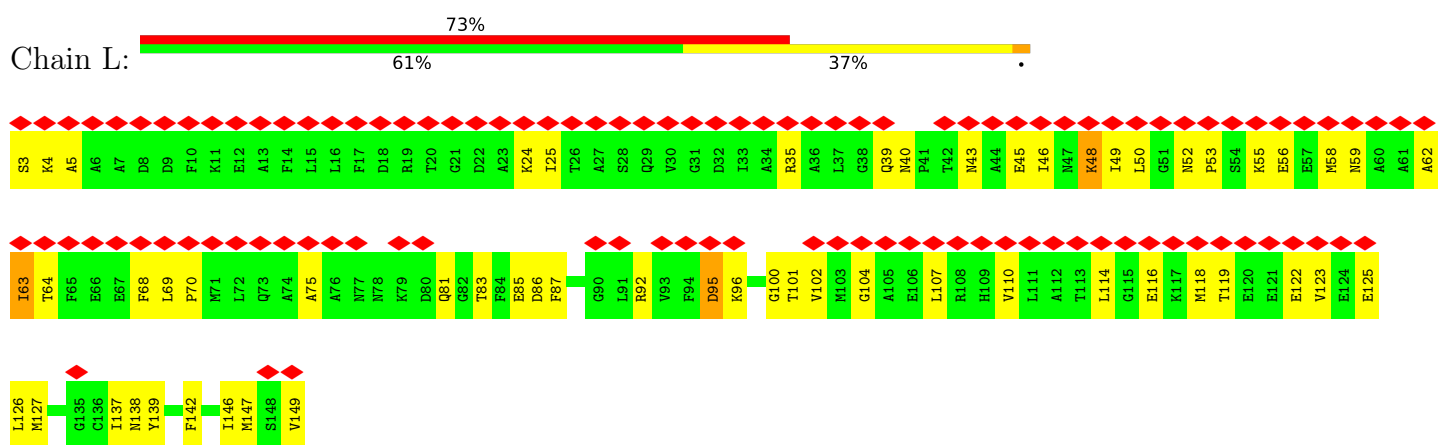
- Molecule 3: SKELETAL MUSCLE MYOSIN II ESSENTIAL LIGHT CHAIN



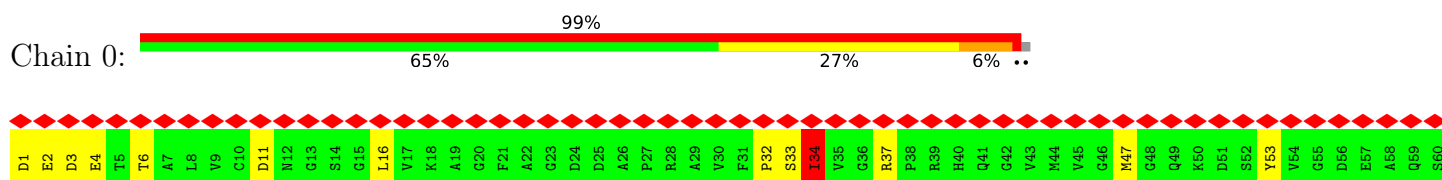
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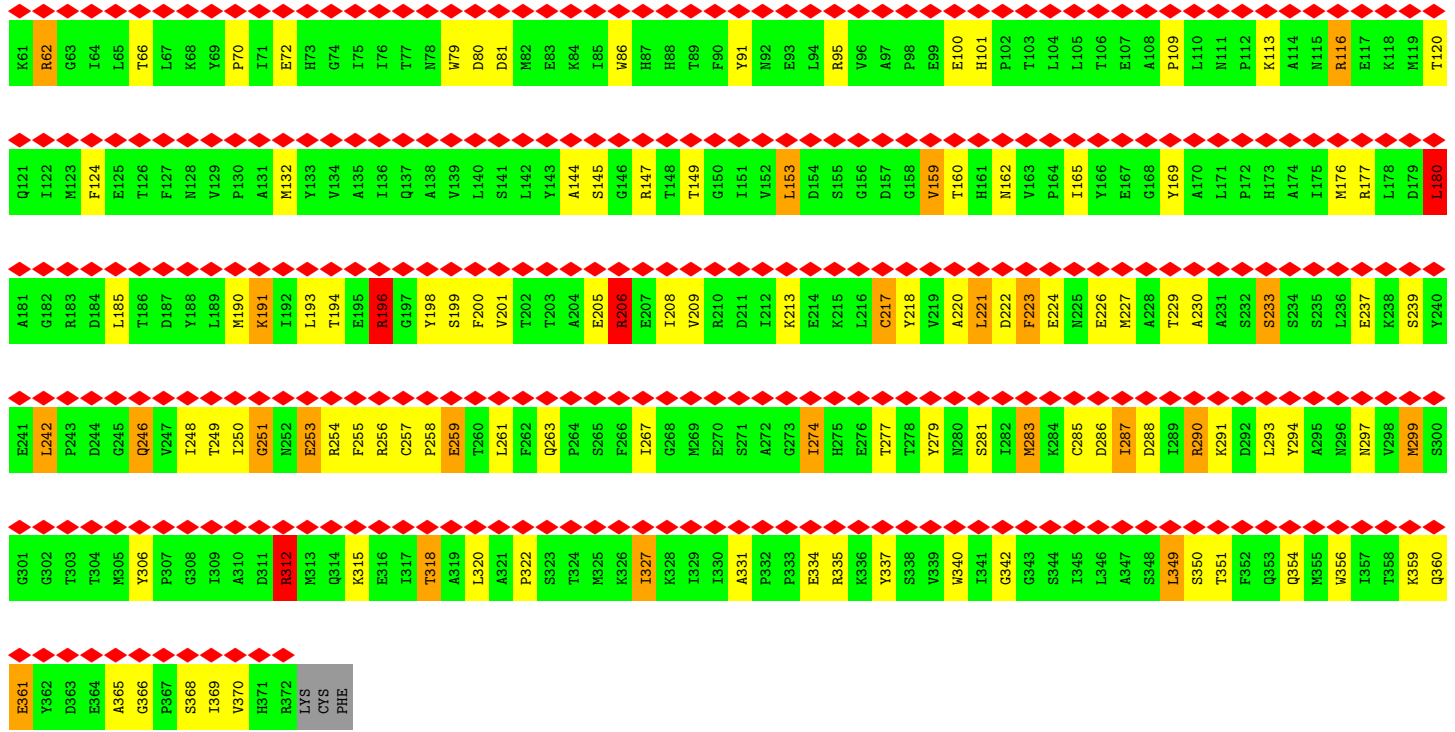


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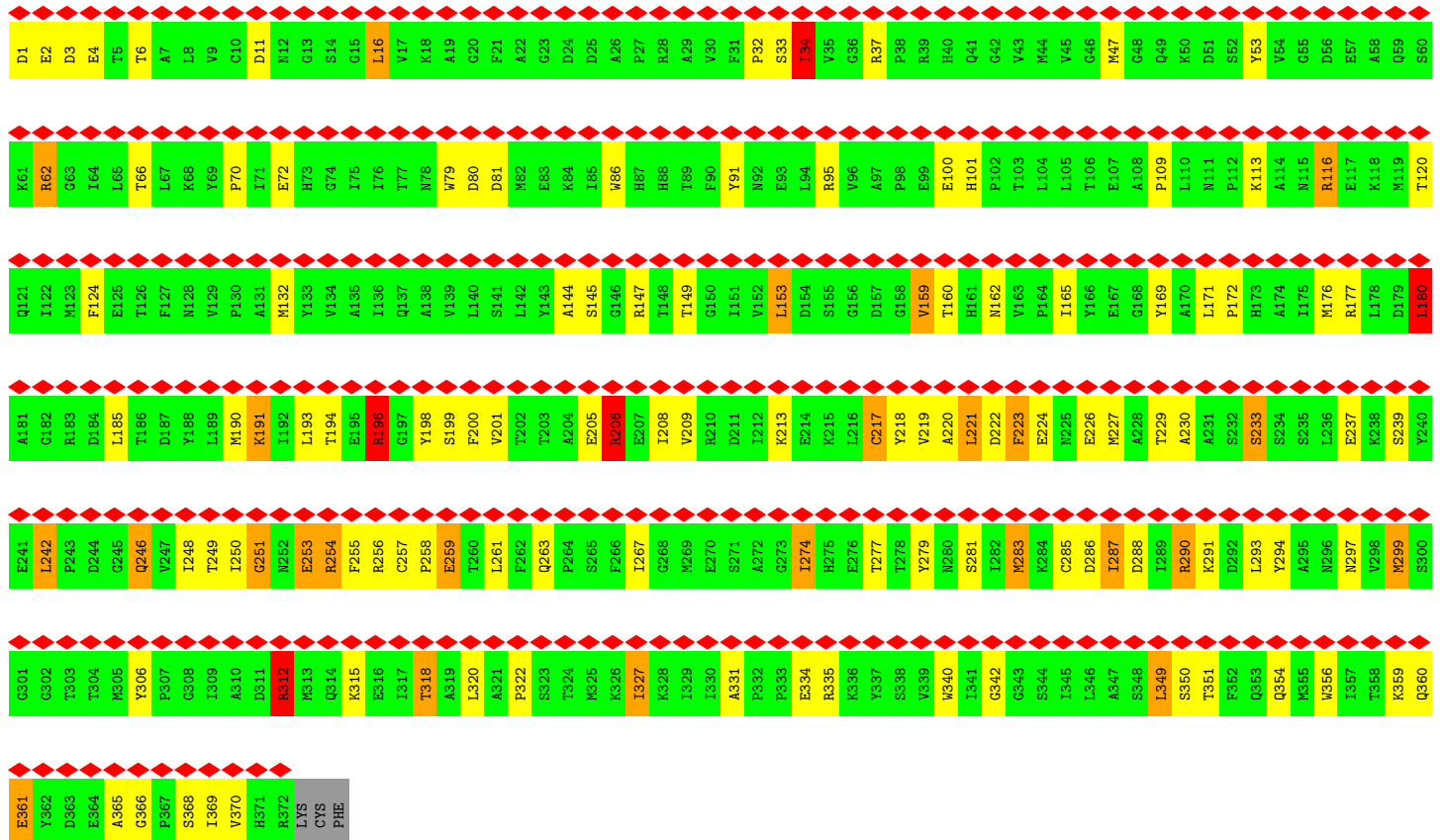


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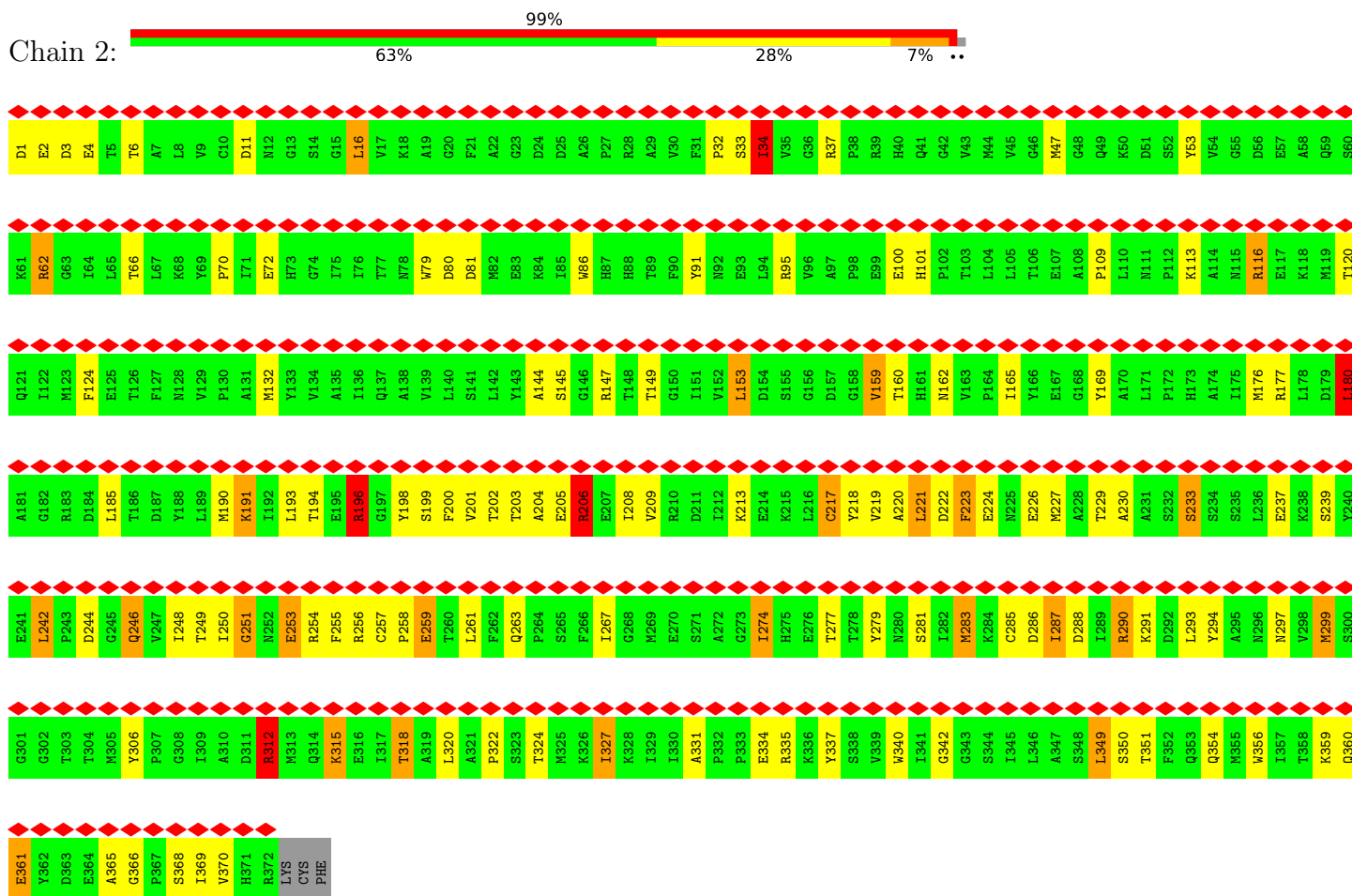




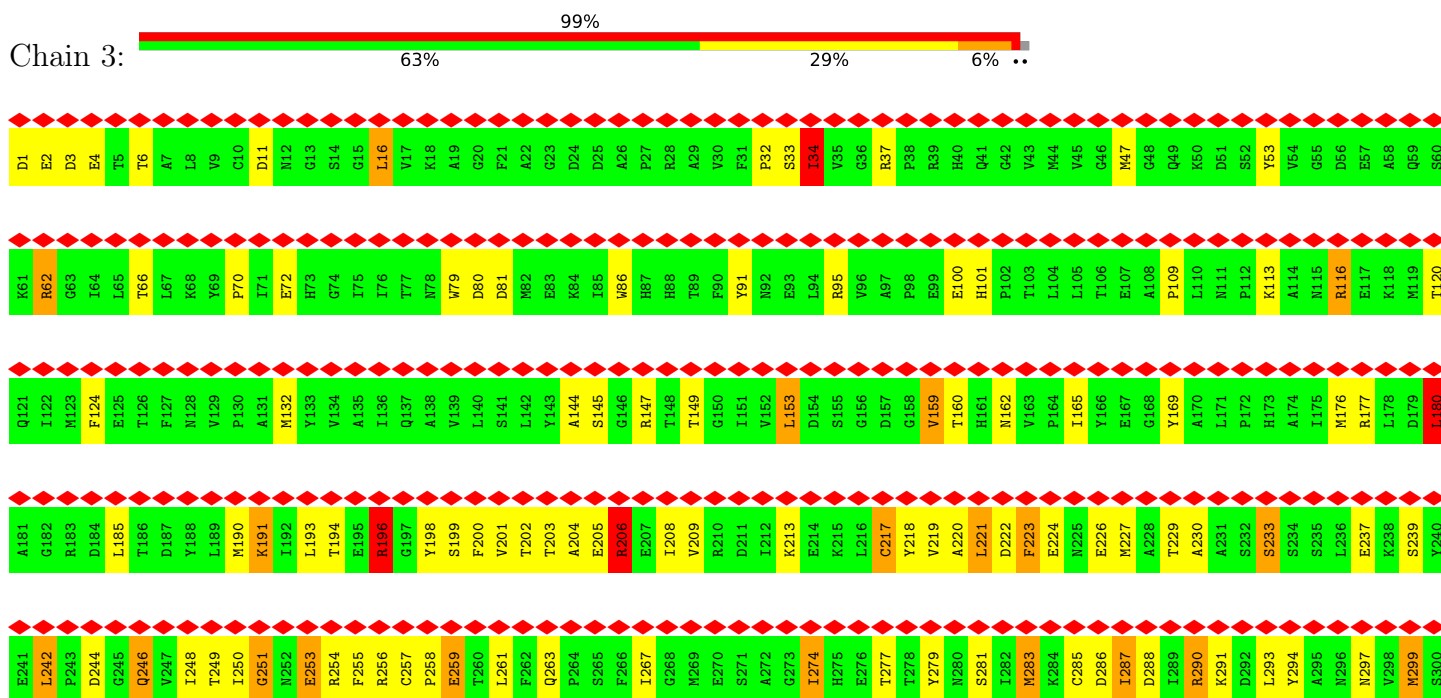
● Molecule 4: SKELETAL MUSCLE ACTIN

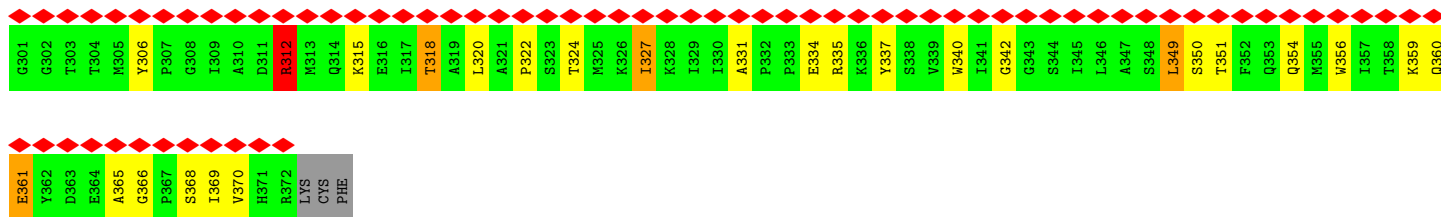


• Molecule 4: SKELETAL MUSCLE ACTIN

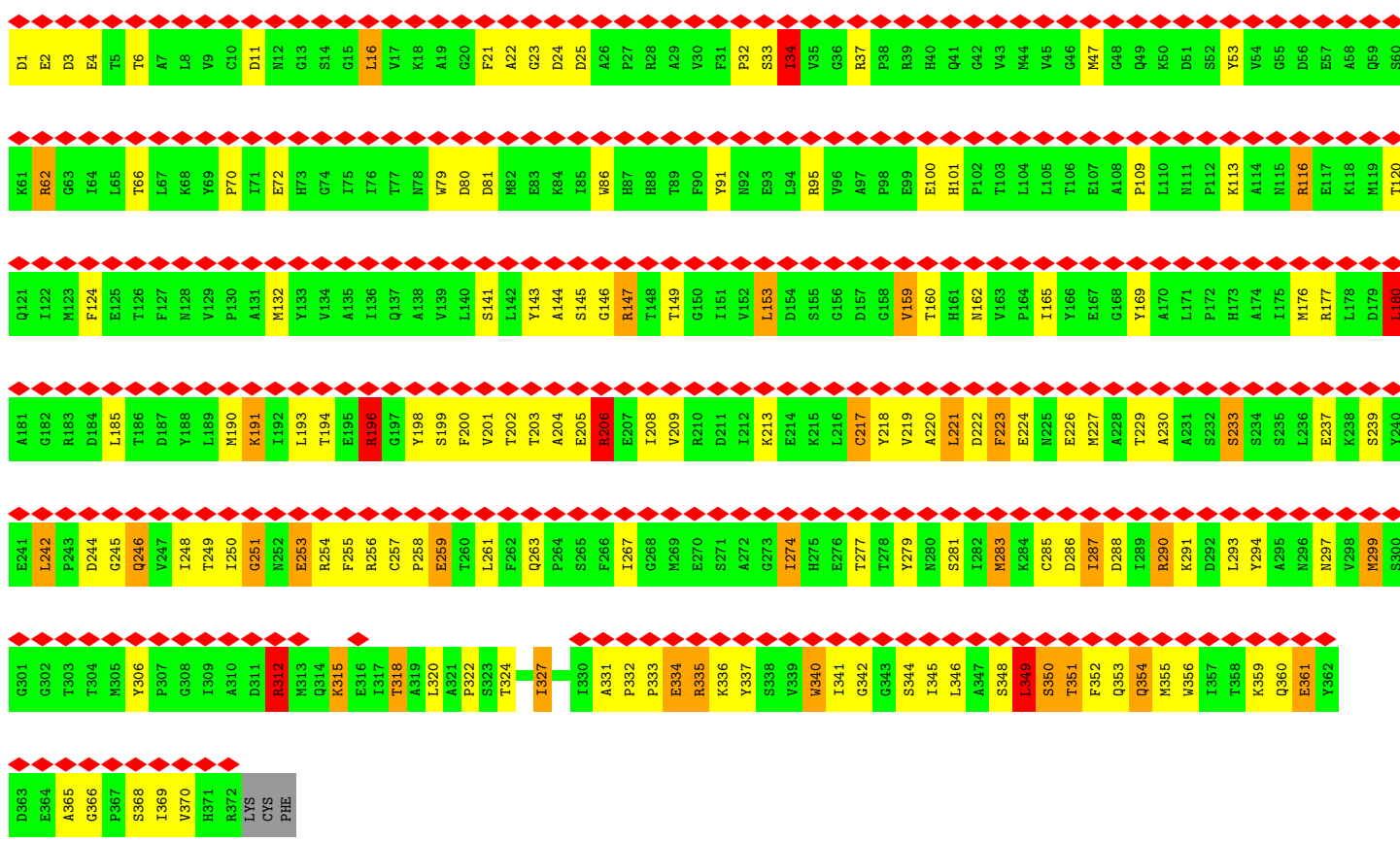
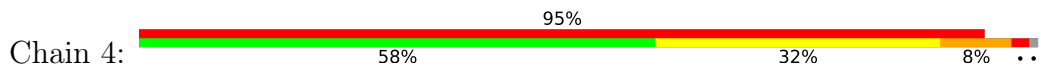


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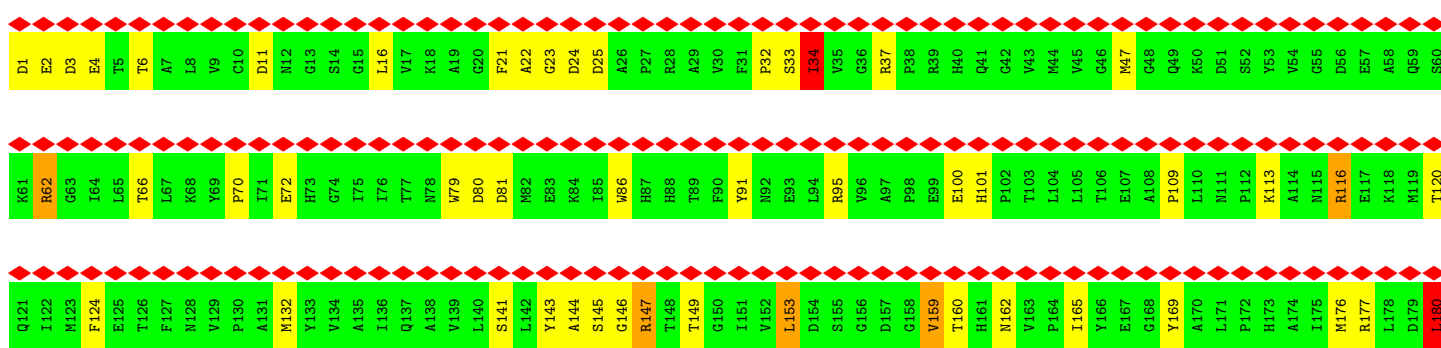




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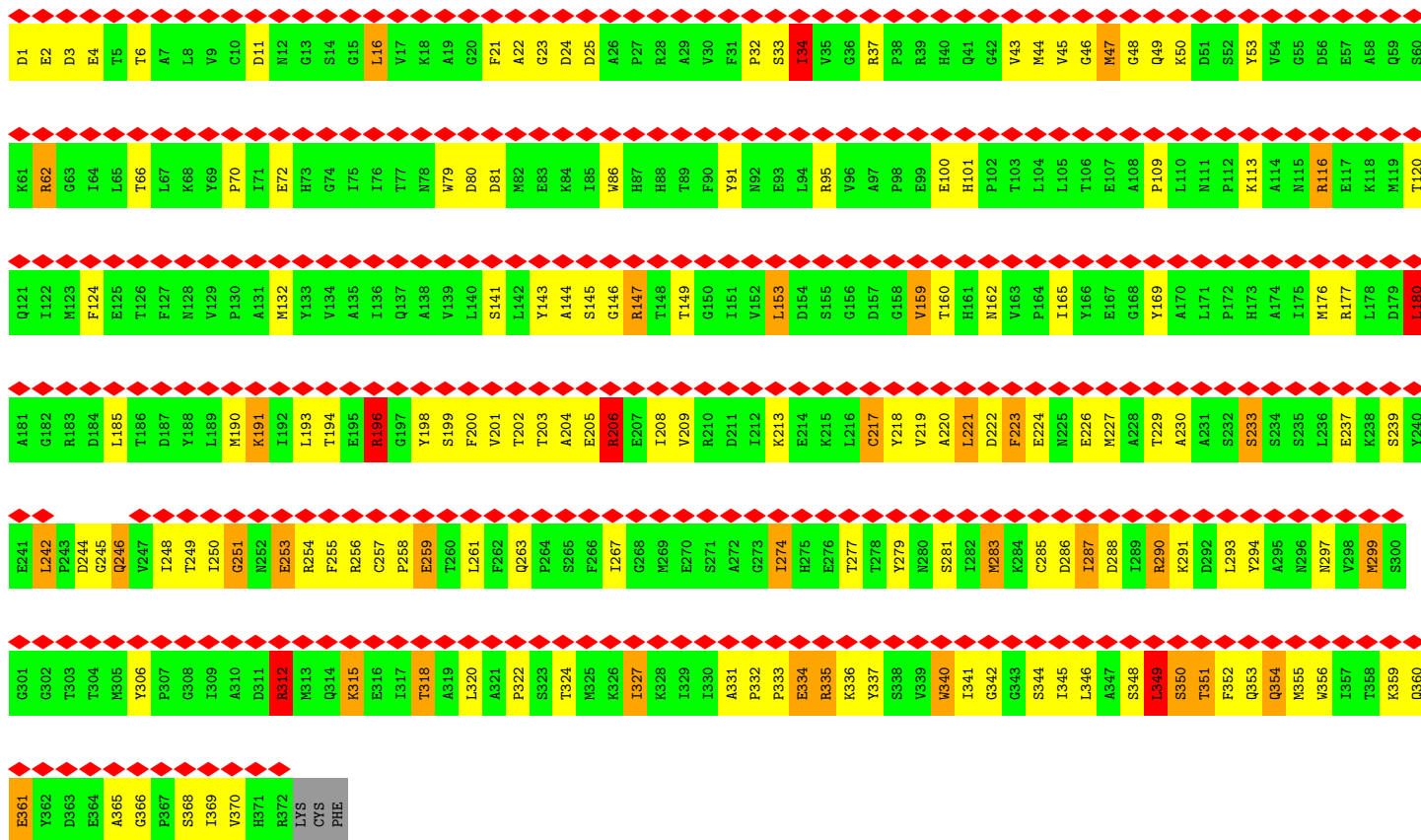
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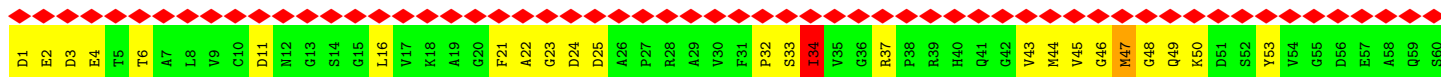


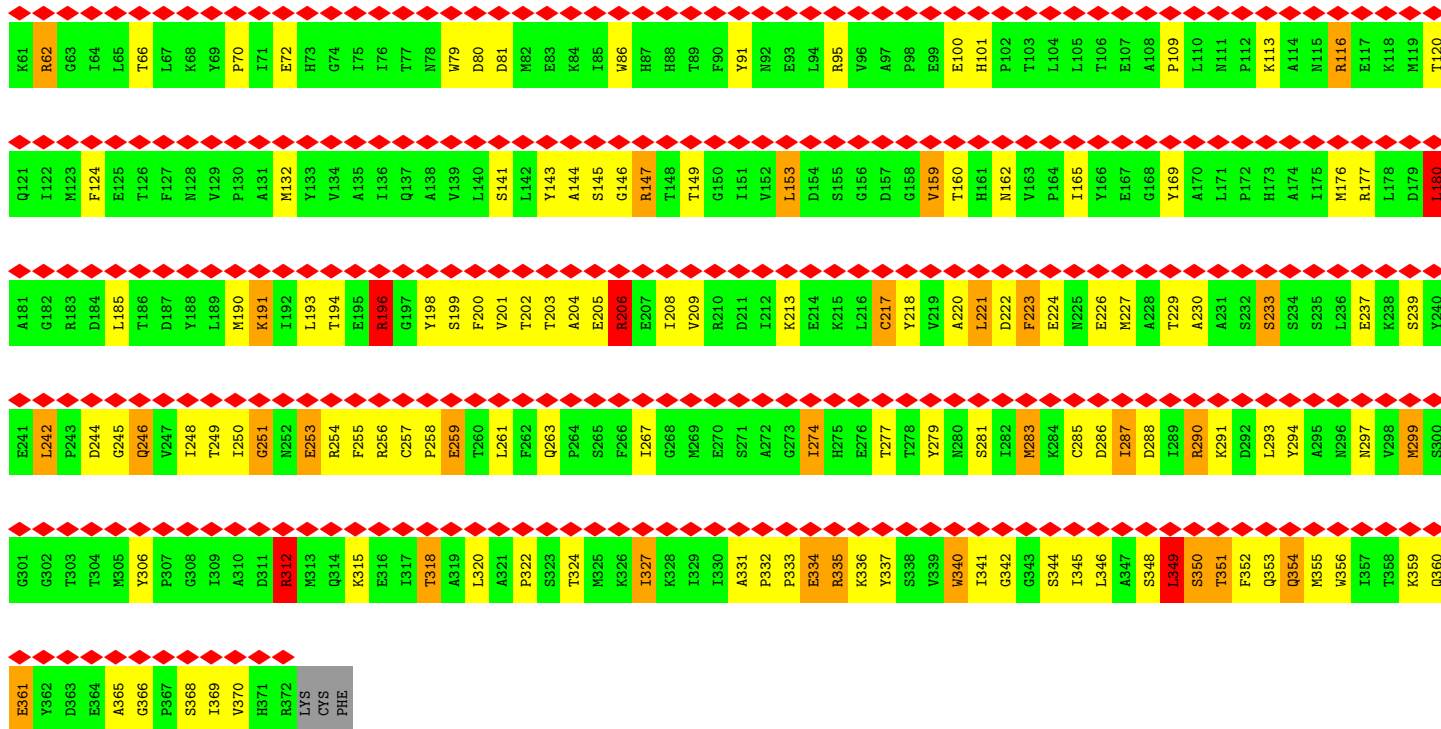


• Molecule 4: SKELETAL MUSCLE ACTIN

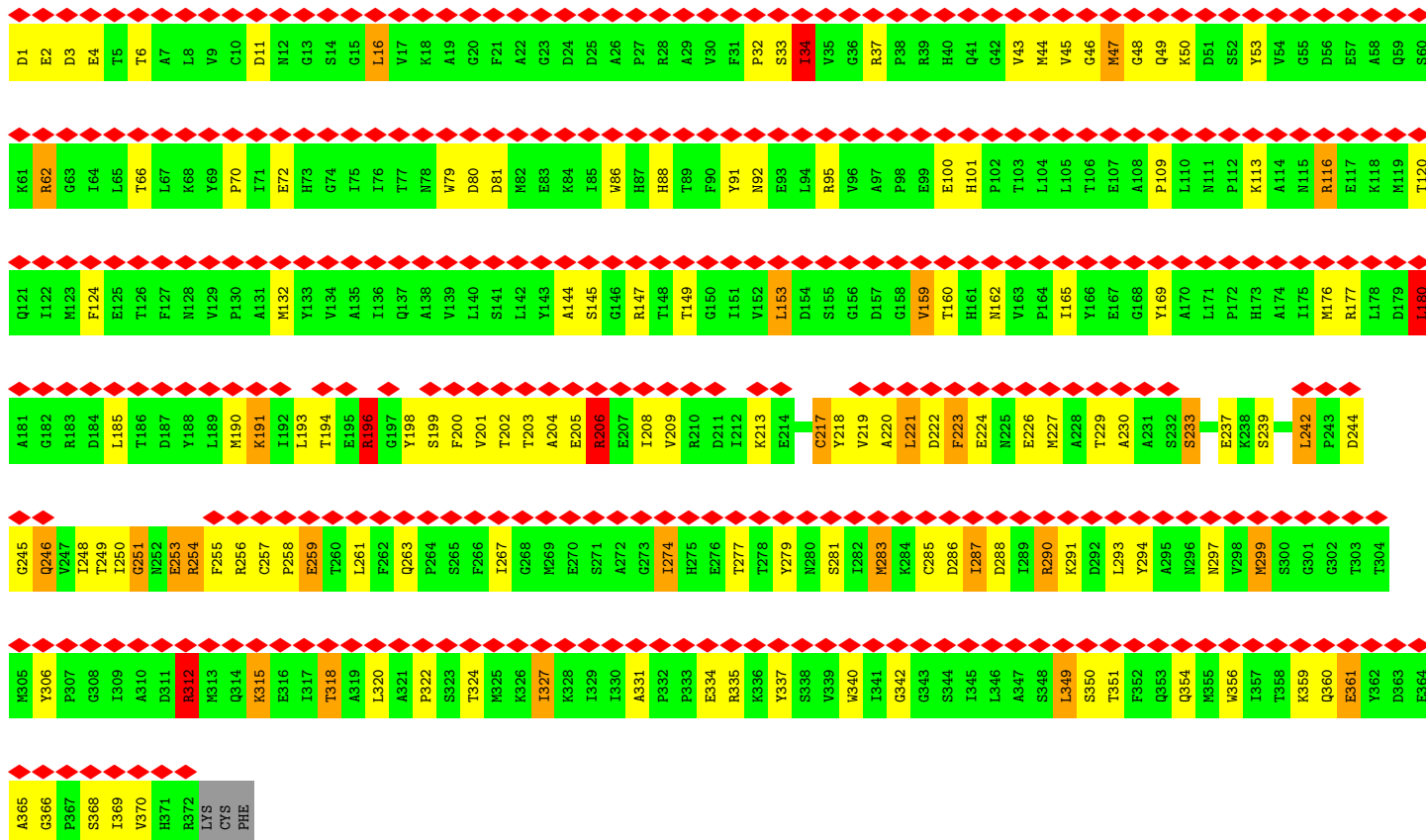
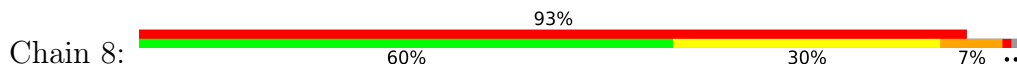


• Molecule 4: SKELETAL MUSCLE ACTIN

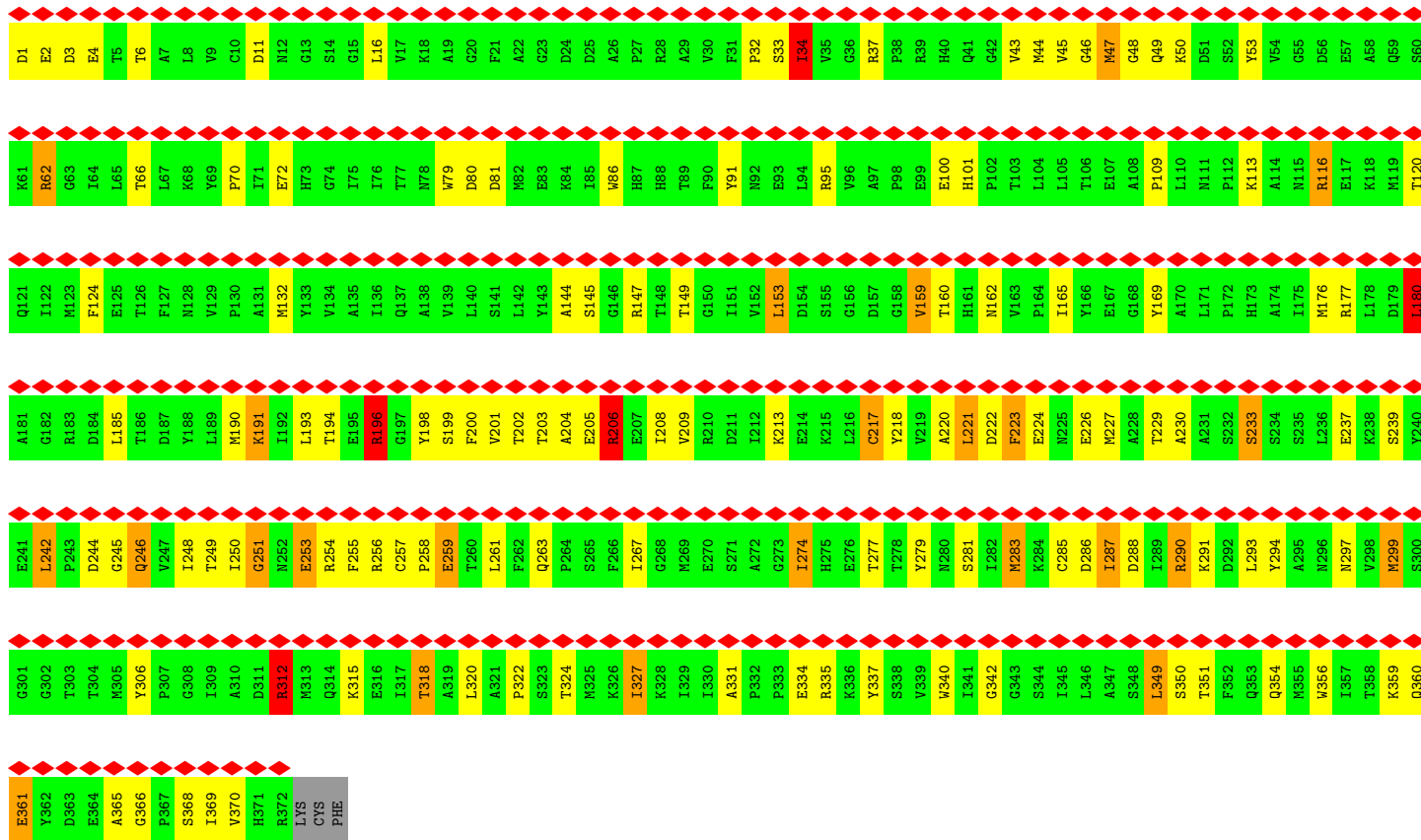




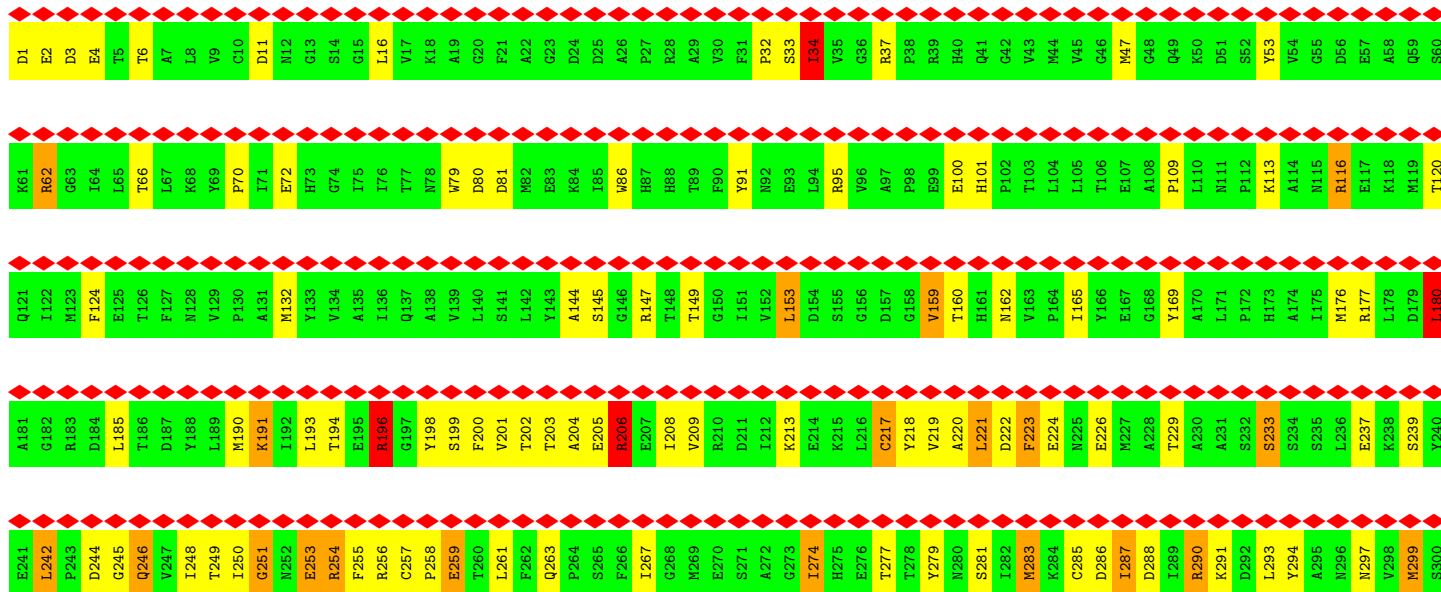
• Molecule 4: SKELETAL MUSCLE ACTIN

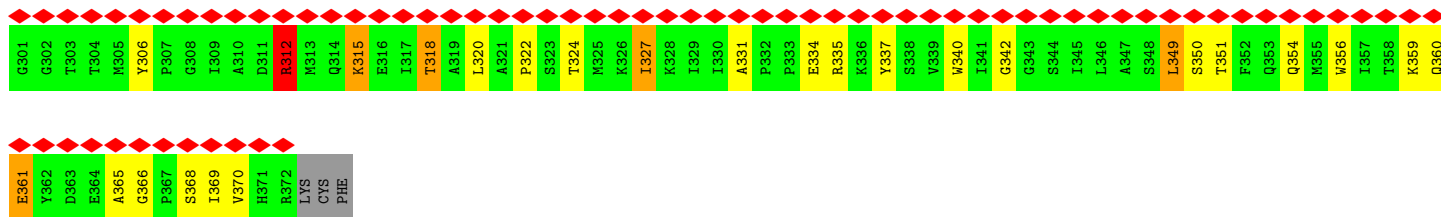


● Molecule 4: SKELETAL MUSCLE ACTIN

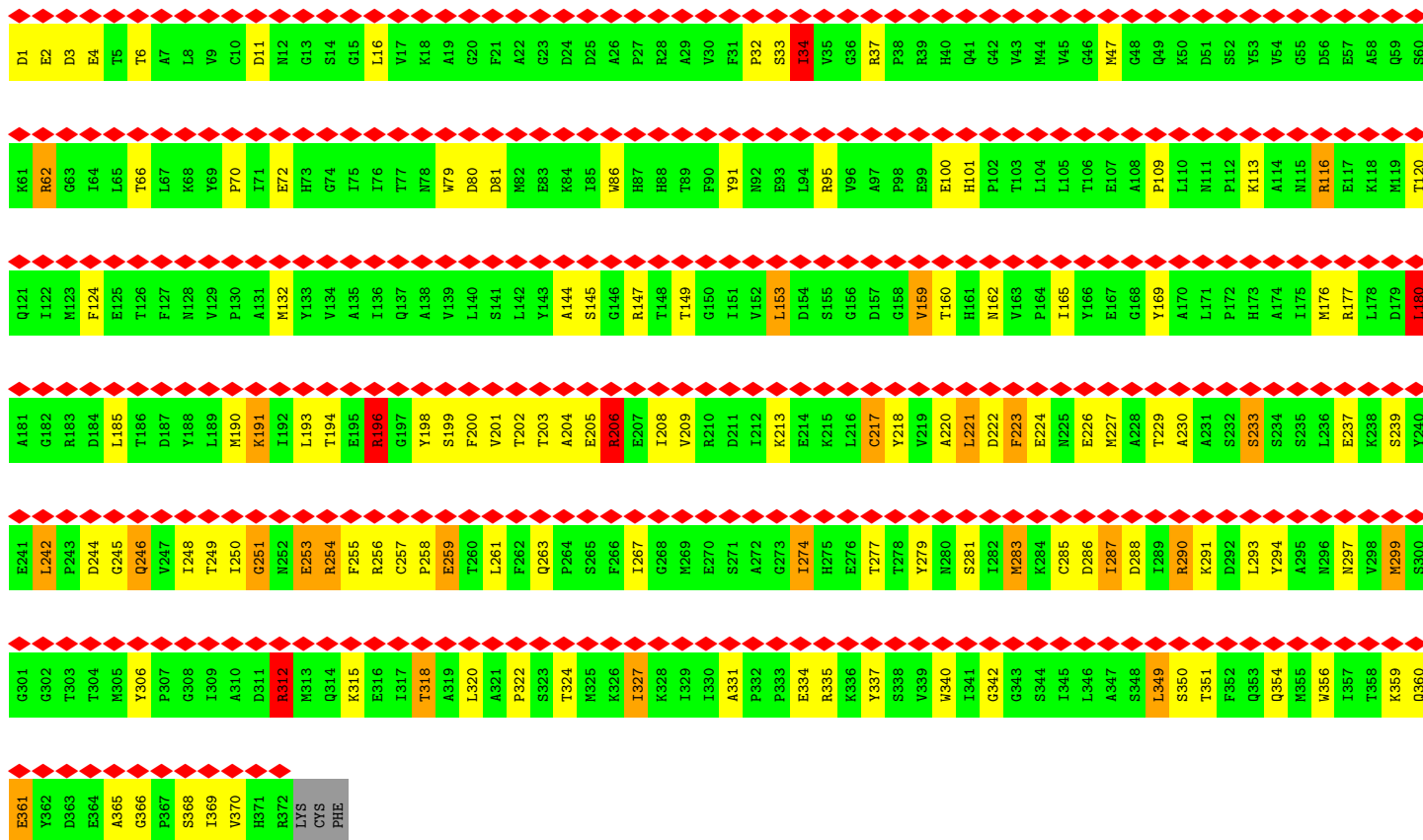


● Molecule 4: SKELETAL MUSCLE ACTIN

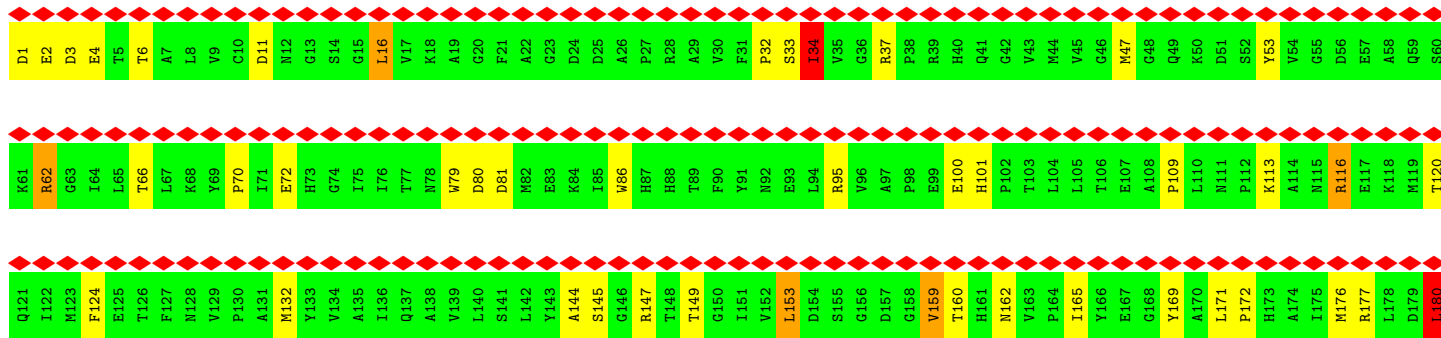


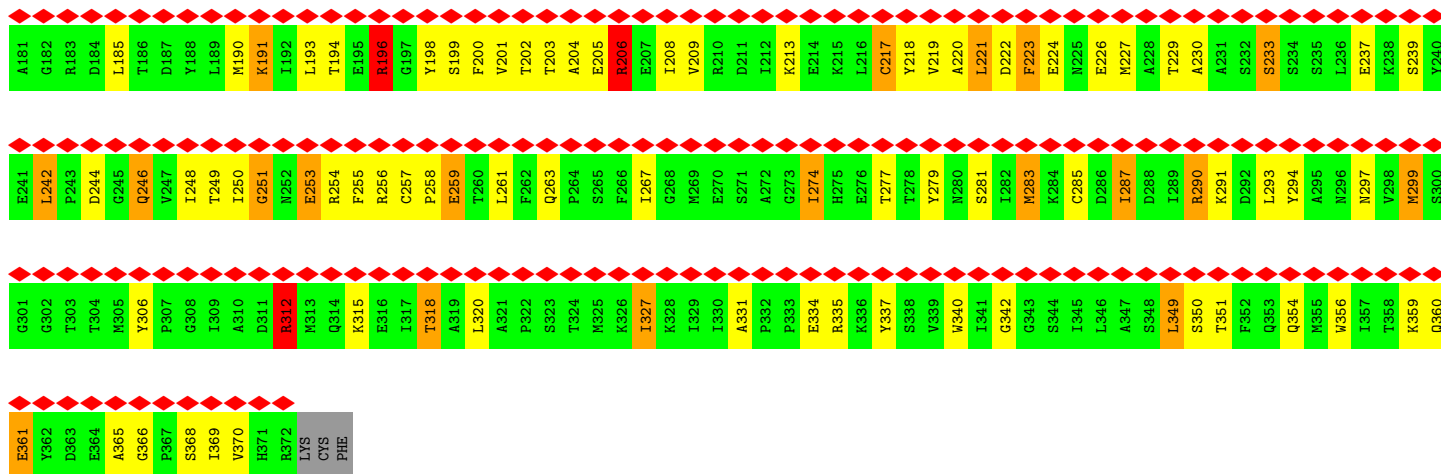


• Molecule 4: SKELETAL MUSCLE ACTIN

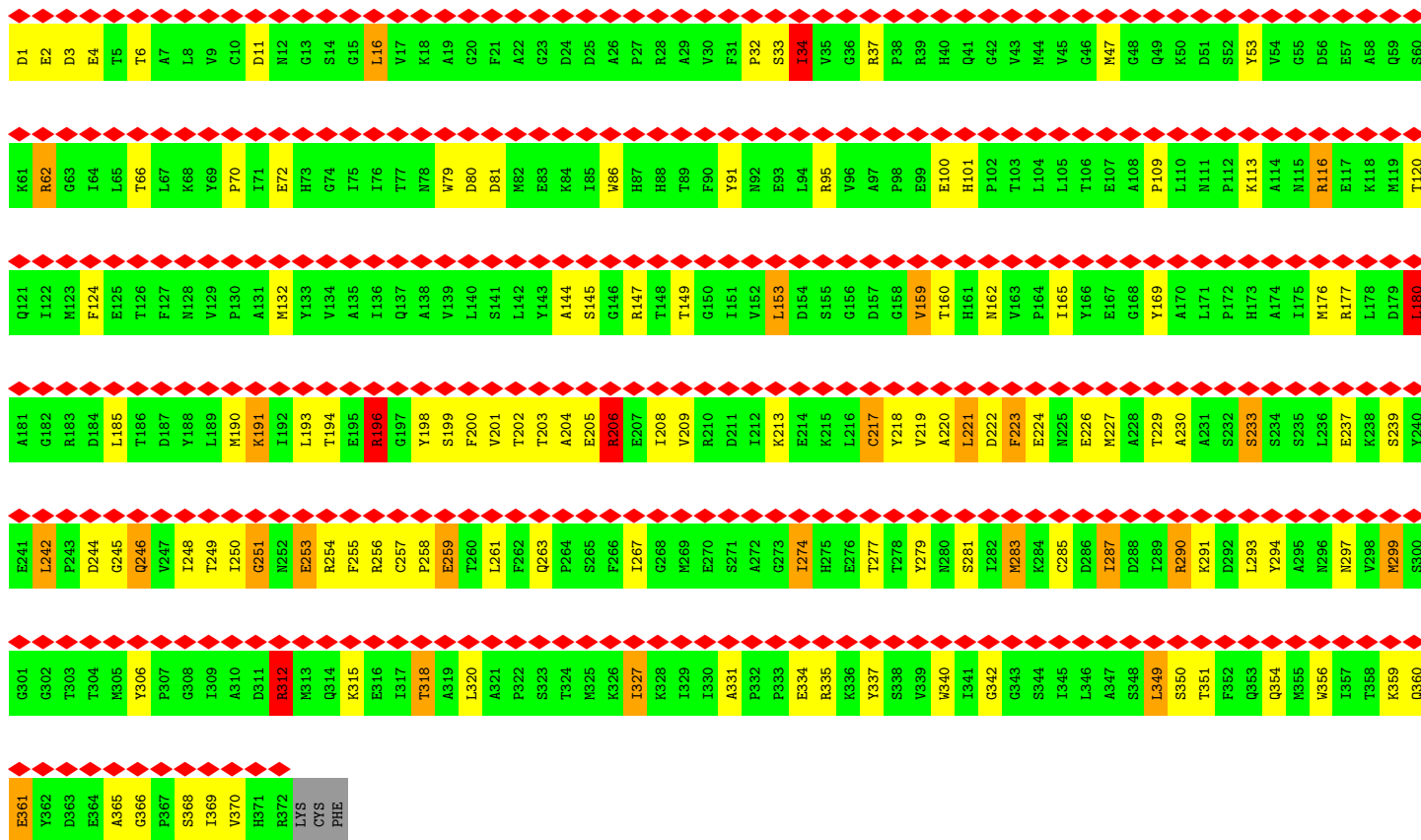


• Molecule 4: SKELETAL MUSCLE ACTIN





● Molecule 4: SKELETAL MUSCLE ACTIN



## 4 Experimental information

Property	Value	Source
EM reconstruction method	TOMOGRAPHY	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of tilted images used	Not provided	
Resolution determination method	Not provided	
CTF correction method	Not provided	
Microscope	FEI/PHILIPS EM400	Depositor
Voltage (kV)	100	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	Not provided	
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	17000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum voxel value	366.680	Depositor
Minimum voxel value	-417.992	Depositor
Average voxel value	1.860	Depositor
Voxel value standard deviation	47.792	Depositor
Recommended contour level	81.2	Depositor
Tomogram size ( $\text{\AA}$ )	9280, 9280, 464	wwPDB
Tomogram dimensions	600, 600, 30	wwPDB
Tomogram angles ( $^\circ$ )	90, 90, 90	wwPDB
Grid spacing ( $\text{\AA}$ )	15.4667, 15.4667, 15.4667	Depositor

## 5 Model quality i

### 5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: MLY

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	1.77	67/6448 (1.0%)	1.82	114/8729 (1.3%)
1	D	1.77	65/6448 (1.0%)	1.82	114/8729 (1.3%)
1	G	1.77	67/6448 (1.0%)	1.82	116/8729 (1.3%)
1	J	1.90	68/6449 (1.1%)	1.84	118/8732 (1.4%)
2	B	1.22	10/1148 (0.9%)	1.61	16/1548 (1.0%)
2	E	1.22	10/1148 (0.9%)	1.61	16/1548 (1.0%)
2	H	1.22	10/1148 (0.9%)	1.62	16/1548 (1.0%)
2	K	1.22	10/1148 (0.9%)	1.61	16/1548 (1.0%)
3	C	0.80	0/1136	0.95	4/1525 (0.3%)
3	F	0.80	0/1136	0.95	4/1525 (0.3%)
3	I	0.80	0/1136	0.95	4/1525 (0.3%)
3	L	0.79	0/1136	0.94	4/1525 (0.3%)
4	0	0.89	1/2968 (0.0%)	1.64	52/4023 (1.3%)
4	1	0.89	2/2968 (0.1%)	1.64	50/4023 (1.2%)
4	2	0.89	1/2968 (0.0%)	1.64	52/4023 (1.3%)
4	3	0.89	1/2968 (0.0%)	1.64	51/4023 (1.3%)
4	4	0.89	1/2968 (0.0%)	1.64	51/4023 (1.3%)
4	5	0.89	2/2968 (0.1%)	1.64	51/4023 (1.3%)
4	6	0.89	2/2968 (0.1%)	1.64	52/4023 (1.3%)
4	7	0.89	2/2968 (0.1%)	1.64	52/4023 (1.3%)
4	8	0.89	2/2968 (0.1%)	1.64	51/4023 (1.3%)
4	V	0.89	1/2968 (0.0%)	1.64	52/4023 (1.3%)
4	W	0.89	2/2968 (0.1%)	1.64	51/4023 (1.3%)
4	X	0.89	2/2968 (0.1%)	1.64	51/4023 (1.3%)
4	Y	0.89	2/2968 (0.1%)	1.64	51/4023 (1.3%)
4	Z	0.89	2/2968 (0.1%)	1.64	52/4023 (1.3%)
All	All	1.29	330/76481 (0.4%)	1.67	1261/103533 (1.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a

sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	1	4
1	D	1	4
1	G	2	4
1	J	1	6
2	B	0	3
2	E	0	3
2	H	0	3
2	K	0	3
3	C	0	2
3	F	0	2
3	I	0	2
3	L	0	2
4	0	0	1
4	1	0	1
4	2	0	1
4	3	0	1
4	4	0	1
4	5	0	1
4	6	0	1
4	7	0	1
4	8	0	1
4	V	0	1
4	W	0	1
4	X	0	1
4	Y	0	1
4	Z	0	1
All	All	5	52

All (330) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	J	709	LYS	C-N	-55.36	0.33	1.33
1	J	649	VAL	CB-CG1	53.26	2.64	1.52
1	G	649	VAL	CB-CG1	53.23	2.64	1.52
1	D	649	VAL	CB-CG1	53.18	2.64	1.52
1	A	649	VAL	CB-CG1	53.16	2.64	1.52
1	D	623	PHE	CB-CG	48.14	2.33	1.51
1	J	623	PHE	CB-CG	48.11	2.33	1.51
1	A	623	PHE	CB-CG	48.09	2.33	1.51
1	G	623	PHE	CB-CG	48.09	2.33	1.51
1	A	649	VAL	CB-CG2	46.26	2.50	1.52
1	G	649	VAL	CB-CG2	46.20	2.49	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	J	649	VAL	CB-CG2	46.17	2.49	1.52
1	D	649	VAL	CB-CG2	46.13	2.49	1.52
1	A	648	THR	CB-OG1	34.37	2.12	1.43
1	G	648	THR	CB-OG1	34.36	2.12	1.43
1	D	648	THR	CB-OG1	34.34	2.12	1.43
1	J	648	THR	CB-OG1	34.31	2.11	1.43
1	A	648	THR	CB-CG2	-30.69	0.51	1.52
1	G	648	THR	CB-CG2	-30.68	0.51	1.52
1	J	648	THR	CB-CG2	-30.67	0.51	1.52
1	D	648	THR	CB-CG2	-30.67	0.51	1.52
1	D	637	LYS	C-N	-15.07	1.05	1.33
1	J	637	LYS	C-N	-15.00	1.06	1.33
1	G	637	LYS	C-N	-14.83	1.06	1.33
1	A	637	LYS	C-N	-14.80	1.06	1.33
1	A	649	VAL	C-N	-13.51	1.02	1.34
1	G	649	VAL	C-N	-13.49	1.03	1.34
1	D	649	VAL	C-N	-13.43	1.03	1.34
1	J	649	VAL	C-N	-13.42	1.03	1.34
2	H	150	TYR	CB-CG	-13.39	1.31	1.51
2	B	150	TYR	CB-CG	-13.36	1.31	1.51
2	E	150	TYR	CB-CG	-13.31	1.31	1.51
2	K	150	TYR	CB-CG	-13.30	1.31	1.51
2	B	140	PHE	C-N	-12.96	1.09	1.34
2	E	140	PHE	C-N	-12.96	1.09	1.34
2	K	140	PHE	C-N	-12.92	1.09	1.34
2	H	140	PHE	C-N	-12.82	1.09	1.34
2	B	150	TYR	CG-CD2	-11.36	1.24	1.39
2	K	150	TYR	CG-CD2	-11.20	1.24	1.39
2	H	150	TYR	CG-CD2	-11.18	1.24	1.39
2	E	150	TYR	CG-CD2	-11.14	1.24	1.39
2	K	141	PRO	N-CD	-10.60	1.33	1.47
2	B	141	PRO	N-CD	-10.50	1.33	1.47
2	E	141	PRO	N-CD	-10.45	1.33	1.47
2	H	141	PRO	N-CD	-10.40	1.33	1.47
1	J	476	GLU	CD-OE1	8.88	1.35	1.25
1	D	476	GLU	CD-OE1	8.81	1.35	1.25
1	G	476	GLU	CD-OE1	8.76	1.35	1.25
1	J	785	GLU	C-N	8.71	1.54	1.34
1	A	622	LEU	C-N	8.68	1.54	1.34
1	A	476	GLU	CD-OE1	8.66	1.35	1.25
1	J	622	LEU	C-N	8.65	1.53	1.34
1	G	622	LEU	C-N	8.64	1.53	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	622	LEU	C-N	8.63	1.53	1.34
1	J	411	GLU	CD-OE1	8.32	1.34	1.25
1	G	411	GLU	CD-OE1	8.30	1.34	1.25
2	K	150	TYR	CA-CB	-8.26	1.35	1.53
1	J	745	GLU	CD-OE2	8.25	1.34	1.25
1	D	745	GLU	CD-OE2	8.25	1.34	1.25
2	B	150	TYR	CA-CB	-8.23	1.35	1.53
1	A	745	GLU	CD-OE2	8.15	1.34	1.25
1	D	411	GLU	CD-OE1	8.11	1.34	1.25
2	H	150	TYR	CA-CB	-8.11	1.36	1.53
1	G	745	GLU	CD-OE2	8.10	1.34	1.25
2	E	150	TYR	CA-CB	-8.08	1.36	1.53
1	A	411	GLU	CD-OE1	8.06	1.34	1.25
1	A	381	GLU	CD-OE1	8.04	1.34	1.25
1	G	108	GLU	CD-OE1	7.96	1.34	1.25
1	A	108	GLU	CD-OE1	7.94	1.34	1.25
1	J	108	GLU	CD-OE1	7.91	1.34	1.25
1	G	381	GLU	CD-OE1	7.89	1.34	1.25
1	J	202	SER	CB-OG	7.84	1.52	1.42
1	J	381	GLU	CD-OE1	7.83	1.34	1.25
1	D	381	GLU	CD-OE1	7.81	1.34	1.25
1	D	202	SER	CB-OG	7.74	1.52	1.42
1	G	202	SER	CB-OG	7.72	1.52	1.42
1	D	108	GLU	CD-OE1	7.65	1.34	1.25
1	A	202	SER	CB-OG	7.64	1.52	1.42
1	D	689	GLU	CD-OE2	7.53	1.33	1.25
1	A	689	GLU	CD-OE2	7.51	1.33	1.25
1	J	689	GLU	CD-OE2	7.45	1.33	1.25
1	G	689	GLU	CD-OE2	7.42	1.33	1.25
1	D	23	GLU	CD-OE1	7.31	1.33	1.25
1	D	347	GLU	CD-OE1	7.27	1.33	1.25
1	J	23	GLU	CD-OE1	7.23	1.33	1.25
1	A	347	GLU	CD-OE1	7.21	1.33	1.25
1	J	511	GLU	CD-OE1	7.19	1.33	1.25
1	G	347	GLU	CD-OE1	7.18	1.33	1.25
1	G	23	GLU	CD-OE1	7.17	1.33	1.25
1	A	23	GLU	CD-OE1	7.17	1.33	1.25
1	J	347	GLU	CD-OE1	7.17	1.33	1.25
1	G	26	GLU	CD-OE1	7.08	1.33	1.25
1	D	68	GLU	CD-OE2	7.05	1.33	1.25
1	J	524	GLU	CD-OE1	7.05	1.33	1.25
1	G	330	GLU	CD-OE1	7.04	1.33	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	68	GLU	CD-OE2	7.04	1.33	1.25
1	D	524	GLU	CD-OE1	7.03	1.33	1.25
1	A	511	GLU	CD-OE1	7.02	1.33	1.25
1	J	330	GLU	CD-OE1	6.99	1.33	1.25
1	D	376	GLU	CD-OE1	6.95	1.33	1.25
1	G	376	GLU	CD-OE1	6.94	1.33	1.25
1	A	376	GLU	CD-OE1	6.93	1.33	1.25
1	J	811	GLU	CD-OE1	6.92	1.33	1.25
1	D	511	GLU	CD-OE1	6.91	1.33	1.25
1	A	330	GLU	CD-OE1	6.90	1.33	1.25
1	G	524	GLU	CD-OE1	6.88	1.33	1.25
1	J	68	GLU	CD-OE2	6.88	1.33	1.25
1	A	68	GLU	CD-OE2	6.87	1.33	1.25
1	A	524	GLU	CD-OE1	6.87	1.33	1.25
1	D	26	GLU	CD-OE1	6.85	1.33	1.25
1	J	376	GLU	CD-OE1	6.85	1.33	1.25
1	G	511	GLU	CD-OE1	6.82	1.33	1.25
1	J	26	GLU	CD-OE1	6.81	1.33	1.25
1	D	811	GLU	CD-OE1	6.81	1.33	1.25
1	A	655	GLU	CD-OE1	6.80	1.33	1.25
1	D	330	GLU	CD-OE1	6.78	1.33	1.25
1	A	26	GLU	CD-OE1	6.76	1.33	1.25
1	A	811	GLU	CD-OE1	6.75	1.33	1.25
1	J	538	GLU	CD-OE1	6.69	1.33	1.25
1	J	655	GLU	CD-OE1	6.67	1.32	1.25
1	J	319	GLU	CD-OE1	6.62	1.32	1.25
2	E	150	TYR	CD2-CE2	-6.60	1.29	1.39
1	A	538	GLU	CD-OE1	6.60	1.32	1.25
1	G	319	GLU	CD-OE1	6.59	1.32	1.25
1	G	811	GLU	CD-OE1	6.59	1.32	1.25
1	G	538	GLU	CD-OE1	6.58	1.32	1.25
1	J	266	GLU	CD-OE2	6.56	1.32	1.25
1	D	655	GLU	CD-OE1	6.55	1.32	1.25
1	G	785	GLU	C-N	6.55	1.49	1.34
1	G	89	GLU	CD-OE1	6.55	1.32	1.25
1	G	655	GLU	CD-OE1	6.55	1.32	1.25
1	A	319	GLU	CD-OE1	6.54	1.32	1.25
1	A	266	GLU	CD-OE2	6.52	1.32	1.25
2	B	150	TYR	CD2-CE2	-6.52	1.29	1.39
1	D	538	GLU	CD-OE1	6.50	1.32	1.25
1	G	99	GLU	CD-OE2	6.48	1.32	1.25
1	D	538	GLU	CD-OE2	-6.46	1.18	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	266	GLU	CD-OE2	6.46	1.32	1.25
1	A	538	GLU	CD-OE2	-6.45	1.18	1.25
1	D	319	GLU	CD-OE1	6.44	1.32	1.25
1	J	89	GLU	CD-OE1	6.44	1.32	1.25
1	D	99	GLU	CD-OE2	6.43	1.32	1.25
1	A	89	GLU	CD-OE1	6.43	1.32	1.25
2	K	150	TYR	CD2-CE2	-6.42	1.29	1.39
1	D	89	GLU	CD-OE1	6.41	1.32	1.25
1	G	502	GLU	CD-OE2	6.41	1.32	1.25
1	A	605	GLU	CD-OE1	6.40	1.32	1.25
1	G	266	GLU	CD-OE2	6.38	1.32	1.25
1	J	538	GLU	CD-OE2	-6.38	1.18	1.25
2	H	150	TYR	CD2-CE2	-6.37	1.29	1.39
1	G	802	GLU	CD-OE1	6.37	1.32	1.25
1	J	808	GLU	CD-OE1	6.37	1.32	1.25
1	J	99	GLU	CD-OE2	6.36	1.32	1.25
1	G	808	GLU	CD-OE1	6.34	1.32	1.25
2	B	150	TYR	N-CA	-6.33	1.33	1.46
1	J	6	GLU	CD-OE1	6.32	1.32	1.25
1	G	605	GLU	CD-OE1	6.32	1.32	1.25
1	G	538	GLU	CD-OE2	-6.31	1.18	1.25
1	D	808	GLU	CD-OE1	6.31	1.32	1.25
1	A	808	GLU	CD-OE1	6.30	1.32	1.25
4	7	259	GLU	CG-CD	6.30	1.61	1.51
4	4	259	GLU	CG-CD	6.29	1.61	1.51
1	D	502	GLU	CD-OE2	6.27	1.32	1.25
1	J	502	GLU	CD-OE2	6.27	1.32	1.25
4	X	259	GLU	CG-CD	6.27	1.61	1.51
1	A	6	GLU	CD-OE1	6.27	1.32	1.25
4	V	259	GLU	CG-CD	6.27	1.61	1.51
4	6	259	GLU	CG-CD	6.26	1.61	1.51
4	W	259	GLU	CG-CD	6.25	1.61	1.51
1	J	802	GLU	CD-OE1	6.25	1.32	1.25
4	5	259	GLU	CG-CD	6.24	1.61	1.51
4	Y	259	GLU	CG-CD	6.24	1.61	1.51
2	K	150	TYR	N-CA	-6.24	1.33	1.46
1	A	502	GLU	CD-OE2	6.24	1.32	1.25
1	G	6	GLU	CD-OE1	6.23	1.32	1.25
4	2	259	GLU	CG-CD	6.23	1.61	1.51
4	8	259	GLU	CG-CD	6.23	1.61	1.51
2	E	150	TYR	N-CA	-6.22	1.33	1.46
4	1	259	GLU	CG-CD	6.22	1.61	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	6	GLU	CD-OE1	6.22	1.32	1.25
4	0	259	GLU	CG-CD	6.22	1.61	1.51
4	Z	259	GLU	CG-CD	6.21	1.61	1.51
1	D	605	GLU	CD-OE1	6.20	1.32	1.25
1	J	605	GLU	CD-OE1	6.20	1.32	1.25
1	A	99	GLU	CD-OE2	6.18	1.32	1.25
4	3	259	GLU	CG-CD	6.18	1.61	1.51
2	H	150	TYR	N-CA	-6.17	1.34	1.46
1	D	509	GLU	CD-OE1	6.16	1.32	1.25
1	D	802	GLU	CD-OE1	6.14	1.32	1.25
1	J	509	GLU	CD-OE1	6.13	1.32	1.25
1	G	509	GLU	CD-OE1	6.11	1.32	1.25
1	A	417	GLU	CD-OE1	6.11	1.32	1.25
1	J	329	GLU	CD-OE1	6.05	1.32	1.25
1	D	417	GLU	CD-OE1	6.01	1.32	1.25
1	G	476	GLU	CD-OE2	-6.01	1.19	1.25
1	A	509	GLU	CD-OE1	6.00	1.32	1.25
1	G	540	CYS	CB-SG	-5.98	1.72	1.81
1	A	329	GLU	CD-OE1	5.97	1.32	1.25
1	G	329	GLU	CD-OE1	5.96	1.32	1.25
1	A	802	GLU	CD-OE1	5.96	1.32	1.25
1	D	329	GLU	CD-OE1	5.91	1.32	1.25
1	J	417	GLU	CD-OE1	5.89	1.32	1.25
1	D	230	GLU	CD-OE2	5.88	1.32	1.25
1	G	417	GLU	CD-OE1	5.88	1.32	1.25
1	G	230	GLU	CD-OE2	5.86	1.32	1.25
1	J	540	CYS	CB-SG	-5.86	1.72	1.81
1	D	468	GLU	CD-OE1	5.85	1.32	1.25
1	J	230	GLU	CD-OE2	5.83	1.32	1.25
1	J	476	GLU	CD-OE2	-5.80	1.19	1.25
1	G	597	GLU	CD-OE1	5.80	1.32	1.25
1	J	527	GLU	CD-OE1	5.80	1.32	1.25
1	D	476	GLU	CD-OE2	-5.79	1.19	1.25
1	G	218	LEU	CB-CG	5.79	1.69	1.52
1	A	468	GLU	CD-OE1	5.79	1.32	1.25
1	J	421	GLU	CD-OE2	5.77	1.32	1.25
1	J	499	GLU	CD-OE2	5.77	1.31	1.25
1	A	540	CYS	CB-SG	-5.76	1.72	1.81
1	D	540	CYS	CB-SG	-5.76	1.72	1.81
1	A	476	GLU	CD-OE2	-5.76	1.19	1.25
1	J	468	GLU	CD-OE1	5.75	1.31	1.25
1	A	625	THR	CB-CG2	5.74	1.71	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	785	GLU	CD-OE2	5.73	1.31	1.25
1	A	230	GLU	CD-OE2	5.73	1.31	1.25
1	G	527	GLU	CD-OE1	5.71	1.31	1.25
1	A	785	GLU	CD-OE2	5.70	1.31	1.25
1	G	625	THR	CB-CG2	5.70	1.71	1.52
1	A	597	GLU	CD-OE1	5.69	1.31	1.25
1	J	625	THR	CB-CG2	5.69	1.71	1.52
1	A	74	GLU	CD-OE2	5.67	1.31	1.25
1	J	74	GLU	CD-OE2	5.67	1.31	1.25
1	D	597	GLU	CD-OE1	5.67	1.31	1.25
1	D	625	THR	CB-CG2	5.67	1.71	1.52
1	J	785	GLU	CD-OE2	5.66	1.31	1.25
1	J	218	LEU	CB-CG	5.66	1.69	1.52
1	A	218	LEU	CB-CG	5.65	1.69	1.52
1	G	785	GLU	CD-OE2	5.65	1.31	1.25
1	D	218	LEU	CB-CG	5.63	1.68	1.52
1	D	499	GLU	CD-OE2	5.62	1.31	1.25
1	G	74	GLU	CD-OE2	5.61	1.31	1.25
1	A	527	GLU	CD-OE1	5.61	1.31	1.25
1	D	687	GLU	CD-OE1	5.60	1.31	1.25
1	D	74	GLU	CD-OE2	5.58	1.31	1.25
1	J	687	GLU	CD-OE1	5.56	1.31	1.25
1	J	373	GLU	CD-OE1	5.56	1.31	1.25
1	A	421	GLU	CD-OE2	5.54	1.31	1.25
1	A	687	GLU	CD-OE1	5.54	1.31	1.25
1	G	421	GLU	CD-OE2	5.54	1.31	1.25
1	G	468	GLU	CD-OE1	5.53	1.31	1.25
1	J	597	GLU	CD-OE1	5.52	1.31	1.25
1	G	687	GLU	CD-OE1	5.51	1.31	1.25
2	H	150	TYR	CE1-CZ	5.51	1.45	1.38
1	A	499	GLU	CD-OE2	5.50	1.31	1.25
1	A	777	GLU	CD-OE2	5.50	1.31	1.25
1	D	373	GLU	CD-OE1	5.50	1.31	1.25
1	G	373	GLU	CD-OE1	5.49	1.31	1.25
2	E	150	TYR	CE1-CZ	5.48	1.45	1.38
1	A	506	GLU	CD-OE2	5.48	1.31	1.25
1	G	499	GLU	CD-OE2	5.48	1.31	1.25
1	D	527	GLU	CD-OE1	5.47	1.31	1.25
1	D	777	GLU	CD-OE2	5.47	1.31	1.25
2	K	150	TYR	CE1-CZ	5.46	1.45	1.38
1	G	479	CYS	CB-SG	-5.45	1.73	1.81
1	A	373	GLU	CD-OE1	5.44	1.31	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	298	GLU	CD-OE2	5.44	1.31	1.25
1	J	479	CYS	CB-SG	-5.44	1.73	1.81
1	G	777	GLU	CD-OE2	5.43	1.31	1.25
2	K	131	GLU	N-CA	5.42	1.57	1.46
2	E	131	GLU	N-CA	5.41	1.57	1.46
2	H	131	GLU	N-CA	5.41	1.57	1.46
1	A	479	CYS	CB-SG	-5.40	1.73	1.81
1	J	777	GLU	CD-OE2	5.39	1.31	1.25
1	G	506	GLU	CD-OE2	5.39	1.31	1.25
2	B	150	TYR	CE1-CZ	5.38	1.45	1.38
1	D	218	LEU	C-N	-5.37	1.21	1.34
1	A	218	LEU	C-N	-5.36	1.21	1.34
1	G	679	GLU	CD-OE2	5.36	1.31	1.25
1	D	421	GLU	CD-OE2	5.35	1.31	1.25
1	J	218	LEU	C-N	-5.34	1.21	1.34
1	D	298	GLU	CD-OE2	5.34	1.31	1.25
1	J	298	GLU	CD-OE2	5.34	1.31	1.25
1	A	65	GLU	CD-OE1	5.32	1.31	1.25
1	A	298	GLU	CD-OE2	5.31	1.31	1.25
1	G	218	LEU	C-N	-5.30	1.21	1.34
2	B	131	GLU	N-CA	5.29	1.56	1.46
1	D	65	GLU	CD-OE1	5.29	1.31	1.25
1	D	479	CYS	CB-SG	-5.28	1.73	1.81
1	J	679	GLU	CD-OE2	5.28	1.31	1.25
1	J	527	GLU	CD-OE2	-5.27	1.19	1.25
1	D	679	GLU	CD-OE2	5.24	1.31	1.25
1	J	65	GLU	CD-OE1	5.21	1.31	1.25
1	D	282	GLU	CD-OE1	5.20	1.31	1.25
2	K	149	ASP	CB-CG	5.19	1.62	1.51
1	J	12	GLU	CD-OE2	5.18	1.31	1.25
1	J	506	GLU	CD-OE2	5.18	1.31	1.25
1	D	702	GLU	CD-OE2	5.16	1.31	1.25
2	E	149	ASP	CB-CG	5.16	1.62	1.51
1	A	679	GLU	CD-OE2	5.15	1.31	1.25
1	G	12	GLU	CD-OE2	5.15	1.31	1.25
1	A	527	GLU	CD-OE2	-5.14	1.20	1.25
1	A	697	CYS	CB-SG	5.14	1.91	1.82
1	A	539	GLU	CD-OE1	5.13	1.31	1.25
1	G	21	GLU	CD-OE2	5.13	1.31	1.25
2	B	149	ASP	CB-CG	5.12	1.62	1.51
1	A	702	GLU	CD-OE2	5.11	1.31	1.25
1	D	506	GLU	CD-OE2	5.11	1.31	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	65	GLU	CD-OE1	5.11	1.31	1.25
1	A	21	GLU	CD-OE2	5.11	1.31	1.25
1	G	702	GLU	CD-OE2	5.10	1.31	1.25
1	J	702	GLU	CD-OE2	5.09	1.31	1.25
1	A	282	GLU	CD-OE1	5.09	1.31	1.25
1	J	282	GLU	CD-OE1	5.09	1.31	1.25
1	A	150	GLU	CD-OE1	5.08	1.31	1.25
1	G	527	GLU	CD-OE2	-5.06	1.20	1.25
1	G	697	CYS	CB-SG	5.05	1.90	1.82
4	Y	259	GLU	CB-CG	5.05	1.61	1.52
2	H	149	ASP	CB-CG	5.05	1.62	1.51
4	1	259	GLU	CB-CG	5.05	1.61	1.52
4	8	259	GLU	CB-CG	5.05	1.61	1.52
1	J	21	GLU	CD-OE2	5.05	1.31	1.25
4	5	259	GLU	CB-CG	5.04	1.61	1.52
1	D	539	GLU	CD-OE1	5.04	1.31	1.25
1	D	21	GLU	CD-OE2	5.03	1.31	1.25
4	6	259	GLU	CB-CG	5.03	1.61	1.52
4	Z	259	GLU	CB-CG	5.03	1.61	1.52
1	G	150	GLU	CD-OE1	5.02	1.31	1.25
4	7	259	GLU	CB-CG	5.02	1.61	1.52
1	J	697	CYS	CB-SG	5.01	1.90	1.82
4	W	259	GLU	CB-CG	5.01	1.61	1.52
4	X	259	GLU	CB-CG	5.01	1.61	1.52
1	D	12	GLU	CD-OE2	5.00	1.31	1.25

All (1261) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	637	LYS	O-C-N	-58.53	23.69	123.20
1	J	637	LYS	O-C-N	-58.47	23.80	123.20
1	D	637	LYS	O-C-N	-58.47	23.81	123.20
1	A	637	LYS	O-C-N	-58.45	23.83	123.20
1	J	649	VAL	CG1-CB-CG2	-34.02	56.47	110.90
1	D	649	VAL	CG1-CB-CG2	-34.00	56.50	110.90
1	A	649	VAL	CG1-CB-CG2	-33.99	56.51	110.90
1	G	649	VAL	CG1-CB-CG2	-33.98	56.53	110.90
1	J	648	THR	CA-CB-OG1	-31.72	42.38	109.00
1	A	648	THR	CA-CB-OG1	-31.70	42.43	109.00
1	D	648	THR	CA-CB-OG1	-31.70	42.43	109.00
1	G	648	THR	CA-CB-OG1	-31.68	42.48	109.00
2	H	150	TYR	CB-CG-CD2	-28.73	103.76	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	150	TYR	CB-CG-CD2	-28.64	103.81	121.00
2	K	150	TYR	CB-CG-CD2	-28.60	103.84	121.00
2	B	150	TYR	CB-CG-CD2	-28.58	103.85	121.00
1	G	649	VAL	CA-CB-CG1	-28.52	68.11	110.90
1	J	649	VAL	CA-CB-CG1	-28.49	68.16	110.90
1	D	649	VAL	CA-CB-CG1	-28.47	68.19	110.90
1	A	649	VAL	CA-CB-CG1	-28.45	68.23	110.90
1	J	649	VAL	CA-CB-CG2	-28.18	68.62	110.90
1	G	649	VAL	CA-CB-CG2	-28.17	68.64	110.90
1	A	649	VAL	CA-CB-CG2	-28.17	68.64	110.90
1	D	649	VAL	CA-CB-CG2	-28.16	68.66	110.90
1	D	648	THR	CA-CB-CG2	-25.60	76.56	112.40
1	J	648	THR	CA-CB-CG2	-25.56	76.61	112.40
1	A	648	THR	CA-CB-CG2	-25.45	76.78	112.40
1	G	648	THR	CA-CB-CG2	-25.36	76.90	112.40
1	J	709	LYS	O-C-N	-21.06	87.39	123.20
2	H	150	TYR	CG-CD2-CE2	-20.84	104.63	121.30
2	K	150	TYR	CG-CD2-CE2	-20.66	104.78	121.30
2	E	150	TYR	CG-CD2-CE2	-20.54	104.86	121.30
2	B	150	TYR	CG-CD2-CE2	-20.43	104.95	121.30
2	K	150	TYR	CD1-CG-CD2	19.49	139.34	117.90
2	H	150	TYR	CD1-CG-CD2	19.45	139.29	117.90
2	E	150	TYR	CD1-CG-CD2	19.40	139.24	117.90
2	B	150	TYR	CD1-CG-CD2	19.38	139.22	117.90
2	H	150	TYR	CG-CD1-CE1	-18.44	106.55	121.30
2	K	150	TYR	CG-CD1-CE1	-18.44	106.55	121.30
2	B	150	TYR	CG-CD1-CE1	-18.39	106.59	121.30
2	E	150	TYR	CG-CD1-CE1	-18.38	106.59	121.30
1	J	800	ARG	NE-CZ-NH2	-16.61	112.00	120.30
1	D	800	ARG	NE-CZ-NH2	-16.48	112.06	120.30
1	G	800	ARG	NE-CZ-NH2	-16.31	112.14	120.30
1	A	800	ARG	NE-CZ-NH2	-16.29	112.16	120.30
1	G	623	PHE	CB-CG-CD2	-13.78	111.16	120.80
1	J	623	PHE	CB-CG-CD2	-13.67	111.23	120.80
1	A	623	PHE	CB-CG-CD2	-13.64	111.25	120.80
1	D	623	PHE	CB-CG-CD2	-13.64	111.25	120.80
1	A	623	PHE	CB-CG-CD1	12.37	129.46	120.80
1	G	623	PHE	CB-CG-CD1	12.35	129.45	120.80
1	J	623	PHE	CB-CG-CD1	12.33	129.43	120.80
1	J	623	PHE	CA-CB-CG	-12.27	84.47	113.90
1	A	623	PHE	CA-CB-CG	-12.26	84.48	113.90
1	D	623	PHE	CA-CB-CG	-12.23	84.54	113.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	623	PHE	CA-CB-CG	-12.21	84.59	113.90
1	D	623	PHE	CB-CG-CD1	12.03	129.22	120.80
1	J	98	HIS	CB-CA-C	-11.57	87.27	110.40
1	A	98	HIS	CB-CA-C	-11.56	87.29	110.40
1	G	98	HIS	CB-CA-C	-11.55	87.29	110.40
1	D	98	HIS	CB-CA-C	-11.54	87.33	110.40
1	G	568	PRO	O-C-N	10.71	139.83	122.70
1	A	568	PRO	O-C-N	10.67	139.78	122.70
1	D	568	PRO	O-C-N	10.66	139.76	122.70
1	J	568	PRO	O-C-N	10.58	139.63	122.70
1	J	709	LYS	C-N-CA	10.30	143.93	122.30
2	E	141	PRO	CA-N-CD	10.30	126.11	111.70
2	H	141	PRO	CA-N-CD	10.27	126.08	111.70
2	K	141	PRO	CA-N-CD	10.21	125.99	111.70
2	B	141	PRO	CA-N-CD	10.18	125.95	111.70
1	G	625	THR	CA-CB-CG2	-10.10	98.26	112.40
1	A	327	ASP	CB-CG-OD1	-10.06	109.24	118.30
1	G	327	ASP	CB-CG-OD1	-10.05	109.25	118.30
1	J	327	ASP	CB-CG-OD1	-10.04	109.26	118.30
1	A	625	THR	CA-CB-CG2	-10.03	98.35	112.40
1	J	625	THR	CA-CB-CG2	-10.03	98.36	112.40
1	D	625	THR	CA-CB-CG2	-10.02	98.38	112.40
1	D	327	ASP	CB-CG-OD1	-10.00	109.30	118.30
1	A	241	ASP	CB-CG-OD1	-9.85	109.44	118.30
1	G	241	ASP	CB-CG-OD1	-9.80	109.48	118.30
3	C	63	ILE	O-C-N	9.80	138.38	122.70
1	D	728	ASN	O-C-N	9.76	138.32	122.70
1	J	241	ASP	CB-CG-OD1	-9.73	109.54	118.30
1	D	241	ASP	CB-CG-OD1	-9.73	109.55	118.30
3	I	63	ILE	O-C-N	9.72	138.25	122.70
3	F	63	ILE	O-C-N	9.71	138.23	122.70
1	A	728	ASN	O-C-N	9.68	138.19	122.70
1	J	728	ASN	O-C-N	9.67	138.17	122.70
3	L	63	ILE	O-C-N	9.66	138.16	122.70
1	G	728	ASN	O-C-N	9.60	138.06	122.70
1	G	264	ASP	CB-CG-OD2	-9.50	109.75	118.30
1	D	264	ASP	CB-CG-OD2	-9.42	109.82	118.30
1	A	264	ASP	CB-CG-OD2	-9.42	109.82	118.30
1	J	709	LYS	CA-C-N	9.42	135.04	116.20
2	E	150	TYR	N-CA-CB	-9.40	93.68	110.60
1	J	264	ASP	CB-CG-OD2	-9.38	109.86	118.30
2	H	150	TYR	N-CA-CB	-9.36	93.75	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	K	150	TYR	N-CA-CB	-9.36	93.75	110.60
2	B	150	TYR	N-CA-CB	-9.28	93.90	110.60
4	W	356	TRP	CD1-CG-CD2	9.18	113.64	106.30
4	8	356	TRP	CD1-CG-CD2	9.17	113.64	106.30
4	Y	356	TRP	CD1-CG-CD2	9.17	113.64	106.30
4	3	356	TRP	CD1-CG-CD2	9.17	113.63	106.30
4	2	356	TRP	CD1-CG-CD2	9.16	113.63	106.30
4	5	356	TRP	CD1-CG-CD2	9.16	113.63	106.30
4	0	356	TRP	CD1-CG-CD2	9.14	113.61	106.30
4	6	356	TRP	CD1-CG-CD2	9.11	113.59	106.30
4	4	356	TRP	CD1-CG-CD2	9.10	113.58	106.30
4	V	356	TRP	CD1-CG-CD2	9.10	113.58	106.30
4	7	356	TRP	CD1-CG-CD2	9.10	113.58	106.30
4	X	356	TRP	CD1-CG-CD2	9.06	113.54	106.30
4	Z	356	TRP	CD1-CG-CD2	9.04	113.53	106.30
4	1	356	TRP	CD1-CG-CD2	9.02	113.51	106.30
1	J	378	ASP	CB-CG-OD2	8.98	126.39	118.30
1	J	352	TYR	CB-CG-CD1	8.97	126.38	121.00
1	D	378	ASP	CB-CG-OD2	8.95	126.35	118.30
1	A	378	ASP	CB-CG-OD2	8.92	126.32	118.30
1	G	378	ASP	CB-CG-OD2	8.91	126.32	118.30
1	G	352	TYR	CB-CG-CD1	8.84	126.30	121.00
4	2	177	ARG	NE-CZ-NH2	-8.80	115.90	120.30
1	D	352	TYR	CB-CG-CD1	8.77	126.26	121.00
2	K	138	ALA	O-C-N	-8.74	108.72	122.70
2	E	138	ALA	O-C-N	-8.72	108.75	122.70
1	A	352	TYR	CB-CG-CD1	8.72	126.23	121.00
4	4	177	ARG	NE-CZ-NH2	-8.70	115.95	120.30
2	B	138	ALA	O-C-N	-8.70	108.79	122.70
2	H	138	ALA	O-C-N	-8.65	108.86	122.70
4	7	177	ARG	NE-CZ-NH2	-8.64	115.98	120.30
4	W	177	ARG	NE-CZ-NH2	-8.57	116.02	120.30
4	4	86	TRP	CD1-CG-CD2	8.53	113.13	106.30
4	Y	86	TRP	CD1-CG-CD2	8.53	113.12	106.30
1	D	601	ASP	CB-CG-OD1	-8.52	110.63	118.30
4	X	177	ARG	NE-CZ-NH2	-8.52	116.04	120.30
4	X	86	TRP	CD1-CG-CD2	8.52	113.11	106.30
1	G	601	ASP	CB-CG-OD1	-8.51	110.64	118.30
4	8	177	ARG	NE-CZ-NH2	-8.50	116.05	120.30
4	7	86	TRP	CD1-CG-CD2	8.49	113.09	106.30
1	J	601	ASP	CB-CG-OD1	-8.49	110.66	118.30
4	0	177	ARG	NE-CZ-NH2	-8.48	116.06	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	5	177	ARG	NE-CZ-NH2	-8.47	116.06	120.30
4	V	177	ARG	NE-CZ-NH2	-8.47	116.06	120.30
4	Z	177	ARG	NE-CZ-NH2	-8.47	116.06	120.30
4	5	86	TRP	CD1-CG-CD2	8.47	113.08	106.30
4	6	86	TRP	CD1-CG-CD2	8.46	113.07	106.30
4	Z	86	TRP	CD1-CG-CD2	8.46	113.07	106.30
4	2	86	TRP	CD1-CG-CD2	8.46	113.07	106.30
4	1	177	ARG	NE-CZ-NH2	-8.46	116.07	120.30
4	3	177	ARG	NE-CZ-NH2	-8.46	116.07	120.30
4	6	177	ARG	NE-CZ-NH2	-8.46	116.07	120.30
4	8	86	TRP	CD1-CG-CD2	8.45	113.06	106.30
1	J	33	ASP	CB-CG-OD1	-8.44	110.71	118.30
4	0	86	TRP	CD1-CG-CD2	8.44	113.05	106.30
4	V	86	TRP	CD1-CG-CD2	8.43	113.04	106.30
1	A	601	ASP	CB-CG-OD1	-8.42	110.72	118.30
4	3	86	TRP	CD1-CG-CD2	8.42	113.03	106.30
4	W	86	TRP	CD1-CG-CD2	8.41	113.03	106.30
1	J	352	TYR	CB-CG-CD2	-8.38	115.97	121.00
1	G	33	ASP	CB-CG-OD1	-8.36	110.78	118.30
4	1	86	TRP	CD1-CG-CD2	8.36	112.99	106.30
1	A	352	TYR	CB-CG-CD2	-8.33	116.00	121.00
1	D	33	ASP	CB-CG-OD1	-8.27	110.85	118.30
4	Y	177	ARG	NE-CZ-NH2	-8.24	116.18	120.30
1	A	33	ASP	CB-CG-OD1	-8.22	110.90	118.30
1	G	352	TYR	CB-CG-CD2	-8.18	116.09	121.00
1	D	352	TYR	CB-CG-CD2	-8.10	116.14	121.00
1	A	339	ASP	CB-CG-OD1	-8.04	111.06	118.30
4	3	356	TRP	CE2-CD2-CG	-8.04	100.87	107.30
4	Y	356	TRP	CE2-CD2-CG	-8.01	100.89	107.30
4	5	356	TRP	CE2-CD2-CG	-8.00	100.90	107.30
4	V	356	TRP	CE2-CD2-CG	-8.00	100.90	107.30
4	8	356	TRP	CE2-CD2-CG	-7.99	100.91	107.30
4	0	356	TRP	CE2-CD2-CG	-7.99	100.91	107.30
4	7	356	TRP	CE2-CD2-CG	-7.99	100.91	107.30
4	6	356	TRP	CE2-CD2-CG	-7.98	100.92	107.30
4	W	356	TRP	CE2-CD2-CG	-7.97	100.92	107.30
1	D	637	LYS	CA-C-N	7.93	132.06	116.20
4	2	356	TRP	CE2-CD2-CG	-7.92	100.96	107.30
4	X	356	TRP	CE2-CD2-CG	-7.92	100.97	107.30
1	A	637	LYS	CA-C-N	7.91	132.01	116.20
1	G	339	ASP	CB-CG-OD1	-7.91	111.18	118.30
1	J	637	LYS	CA-C-N	7.91	132.01	116.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	Z	356	TRP	CE2-CD2-CG	-7.90	100.98	107.30
2	E	150	TYR	CD1-CE1-CZ	-7.90	112.69	119.80
1	G	637	LYS	CA-C-N	7.89	131.97	116.20
1	D	339	ASP	CB-CG-OD1	-7.88	111.21	118.30
4	1	356	TRP	CE2-CD2-CG	-7.87	101.00	107.30
2	H	150	TYR	CD1-CE1-CZ	-7.87	112.72	119.80
4	4	356	TRP	CE2-CD2-CG	-7.86	101.01	107.30
1	J	339	ASP	CB-CG-OD1	-7.84	111.24	118.30
1	A	202	SER	CB-CA-C	-7.78	95.31	110.10
2	B	150	TYR	CD1-CE1-CZ	-7.76	112.81	119.80
1	D	202	SER	CB-CA-C	-7.76	95.35	110.10
2	K	150	TYR	CD1-CE1-CZ	-7.74	112.83	119.80
1	J	202	SER	CB-CA-C	-7.73	95.41	110.10
4	0	312	ARG	NE-CZ-NH2	7.73	124.17	120.30
1	G	202	SER	CB-CA-C	-7.72	95.44	110.10
4	1	312	ARG	NE-CZ-NH2	7.69	124.15	120.30
1	G	654	ARG	NE-CZ-NH1	7.68	124.14	120.30
4	X	312	ARG	NE-CZ-NH2	7.68	124.14	120.30
4	5	312	ARG	NE-CZ-NH2	7.68	124.14	120.30
4	3	312	ARG	NE-CZ-NH2	7.66	124.13	120.30
1	J	653	PHE	CB-CG-CD1	-7.66	115.44	120.80
4	Y	312	ARG	NE-CZ-NH2	7.65	124.13	120.30
1	D	653	PHE	CB-CG-CD1	-7.65	115.45	120.80
4	X	86	TRP	CE2-CD2-CG	-7.63	101.19	107.30
4	Z	312	ARG	NE-CZ-NH2	7.63	124.12	120.30
4	4	312	ARG	NE-CZ-NH2	7.63	124.11	120.30
4	8	312	ARG	NE-CZ-NH2	7.62	124.11	120.30
4	2	312	ARG	NE-CZ-NH2	7.60	124.10	120.30
4	8	86	TRP	CE2-CD2-CG	-7.59	101.22	107.30
4	4	86	TRP	CE2-CD2-CG	-7.58	101.24	107.30
4	V	312	ARG	NE-CZ-NH2	7.56	124.08	120.30
4	7	86	TRP	CE2-CD2-CG	-7.56	101.25	107.30
4	0	86	TRP	CE2-CD2-CG	-7.56	101.25	107.30
4	6	312	ARG	NE-CZ-NH2	7.56	124.08	120.30
1	A	654	ARG	NE-CZ-NH1	7.55	124.08	120.30
4	Y	86	TRP	CE2-CD2-CG	-7.55	101.26	107.30
1	G	653	PHE	CB-CG-CD1	-7.54	115.52	120.80
4	7	312	ARG	NE-CZ-NH2	7.53	124.06	120.30
2	E	127	ARG	NE-CZ-NH2	7.52	124.06	120.30
4	2	86	TRP	CE2-CD2-CG	-7.52	101.28	107.30
4	V	86	TRP	CE2-CD2-CG	-7.52	101.28	107.30
3	C	63	ILE	CG1-CB-CG2	-7.52	94.86	111.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	5	86	TRP	CE2-CD2-CG	-7.51	101.29	107.30
4	W	86	TRP	CE2-CD2-CG	-7.51	101.29	107.30
4	W	312	ARG	NE-CZ-NH2	7.49	124.05	120.30
4	3	86	TRP	CE2-CD2-CG	-7.49	101.31	107.30
3	F	63	ILE	CG1-CB-CG2	-7.48	94.94	111.40
1	G	346	ASP	CB-CG-OD2	-7.48	111.57	118.30
1	J	654	ARG	NE-CZ-NH1	7.47	124.04	120.30
3	L	63	ILE	CG1-CB-CG2	-7.47	94.96	111.40
3	I	63	ILE	CG1-CB-CG2	-7.47	94.97	111.40
4	6	86	TRP	CE2-CD2-CG	-7.46	101.33	107.30
4	Z	86	TRP	CE2-CD2-CG	-7.46	101.33	107.30
4	1	86	TRP	CE2-CD2-CG	-7.46	101.33	107.30
1	A	653	PHE	CB-CG-CD1	-7.46	115.58	120.80
1	J	518	ASP	CB-CG-OD1	-7.43	111.61	118.30
1	A	518	ASP	CB-CG-OD1	-7.40	111.64	118.30
4	1	254	ARG	NE-CZ-NH2	-7.40	116.60	120.30
3	I	63	ILE	CA-C-N	-7.39	100.94	117.20
4	W	180	LEU	CA-CB-CG	7.39	132.29	115.30
4	0	233	SER	CA-C-N	-7.38	100.95	117.20
4	W	233	SER	CA-C-N	-7.38	100.96	117.20
4	6	233	SER	CA-C-N	-7.38	100.97	117.20
4	X	233	SER	CA-C-N	-7.37	100.98	117.20
4	1	233	SER	CA-C-N	-7.37	100.98	117.20
2	B	127	ARG	NE-CZ-NH2	7.37	123.98	120.30
1	D	346	ASP	CB-CG-OD2	-7.37	111.67	118.30
1	D	654	ARG	NE-CZ-NH1	7.37	123.98	120.30
4	8	233	SER	CA-C-N	-7.37	101.00	117.20
4	3	233	SER	CA-C-N	-7.36	101.00	117.20
4	5	233	SER	CA-C-N	-7.36	101.00	117.20
1	D	518	ASP	CB-CG-OD1	-7.36	111.68	118.30
4	4	233	SER	CA-C-N	-7.36	101.02	117.20
4	7	233	SER	CA-C-N	-7.36	101.01	117.20
3	C	63	ILE	CA-C-N	-7.36	101.02	117.20
4	V	233	SER	CA-C-N	-7.36	101.02	117.20
4	7	180	LEU	CA-CB-CG	7.35	132.21	115.30
4	1	180	LEU	CA-CB-CG	7.35	132.20	115.30
4	Z	233	SER	CA-C-N	-7.35	101.03	117.20
4	2	233	SER	CA-C-N	-7.35	101.04	117.20
4	6	180	LEU	CA-CB-CG	7.34	132.19	115.30
4	3	180	LEU	CA-CB-CG	7.34	132.19	115.30
4	5	180	LEU	CA-CB-CG	7.34	132.19	115.30
3	L	63	ILE	CA-C-N	-7.34	101.05	117.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	X	180	LEU	CA-CB-CG	7.34	132.18	115.30
4	0	180	LEU	CA-CB-CG	7.33	132.17	115.30
4	V	180	LEU	CA-CB-CG	7.33	132.16	115.30
4	Y	233	SER	CA-C-N	-7.33	101.08	117.20
1	A	346	ASP	CB-CG-OD2	-7.33	111.71	118.30
4	4	180	LEU	CA-CB-CG	7.33	132.15	115.30
4	8	180	LEU	CA-CB-CG	7.32	132.14	115.30
3	F	63	ILE	CA-C-N	-7.31	101.11	117.20
4	2	180	LEU	CA-CB-CG	7.31	132.12	115.30
4	Y	180	LEU	CA-CB-CG	7.31	132.10	115.30
4	Z	180	LEU	CA-CB-CG	7.30	132.09	115.30
1	G	104	TYR	CB-CG-CD2	7.30	125.38	121.00
4	2	254	ARG	NE-CZ-NH2	-7.30	116.65	120.30
1	J	346	ASP	CB-CG-OD2	-7.29	111.73	118.30
4	W	254	ARG	NE-CZ-NH2	-7.29	116.66	120.30
4	4	254	ARG	NE-CZ-NH2	-7.28	116.66	120.30
4	X	79	TRP	CD1-CG-CD2	7.26	112.11	106.30
1	J	104	TYR	CB-CG-CD2	7.26	125.36	121.00
1	G	518	ASP	CB-CG-OD1	-7.25	111.78	118.30
4	V	254	ARG	NE-CZ-NH2	-7.25	116.68	120.30
4	5	254	ARG	NE-CZ-NH2	-7.23	116.69	120.30
4	1	79	TRP	CD1-CG-CD2	7.22	112.07	106.30
4	V	340	TRP	CE2-CD2-CG	-7.21	101.53	107.30
4	X	254	ARG	NE-CZ-NH2	-7.21	116.69	120.30
4	8	254	ARG	NE-CZ-NH2	-7.21	116.70	120.30
4	5	79	TRP	CD1-CG-CD2	7.21	112.06	106.30
4	6	340	TRP	CE2-CD2-CG	-7.20	101.54	107.30
4	W	340	TRP	CE2-CD2-CG	-7.20	101.54	107.30
4	5	340	TRP	CE2-CD2-CG	-7.20	101.54	107.30
4	2	79	TRP	CD1-CG-CD2	7.19	112.06	106.30
4	V	206	ARG	NE-CZ-NH1	7.19	123.90	120.30
4	3	340	TRP	CE2-CD2-CG	-7.18	101.55	107.30
4	0	79	TRP	CD1-CG-CD2	7.17	112.04	106.30
4	2	340	TRP	CE2-CD2-CG	-7.17	101.56	107.30
4	0	340	TRP	CE2-CD2-CG	-7.16	101.57	107.30
4	3	206	ARG	NE-CZ-NH1	7.16	123.88	120.30
4	8	79	TRP	CD1-CG-CD2	7.16	112.02	106.30
1	A	148	ARG	NE-CZ-NH2	-7.15	116.72	120.30
4	6	79	TRP	CD1-CG-CD2	7.15	112.02	106.30
4	Y	340	TRP	CE2-CD2-CG	-7.15	101.58	107.30
4	Z	340	TRP	CE2-CD2-CG	-7.15	101.58	107.30
4	Y	254	ARG	NE-CZ-NH2	-7.15	116.73	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	1	340	TRP	CE2-CD2-CG	-7.15	101.58	107.30
4	Z	79	TRP	CD1-CG-CD2	7.15	112.02	106.30
4	W	206	ARG	NE-CZ-NH1	7.14	123.87	120.30
4	7	340	TRP	CE2-CD2-CG	-7.14	101.59	107.30
4	1	206	ARG	NE-CZ-NH1	7.14	123.87	120.30
4	4	79	TRP	CD1-CG-CD2	7.14	112.01	106.30
4	4	340	TRP	CE2-CD2-CG	-7.14	101.59	107.30
4	V	79	TRP	CD1-CG-CD2	7.14	112.01	106.30
1	G	568	PRO	CA-C-N	-7.13	101.51	117.20
1	A	104	TYR	CB-CG-CD2	7.13	125.28	121.00
4	Y	79	TRP	CD1-CG-CD2	7.13	112.01	106.30
2	K	150	TYR	CB-CG-CD1	-7.12	116.73	121.00
4	7	79	TRP	CD1-CG-CD2	7.12	112.00	106.30
4	W	79	TRP	CD1-CG-CD2	7.12	112.00	106.30
4	X	340	TRP	CE2-CD2-CG	-7.12	101.61	107.30
4	6	254	ARG	NE-CZ-NH2	-7.11	116.75	120.30
4	8	206	ARG	NE-CZ-NH1	7.11	123.85	120.30
1	A	568	PRO	CA-C-N	-7.10	101.57	117.20
2	K	127	ARG	NE-CZ-NH2	7.10	123.85	120.30
4	7	254	ARG	NE-CZ-NH2	-7.10	116.75	120.30
4	X	79	TRP	CE2-CD2-CG	-7.10	101.62	107.30
4	3	340	TRP	CD1-CG-CD2	7.09	111.97	106.30
4	5	206	ARG	NE-CZ-NH1	7.09	123.84	120.30
4	3	79	TRP	CD1-CG-CD2	7.08	111.97	106.30
1	D	568	PRO	CA-C-N	-7.08	101.63	117.20
4	0	254	ARG	NE-CZ-NH2	-7.08	116.76	120.30
4	6	206	ARG	NE-CZ-NH1	7.08	123.84	120.30
1	J	568	PRO	CA-C-N	-7.07	101.64	117.20
4	2	206	ARG	NE-CZ-NH1	7.07	123.84	120.30
4	4	206	ARG	NE-CZ-NH1	7.07	123.83	120.30
2	H	127	ARG	NE-CZ-NH2	7.06	123.83	120.30
4	X	206	ARG	NE-CZ-NH1	7.06	123.83	120.30
1	D	218	LEU	CB-CG-CD1	7.05	122.99	111.00
4	1	47	MET	CA-CB-CG	-7.05	101.31	113.30
1	A	264	ASP	N-CA-CB	-7.04	97.92	110.60
4	6	47	MET	CA-CB-CG	-7.04	101.34	113.30
4	7	206	ARG	NE-CZ-NH1	7.04	123.82	120.30
4	8	47	MET	CA-CB-CG	-7.04	101.34	113.30
4	0	47	MET	CA-CB-CG	-7.03	101.35	113.30
4	Z	254	ARG	NE-CZ-NH2	-7.03	116.78	120.30
4	8	340	TRP	CE2-CD2-CG	-7.02	101.68	107.30
4	Z	47	MET	CA-CB-CG	-7.02	101.36	113.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	Y	206	ARG	NE-CZ-NH1	7.02	123.81	120.30
1	D	217	THR	N-CA-CB	7.01	123.63	110.30
4	8	79	TRP	CE2-CD2-CG	-7.01	101.69	107.30
4	X	47	MET	CA-CB-CG	-7.01	101.38	113.30
4	0	206	ARG	NE-CZ-NH1	7.01	123.81	120.30
4	3	47	MET	CA-CB-CG	-7.01	101.38	113.30
4	V	47	MET	CA-CB-CG	-7.01	101.38	113.30
4	W	47	MET	CA-CB-CG	-7.01	101.38	113.30
1	J	264	ASP	N-CA-CB	-7.01	97.99	110.60
4	0	79	TRP	CE2-CD2-CG	-7.01	101.69	107.30
4	2	47	MET	CA-CB-CG	-7.01	101.39	113.30
1	D	104	TYR	CB-CG-CD2	7.00	125.20	121.00
1	J	218	LEU	CB-CG-CD1	7.00	122.90	111.00
4	W	79	TRP	CE2-CD2-CG	-7.00	101.70	107.30
4	4	47	MET	CA-CB-CG	-7.00	101.40	113.30
4	5	47	MET	CA-CB-CG	-7.00	101.40	113.30
4	7	47	MET	CA-CB-CG	-7.00	101.41	113.30
4	Z	206	ARG	NE-CZ-NH1	7.00	123.80	120.30
1	D	264	ASP	N-CA-CB	-7.00	98.01	110.60
1	G	217	THR	N-CA-CB	6.99	123.58	110.30
1	G	218	LEU	CB-CG-CD1	6.99	122.89	111.00
4	W	340	TRP	CD1-CG-CD2	6.99	111.89	106.30
4	5	79	TRP	CE2-CD2-CG	-6.98	101.71	107.30
4	1	79	TRP	CE2-CD2-CG	-6.98	101.72	107.30
1	G	264	ASP	N-CA-CB	-6.98	98.04	110.60
4	2	79	TRP	CE2-CD2-CG	-6.97	101.72	107.30
1	J	148	ARG	NE-CZ-NH2	-6.97	116.81	120.30
4	Z	79	TRP	CE2-CD2-CG	-6.97	101.72	107.30
4	Z	340	TRP	CD1-CG-CD2	6.97	111.88	106.30
4	Y	47	MET	CA-CB-CG	-6.97	101.45	113.30
1	J	217	THR	N-CA-CB	6.96	123.52	110.30
1	A	218	LEU	CB-CG-CD1	6.96	122.83	111.00
4	7	340	TRP	CD1-CG-CD2	6.96	111.86	106.30
2	B	150	TYR	CB-CG-CD1	-6.95	116.83	121.00
4	2	340	TRP	CD1-CG-CD2	6.95	111.86	106.30
4	Y	340	TRP	CD1-CG-CD2	6.95	111.86	106.30
4	5	340	TRP	CD1-CG-CD2	6.95	111.86	106.30
1	A	217	THR	N-CA-CB	6.94	123.49	110.30
4	6	340	TRP	CD1-CG-CD2	6.94	111.86	106.30
4	V	79	TRP	CE2-CD2-CG	-6.94	101.75	107.30
2	H	150	TYR	CB-CG-CD1	-6.93	116.84	121.00
4	3	254	ARG	NE-CZ-NH2	-6.93	116.83	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	4	340	TRP	CD1-CG-CD2	6.93	111.85	106.30
4	Y	79	TRP	CE2-CD2-CG	-6.93	101.75	107.30
4	X	340	TRP	CD1-CG-CD2	6.93	111.84	106.30
4	1	340	TRP	CD1-CG-CD2	6.93	111.84	106.30
4	4	79	TRP	CE2-CD2-CG	-6.92	101.76	107.30
4	0	340	TRP	CD1-CG-CD2	6.92	111.84	106.30
4	7	79	TRP	CE2-CD2-CG	-6.92	101.76	107.30
4	3	79	TRP	CE2-CD2-CG	-6.92	101.76	107.30
4	V	340	TRP	CD1-CG-CD2	6.92	111.83	106.30
2	E	150	TYR	CB-CG-CD1	-6.91	116.85	121.00
4	6	79	TRP	CE2-CD2-CG	-6.91	101.77	107.30
1	A	75	ASP	N-CA-CB	6.91	123.03	110.60
1	D	728	ASN	CA-C-N	-6.90	102.02	117.20
1	G	75	ASP	N-CA-CB	6.90	123.02	110.60
4	8	340	TRP	CD1-CG-CD2	6.89	111.81	106.30
1	G	148	ARG	NE-CZ-NH2	-6.88	116.86	120.30
1	J	75	ASP	N-CA-CB	6.86	122.94	110.60
1	J	728	ASN	CA-C-N	-6.85	102.13	117.20
1	G	728	ASN	CA-C-N	-6.85	102.14	117.20
1	G	450	ASP	CB-CG-OD2	6.85	124.46	118.30
1	A	728	ASN	CA-C-N	-6.84	102.14	117.20
1	D	450	ASP	CB-CG-OD2	6.83	124.45	118.30
1	J	450	ASP	CB-CG-OD2	6.83	124.45	118.30
1	D	148	ARG	NE-CZ-NH2	-6.81	116.89	120.30
1	A	450	ASP	CB-CG-OD2	6.79	124.41	118.30
1	D	75	ASP	N-CA-CB	6.76	122.77	110.60
1	D	781	ASP	CB-CG-OD1	-6.73	112.24	118.30
1	J	75	ASP	CB-CG-OD2	6.70	124.33	118.30
1	J	219	GLU	N-CA-C	-6.69	92.94	111.00
1	G	756	THR	N-CA-CB	-6.68	97.61	110.30
1	D	756	THR	N-CA-CB	-6.66	97.64	110.30
1	J	756	THR	N-CA-CB	-6.66	97.64	110.30
4	V	169	TYR	CB-CG-CD2	-6.65	117.01	121.00
1	G	219	GLU	N-CA-C	-6.65	93.04	111.00
1	A	343	PHE	CB-CG-CD1	6.65	125.45	120.80
1	G	781	ASP	CB-CG-OD1	-6.64	112.32	118.30
1	G	555	TYR	CB-CG-CD2	-6.64	117.01	121.00
1	J	555	TYR	CB-CG-CD2	-6.64	117.02	121.00
1	A	75	ASP	CB-CG-OD2	6.63	124.27	118.30
1	A	756	THR	N-CA-CB	-6.63	97.70	110.30
4	2	169	TYR	CB-CG-CD2	-6.63	117.02	121.00
4	5	196	ARG	NE-CZ-NH1	6.62	123.61	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	J	781	ASP	CB-CG-OD1	-6.62	112.34	118.30
1	A	781	ASP	CB-CG-OD1	-6.60	112.36	118.30
1	D	555	TYR	CB-CG-CD2	-6.60	117.04	121.00
1	A	219	GLU	N-CA-C	-6.60	93.19	111.00
4	4	169	TYR	CB-CG-CD2	-6.57	117.06	121.00
1	D	75	ASP	CB-CG-OD2	6.57	124.21	118.30
4	X	169	TYR	CB-CG-CD2	-6.57	117.06	121.00
1	A	332	MET	CG-SD-CE	-6.56	89.70	100.20
1	D	219	GLU	N-CA-C	-6.56	93.28	111.00
1	A	555	TYR	CB-CG-CD2	-6.56	117.06	121.00
4	7	169	TYR	CB-CG-CD2	-6.55	117.07	121.00
1	G	169	ASP	CB-CG-OD1	-6.55	112.40	118.30
1	D	332	MET	CG-SD-CE	-6.55	89.72	100.20
4	W	283	MET	CG-SD-CE	6.54	110.67	100.20
1	J	332	MET	CG-SD-CE	-6.54	89.73	100.20
4	4	283	MET	CG-SD-CE	6.54	110.67	100.20
4	6	283	MET	CG-SD-CE	6.54	110.67	100.20
4	Y	169	TYR	CB-CG-CD2	-6.54	117.08	121.00
4	5	283	MET	CG-SD-CE	6.54	110.66	100.20
4	W	196	ARG	NE-CZ-NH1	6.54	123.57	120.30
1	G	332	MET	CG-SD-CE	-6.54	89.74	100.20
4	X	283	MET	CG-SD-CE	6.53	110.65	100.20
4	3	169	TYR	CB-CG-CD2	-6.53	117.08	121.00
4	1	283	MET	CG-SD-CE	6.53	110.65	100.20
4	6	196	ARG	NE-CZ-NH1	6.53	123.56	120.30
4	8	169	TYR	CB-CG-CD2	-6.52	117.09	121.00
4	0	283	MET	CG-SD-CE	6.52	110.63	100.20
4	2	283	MET	CG-SD-CE	6.52	110.63	100.20
4	Z	169	TYR	CB-CG-CD2	-6.52	117.09	121.00
4	5	169	TYR	CB-CG-CD2	-6.52	117.09	121.00
4	8	283	MET	CG-SD-CE	6.52	110.63	100.20
1	J	141	LEU	CB-CA-C	-6.51	97.82	110.20
4	1	169	TYR	CB-CG-CD2	-6.51	117.09	121.00
4	3	283	MET	CG-SD-CE	6.51	110.62	100.20
4	7	283	MET	CG-SD-CE	6.51	110.62	100.20
4	Y	283	MET	CG-SD-CE	6.51	110.61	100.20
4	3	159	VAL	CB-CA-C	-6.51	99.04	111.40
4	8	196	ARG	NE-CZ-NH1	6.51	123.55	120.30
4	V	283	MET	CG-SD-CE	6.51	110.61	100.20
1	J	334	THR	CA-CB-CG2	-6.50	103.30	112.40
1	G	590	TYR	CB-CG-CD2	6.50	124.90	121.00
1	D	334	THR	CA-CB-CG2	-6.50	103.31	112.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	141	LEU	CB-CA-C	-6.50	97.86	110.20
4	V	196	ARG	NE-CZ-NH1	6.50	123.55	120.30
4	Z	159	VAL	CB-CA-C	-6.49	99.07	111.40
4	Z	283	MET	CG-SD-CE	6.49	110.59	100.20
1	A	169	ASP	CB-CG-OD1	-6.49	112.46	118.30
4	0	169	TYR	CB-CG-CD2	-6.49	117.11	121.00
2	E	141	PRO	N-CD-CG	-6.49	93.47	103.20
4	2	159	VAL	CB-CA-C	-6.49	99.08	111.40
4	V	159	VAL	CB-CA-C	-6.49	99.08	111.40
1	J	169	ASP	CB-CG-OD1	-6.48	112.47	118.30
4	5	159	VAL	CB-CA-C	-6.48	99.09	111.40
4	Y	196	ARG	NE-CZ-NH1	6.48	123.54	120.30
1	G	334	THR	CA-CB-CG2	-6.48	103.33	112.40
4	0	159	VAL	CB-CA-C	-6.48	99.09	111.40
4	1	159	VAL	CB-CA-C	-6.48	99.09	111.40
4	6	159	VAL	CB-CA-C	-6.47	99.10	111.40
4	8	159	VAL	CB-CA-C	-6.47	99.10	111.40
4	0	196	ARG	NE-CZ-NH1	6.47	123.54	120.30
4	7	196	ARG	NE-CZ-NH1	6.47	123.54	120.30
1	D	141	LEU	CB-CA-C	-6.47	97.91	110.20
2	H	141	PRO	N-CD-CG	-6.47	93.50	103.20
4	4	159	VAL	CB-CA-C	-6.47	99.11	111.40
4	X	159	VAL	CB-CA-C	-6.47	99.11	111.40
4	6	169	TYR	CB-CG-CD2	-6.46	117.12	121.00
4	W	159	VAL	CB-CA-C	-6.46	99.12	111.40
4	1	196	ARG	NE-CZ-NH1	6.46	123.53	120.30
4	Y	159	VAL	CB-CA-C	-6.46	99.13	111.40
1	D	169	ASP	CB-CG-OD1	-6.46	112.49	118.30
4	7	159	VAL	CB-CA-C	-6.46	99.13	111.40
4	W	169	TYR	CB-CG-CD2	-6.46	117.13	121.00
4	Z	196	ARG	NE-CZ-NH1	6.45	123.53	120.30
1	A	334	THR	CA-CB-CG2	-6.45	103.37	112.40
4	2	196	ARG	NE-CZ-NH1	6.44	123.52	120.30
1	A	141	LEU	CB-CA-C	-6.44	97.96	110.20
1	D	343	PHE	CB-CG-CD1	6.44	125.31	120.80
4	0	34	ILE	CA-CB-CG2	-6.44	98.03	110.90
1	G	589	ASP	CB-CG-OD1	-6.43	112.51	118.30
1	G	343	PHE	CB-CG-CD1	6.42	125.30	120.80
1	G	75	ASP	CB-CG-OD2	6.41	124.07	118.30
4	W	34	ILE	CA-CB-CG2	-6.41	98.07	110.90
1	J	589	ASP	CB-CG-OD1	-6.41	112.53	118.30
4	7	34	ILE	CA-CB-CG2	-6.41	98.08	110.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	6	34	ILE	CA-CB-CG2	-6.41	98.09	110.90
1	A	589	ASP	CB-CG-OD1	-6.41	112.54	118.30
4	4	34	ILE	CA-CB-CG2	-6.41	98.09	110.90
4	8	34	ILE	CA-CB-CG2	-6.41	98.09	110.90
4	X	34	ILE	CA-CB-CG2	-6.41	98.09	110.90
4	Z	34	ILE	CA-CB-CG2	-6.40	98.09	110.90
4	2	34	ILE	CA-CB-CG2	-6.40	98.10	110.90
4	3	34	ILE	CA-CB-CG2	-6.39	98.11	110.90
4	3	196	ARG	NE-CZ-NH1	6.39	123.50	120.30
4	1	34	ILE	CA-CB-CG2	-6.39	98.13	110.90
1	J	810	ARG	NE-CZ-NH1	6.38	123.49	120.30
4	4	196	ARG	NE-CZ-NH1	6.38	123.49	120.30
2	K	141	PRO	N-CD-CG	-6.37	93.64	103.20
4	5	34	ILE	CA-CB-CG2	-6.37	98.15	110.90
4	V	34	ILE	CA-CB-CG2	-6.37	98.15	110.90
1	D	129	TYR	CB-CG-CD2	-6.37	117.18	121.00
1	J	327	ASP	CB-CG-OD2	6.37	124.03	118.30
4	Y	34	ILE	CA-CB-CG2	-6.36	98.17	110.90
4	X	196	ARG	NE-CZ-NH1	6.36	123.48	120.30
2	B	141	PRO	N-CD-CG	-6.35	93.68	103.20
1	D	589	ASP	CB-CG-OD1	-6.35	112.59	118.30
1	G	578	HIS	N-CA-CB	6.33	122.00	110.60
1	J	129	TYR	CB-CG-CD2	-6.33	117.20	121.00
1	A	341	LEU	CB-CA-C	6.33	122.23	110.20
1	G	341	LEU	CB-CA-C	6.33	122.22	110.20
1	J	341	LEU	CB-CA-C	6.32	122.20	110.20
4	Z	217	CYS	CA-CB-SG	-6.31	102.64	114.00
1	J	779	ARG	NE-CZ-NH1	6.30	123.45	120.30
1	G	129	TYR	CB-CG-CD2	-6.30	117.22	121.00
4	3	217	CYS	CA-CB-SG	-6.30	102.67	114.00
4	7	217	CYS	CA-CB-SG	-6.30	102.67	114.00
1	A	578	HIS	N-CA-CB	6.29	121.93	110.60
4	5	217	CYS	CA-CB-SG	-6.29	102.67	114.00
4	2	217	CYS	CA-CB-SG	-6.29	102.67	114.00
4	4	217	CYS	CA-CB-SG	-6.29	102.68	114.00
4	0	217	CYS	CA-CB-SG	-6.28	102.69	114.00
4	Y	217	CYS	CA-CB-SG	-6.28	102.69	114.00
1	J	343	PHE	CB-CG-CD1	6.28	125.19	120.80
1	J	578	HIS	N-CA-CB	6.28	121.90	110.60
4	8	217	CYS	CA-CB-SG	-6.28	102.70	114.00
4	W	217	CYS	CA-CB-SG	-6.27	102.71	114.00
4	V	217	CYS	CA-CB-SG	-6.27	102.72	114.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	1	217	CYS	CA-CB-SG	-6.27	102.72	114.00
1	D	341	LEU	CB-CA-C	6.27	122.11	110.20
4	X	217	CYS	CA-CB-SG	-6.27	102.72	114.00
4	6	217	CYS	CA-CB-SG	-6.26	102.73	114.00
1	A	129	TYR	CB-CG-CD2	-6.25	117.25	121.00
1	D	578	HIS	N-CA-CB	6.24	121.83	110.60
1	J	760	PHE	CB-CG-CD2	-6.22	116.45	120.80
2	K	129	THR	CB-CA-C	-6.22	94.81	111.60
1	A	780	ASP	CB-CG-OD2	6.21	123.89	118.30
1	D	760	PHE	CB-CG-CD2	-6.21	116.45	120.80
1	A	463	ASP	CB-CG-OD2	-6.20	112.72	118.30
1	A	327	ASP	CB-CG-OD2	6.20	123.88	118.30
2	B	129	THR	CB-CA-C	-6.19	94.88	111.60
1	D	327	ASP	CB-CG-OD2	6.19	123.87	118.30
1	A	698	ASN	CB-CA-C	-6.19	98.02	110.40
2	H	129	THR	CB-CA-C	-6.19	94.89	111.60
1	J	214	MET	CG-SD-CE	6.18	110.10	100.20
2	E	129	THR	CB-CA-C	-6.17	94.94	111.60
1	D	214	MET	CG-SD-CE	6.17	110.07	100.20
2	K	141	PRO	N-CA-CB	-6.17	95.82	102.60
1	G	214	MET	CG-SD-CE	6.16	110.06	100.20
1	G	327	ASP	CB-CG-OD2	6.16	123.84	118.30
1	J	463	ASP	CB-CG-OD2	-6.16	112.76	118.30
2	H	141	PRO	N-CA-CB	-6.15	95.84	102.60
1	A	214	MET	CG-SD-CE	6.14	110.03	100.20
4	4	259	GLU	CA-CB-CG	6.14	126.92	113.40
1	D	590	TYR	CB-CG-CD2	6.14	124.69	121.00
3	F	58	MET	CG-SD-CE	6.14	110.02	100.20
4	X	259	GLU	CA-CB-CG	6.14	126.91	113.40
1	G	104	TYR	CB-CG-CD1	-6.13	117.32	121.00
4	1	259	GLU	CA-CB-CG	6.13	126.90	113.40
4	Y	259	GLU	CA-CB-CG	6.13	126.89	113.40
4	2	259	GLU	CA-CB-CG	6.13	126.89	113.40
4	3	259	GLU	CA-CB-CG	6.13	126.89	113.40
4	Z	259	GLU	CA-CB-CG	6.13	126.89	113.40
1	A	760	PHE	CB-CG-CD2	-6.13	116.51	120.80
1	D	698	ASN	CB-CA-C	-6.13	98.14	110.40
4	W	259	GLU	CA-CB-CG	6.13	126.88	113.40
4	V	259	GLU	CA-CB-CG	6.13	126.88	113.40
4	0	259	GLU	CA-CB-CG	6.12	126.87	113.40
2	E	129	THR	CA-CB-CG2	6.12	120.96	112.40
4	6	259	GLU	CA-CB-CG	6.12	126.86	113.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	590	TYR	CB-CG-CD2	6.12	124.67	121.00
1	D	104	TYR	CB-CG-CD1	-6.12	117.33	121.00
4	5	259	GLU	CA-CB-CG	6.12	126.85	113.40
2	E	141	PRO	N-CA-CB	-6.11	95.87	102.60
4	7	259	GLU	CA-CB-CG	6.11	126.85	113.40
4	8	259	GLU	CA-CB-CG	6.11	126.85	113.40
1	J	752	ASP	CB-CG-OD2	6.11	123.80	118.30
1	J	104	TYR	CB-CG-CD1	-6.11	117.33	121.00
1	J	698	ASN	CB-CA-C	-6.11	98.18	110.40
3	L	58	MET	CG-SD-CE	6.10	109.97	100.20
1	G	779	ARG	NE-CZ-NH1	6.10	123.35	120.30
4	5	335	ARG	NE-CZ-NH2	-6.10	117.25	120.30
1	G	810	ARG	NE-CZ-NH1	6.09	123.34	120.30
1	J	682	THR	CA-CB-CG2	-6.09	103.87	112.40
1	G	698	ASN	CB-CA-C	-6.09	98.23	110.40
1	G	346	ASP	CB-CG-OD1	6.08	123.78	118.30
4	W	349	LEU	CA-C-N	-6.08	103.82	117.20
1	G	463	ASP	CB-CG-OD2	-6.08	112.83	118.30
1	G	625	THR	CA-CB-OG1	6.07	121.75	109.00
1	D	346	ASP	CB-CG-OD1	6.07	123.76	118.30
2	H	129	THR	CA-CB-CG2	6.07	120.89	112.40
4	3	349	LEU	CA-C-N	-6.07	103.86	117.20
3	I	58	MET	CG-SD-CE	6.06	109.90	100.20
4	2	349	LEU	CA-C-N	-6.06	103.87	117.20
2	B	141	PRO	N-CA-CB	-6.06	95.94	102.60
1	G	682	THR	CA-CB-CG2	-6.06	103.92	112.40
1	J	625	THR	CA-CB-OG1	6.06	121.72	109.00
1	J	590	TYR	CB-CG-CD2	6.05	124.63	121.00
4	0	349	LEU	CA-C-N	-6.05	103.89	117.20
4	7	16	LEU	CA-CB-CG	6.05	129.21	115.30
1	D	810	ARG	NE-CZ-NH1	6.05	123.32	120.30
4	0	16	LEU	CA-CB-CG	6.05	129.21	115.30
4	4	349	LEU	CA-C-N	-6.05	103.89	117.20
4	4	16	LEU	CA-CB-CG	6.05	129.21	115.30
4	V	16	LEU	CA-CB-CG	6.05	129.21	115.30
3	C	58	MET	CG-SD-CE	6.04	109.87	100.20
4	2	16	LEU	CA-CB-CG	6.04	129.20	115.30
1	D	463	ASP	CB-CG-OD2	-6.04	112.86	118.30
1	J	450	ASP	CB-CG-OD1	-6.04	112.86	118.30
4	Y	349	LEU	CA-C-N	-6.04	103.90	117.20
2	K	129	THR	CA-CB-CG2	6.04	120.86	112.40
4	1	349	LEU	CA-C-N	-6.04	103.91	117.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	6	349	LEU	CA-C-N	-6.04	103.91	117.20
4	5	16	LEU	CA-CB-CG	6.04	129.19	115.30
4	8	16	LEU	CA-CB-CG	6.04	129.19	115.30
4	X	16	LEU	CA-CB-CG	6.04	129.19	115.30
4	Y	16	LEU	CA-CB-CG	6.04	129.18	115.30
4	3	16	LEU	CA-CB-CG	6.03	129.17	115.30
4	8	349	LEU	CA-C-N	-6.03	103.93	117.20
4	W	16	LEU	CA-CB-CG	6.03	129.17	115.30
1	J	192	VAL	CA-CB-CG1	-6.03	101.85	110.90
4	1	16	LEU	CA-CB-CG	6.03	129.17	115.30
1	G	760	PHE	CB-CG-CD2	-6.03	116.58	120.80
4	5	349	LEU	CA-C-N	-6.03	103.94	117.20
4	6	16	LEU	CA-CB-CG	6.03	129.16	115.30
4	Z	349	LEU	CA-C-N	-6.03	103.94	117.20
4	Z	16	LEU	CA-CB-CG	6.02	129.16	115.30
1	A	682	THR	CA-CB-CG2	-6.02	103.97	112.40
1	J	665	ARG	NE-CZ-NH2	-6.02	117.29	120.30
4	7	349	LEU	CA-C-N	-6.02	103.95	117.20
1	A	779	ARG	NE-CZ-NH1	6.02	123.31	120.30
2	B	129	THR	CA-CB-CG2	6.02	120.82	112.40
1	D	378	ASP	CB-CG-OD1	-6.01	112.89	118.30
4	6	335	ARG	NE-CZ-NH2	-6.01	117.29	120.30
4	X	349	LEU	CA-C-N	-6.01	103.97	117.20
1	A	625	THR	CA-CB-OG1	6.01	121.62	109.00
1	D	192	VAL	CA-CB-CG1	-6.01	101.89	110.90
1	D	447	GLN	N-CA-CB	6.01	121.42	110.60
1	D	682	THR	CA-CB-CG2	-6.01	103.99	112.40
4	V	349	LEU	CA-C-N	-6.01	103.98	117.20
1	A	810	ARG	NE-CZ-NH1	6.01	123.30	120.30
1	A	447	GLN	N-CA-CB	6.00	121.41	110.60
1	G	447	GLN	N-CA-CB	6.00	121.41	110.60
1	D	625	THR	CA-CB-OG1	6.00	121.59	109.00
1	G	192	VAL	CA-CB-CG1	-5.99	101.91	110.90
1	J	447	GLN	N-CA-CB	5.99	121.38	110.60
4	Z	116	ARG	NE-CZ-NH1	5.99	123.30	120.30
4	6	116	ARG	NE-CZ-NH1	5.99	123.29	120.30
4	1	79	TRP	CG-CD2-CE3	5.98	139.28	133.90
1	D	450	ASP	CB-CG-OD1	-5.98	112.92	118.30
1	D	780	ASP	CB-CG-OD2	5.97	123.67	118.30
1	G	780	ASP	CB-CG-OD2	5.96	123.67	118.30
1	D	754	ASP	CB-CG-OD2	-5.96	112.94	118.30
1	G	752	ASP	CB-CG-OD2	5.96	123.66	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	V	116	ARG	NE-CZ-NH1	5.96	123.28	120.30
4	X	79	TRP	CG-CD2-CE3	5.95	139.26	133.90
1	G	378	ASP	CB-CG-OD1	-5.95	112.94	118.30
4	Z	335	ARG	NE-CZ-NH2	-5.95	117.33	120.30
4	3	335	ARG	NE-CZ-NH2	-5.94	117.33	120.30
1	A	665	ARG	NE-CZ-NH2	-5.94	117.33	120.30
1	J	378	ASP	CB-CG-OD1	-5.94	112.95	118.30
1	G	754	ASP	CB-CG-OD2	-5.94	112.96	118.30
4	Y	335	ARG	NE-CZ-NH2	-5.93	117.33	120.30
1	A	192	VAL	CA-CB-CG1	-5.93	102.00	110.90
4	3	116	ARG	NE-CZ-NH1	5.93	123.27	120.30
4	4	335	ARG	NE-CZ-NH2	-5.93	117.33	120.30
1	D	556	ASP	CB-CG-OD1	-5.93	112.97	118.30
4	8	79	TRP	CG-CD2-CE3	5.92	139.23	133.90
1	A	815	CYS	CA-CB-SG	-5.92	103.34	114.00
1	A	104	TYR	CB-CG-CD1	-5.92	117.45	121.00
1	D	665	ARG	NE-CZ-NH2	-5.92	117.34	120.30
1	G	450	ASP	CB-CG-OD1	-5.91	112.98	118.30
1	J	780	ASP	CB-CG-OD2	5.91	123.62	118.30
4	V	335	ARG	NE-CZ-NH2	-5.91	117.35	120.30
4	W	335	ARG	NE-CZ-NH2	-5.91	117.34	120.30
1	D	339	ASP	CB-CG-OD2	5.90	123.61	118.30
1	G	665	ARG	NE-CZ-NH2	-5.90	117.35	120.30
4	5	254	ARG	NE-CZ-NH1	5.90	123.25	120.30
4	5	116	ARG	NE-CZ-NH1	5.90	123.25	120.30
1	D	471	ASP	CB-CG-OD1	-5.89	113.00	118.30
4	X	335	ARG	NE-CZ-NH2	-5.89	117.36	120.30
1	G	339	ASP	CB-CG-OD2	5.89	123.60	118.30
1	J	754	ASP	CB-CG-OD2	-5.88	113.00	118.30
4	1	200	PHE	CA-C-N	-5.88	104.25	117.20
4	5	200	PHE	CA-C-N	-5.88	104.26	117.20
1	D	779	ARG	NE-CZ-NH1	5.88	123.24	120.30
4	4	200	PHE	CA-C-N	-5.88	104.26	117.20
4	7	200	PHE	CA-C-N	-5.88	104.26	117.20
4	X	200	PHE	CA-C-N	-5.88	104.26	117.20
4	5	79	TRP	CG-CD2-CE3	5.88	139.19	133.90
4	W	116	ARG	NE-CZ-NH1	5.88	123.24	120.30
4	6	200	PHE	CA-C-N	-5.88	104.28	117.20
4	W	200	PHE	CA-C-N	-5.88	104.28	117.20
1	A	450	ASP	CB-CG-OD1	-5.87	113.02	118.30
1	A	752	ASP	CB-CG-OD2	5.87	123.58	118.30
4	Y	200	PHE	CA-C-N	-5.87	104.29	117.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	738	MET	CG-SD-CE	5.86	109.58	100.20
1	J	471	ASP	CB-CG-OD1	-5.86	113.02	118.30
4	8	116	ARG	NE-CZ-NH1	5.86	123.23	120.30
1	A	754	ASP	CB-CG-OD2	-5.86	113.03	118.30
1	G	738	MET	CG-SD-CE	5.86	109.58	100.20
4	0	79	TRP	CG-CD2-CE3	5.86	139.17	133.90
4	3	200	PHE	CA-C-N	-5.86	104.31	117.20
1	G	809	ARG	NE-CZ-NH2	-5.86	117.37	120.30
4	8	254	ARG	NE-CZ-NH1	5.86	123.23	120.30
4	2	335	ARG	NE-CZ-NH2	-5.86	117.37	120.30
1	D	738	MET	CG-SD-CE	5.86	109.57	100.20
1	J	738	MET	CG-SD-CE	5.86	109.57	100.20
4	2	200	PHE	CA-C-N	-5.85	104.32	117.20
1	A	378	ASP	CB-CG-OD1	-5.85	113.03	118.30
4	0	200	PHE	CA-C-N	-5.85	104.33	117.20
4	V	200	PHE	CA-C-N	-5.85	104.33	117.20
4	Z	200	PHE	CA-C-N	-5.85	104.33	117.20
1	J	346	ASP	CB-CG-OD1	5.85	123.56	118.30
4	2	116	ARG	NE-CZ-NH1	5.84	123.22	120.30
1	G	780	ASP	CB-CG-OD1	-5.84	113.04	118.30
1	D	752	ASP	CB-CG-OD2	5.84	123.56	118.30
1	J	556	ASP	CB-CG-OD1	-5.84	113.04	118.30
4	8	200	PHE	CA-C-N	-5.84	104.36	117.20
4	4	79	TRP	CG-CD2-CE3	5.83	139.15	133.90
4	V	254	ARG	NE-CZ-NH1	5.83	123.21	120.30
1	J	815	CYS	CA-CB-SG	-5.83	103.51	114.00
4	2	79	TRP	CG-CD2-CE3	5.82	139.14	133.90
4	Y	116	ARG	NE-CZ-NH1	5.82	123.21	120.30
4	Y	254	ARG	NE-CZ-NH1	5.82	123.21	120.30
4	8	95	ARG	CA-CB-CG	5.82	126.20	113.40
1	D	809	ARG	NE-CZ-NH2	-5.82	117.39	120.30
4	6	79	TRP	CG-CD2-CE3	5.82	139.13	133.90
4	Z	79	TRP	CG-CD2-CE3	5.82	139.13	133.90
4	1	335	ARG	NE-CZ-NH2	-5.82	117.39	120.30
1	G	471	ASP	CB-CG-OD1	-5.81	113.07	118.30
4	1	95	ARG	CA-CB-CG	5.81	126.19	113.40
1	A	780	ASP	CB-CG-OD1	-5.81	113.07	118.30
4	V	95	ARG	CA-CB-CG	5.81	126.18	113.40
4	Z	95	ARG	CA-CB-CG	5.81	126.17	113.40
4	3	79	TRP	CG-CD2-CE3	5.80	139.12	133.90
4	7	95	ARG	CA-CB-CG	5.80	126.16	113.40
4	X	95	ARG	CA-CB-CG	5.80	126.16	113.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	Y	79	TRP	CG-CD2-CE3	5.80	139.12	133.90
4	4	254	ARG	NE-CZ-NH1	5.80	123.20	120.30
1	D	815	CYS	CA-CB-SG	-5.79	103.57	114.00
4	1	254	ARG	NE-CZ-NH1	5.79	123.20	120.30
4	W	79	TRP	CG-CD2-CE3	5.79	139.11	133.90
4	8	335	ARG	NE-CZ-NH2	-5.79	117.41	120.30
1	A	346	ASP	CB-CG-OD1	5.79	123.51	118.30
4	7	79	TRP	CG-CD2-CE3	5.79	139.11	133.90
1	G	556	ASP	CB-CG-OD1	-5.78	113.09	118.30
4	4	95	ARG	CA-CB-CG	5.78	126.12	113.40
4	6	95	ARG	CA-CB-CG	5.78	126.12	113.40
4	Y	95	ARG	CA-CB-CG	5.78	126.12	113.40
1	A	4	ASP	CB-CG-OD2	5.78	123.50	118.30
1	J	339	ASP	CB-CG-OD2	5.78	123.50	118.30
1	J	809	ARG	NE-CZ-NH2	-5.78	117.41	120.30
4	0	95	ARG	CA-CB-CG	5.78	126.11	113.40
1	A	556	ASP	CB-CG-OD1	-5.77	113.10	118.30
1	A	471	ASP	CB-CG-OD1	-5.77	113.11	118.30
4	0	254	ARG	NE-CZ-NH1	5.77	123.19	120.30
4	0	335	ARG	NE-CZ-NH2	-5.77	117.42	120.30
4	2	95	ARG	CA-CB-CG	5.77	126.09	113.40
4	W	95	ARG	CA-CB-CG	5.77	126.09	113.40
4	7	335	ARG	NE-CZ-NH2	-5.76	117.42	120.30
4	V	79	TRP	CG-CD2-CE3	5.76	139.09	133.90
4	Z	254	ARG	NE-CZ-NH1	5.76	123.18	120.30
4	0	116	ARG	NE-CZ-NH1	5.76	123.18	120.30
4	5	95	ARG	CA-CB-CG	5.76	126.07	113.40
4	1	116	ARG	NE-CZ-NH1	5.76	123.18	120.30
4	3	95	ARG	CA-CB-CG	5.75	126.06	113.40
1	D	352	TYR	N-CA-CB	5.75	120.94	110.60
1	A	809	ARG	NE-CZ-NH2	-5.74	117.43	120.30
1	D	781	ASP	CB-CG-OD2	5.74	123.47	118.30
2	B	149	ASP	N-CA-CB	5.74	120.93	110.60
1	D	4	ASP	CB-CG-OD2	5.74	123.46	118.30
1	A	339	ASP	CB-CG-OD2	5.73	123.46	118.30
2	H	149	ASP	N-CA-CB	5.73	120.91	110.60
1	J	165	PHE	N-CA-CB	-5.73	100.29	110.60
4	W	254	ARG	NE-CZ-NH1	5.73	123.16	120.30
2	K	149	ASP	N-CA-CB	5.72	120.90	110.60
4	0	335	ARG	CA-CB-CG	5.72	125.99	113.40
4	X	254	ARG	NE-CZ-NH1	5.72	123.16	120.30
1	A	165	PHE	N-CA-CB	-5.72	100.31	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	6	254	ARG	NE-CZ-NH1	5.72	123.16	120.30
1	G	815	CYS	CA-CB-SG	-5.72	103.71	114.00
4	7	335	ARG	CA-CB-CG	5.72	125.98	113.40
4	V	335	ARG	CA-CB-CG	5.72	125.98	113.40
1	J	4	ASP	CB-CG-OD2	5.71	123.44	118.30
4	1	335	ARG	CA-CB-CG	5.71	125.96	113.40
4	2	335	ARG	CA-CB-CG	5.71	125.96	113.40
1	G	4	ASP	CB-CG-OD2	5.71	123.44	118.30
4	5	335	ARG	CA-CB-CG	5.71	125.95	113.40
4	7	254	ARG	NE-CZ-NH1	5.71	123.15	120.30
4	3	335	ARG	CA-CB-CG	5.71	125.95	113.40
4	4	335	ARG	CA-CB-CG	5.70	125.94	113.40
4	X	335	ARG	CA-CB-CG	5.70	125.94	113.40
1	G	165	PHE	N-CA-CB	-5.70	100.35	110.60
4	6	335	ARG	CA-CB-CG	5.70	125.93	113.40
4	8	335	ARG	CA-CB-CG	5.70	125.93	113.40
4	W	335	ARG	CA-CB-CG	5.69	125.92	113.40
4	4	116	ARG	NE-CZ-NH1	5.68	123.14	120.30
4	Z	335	ARG	CA-CB-CG	5.68	125.90	113.40
4	Y	335	ARG	CA-CB-CG	5.68	125.89	113.40
4	2	254	ARG	NE-CZ-NH1	5.67	123.14	120.30
1	D	780	ASP	CB-CG-OD1	-5.67	113.20	118.30
1	G	352	TYR	N-CA-CB	5.66	120.79	110.60
1	D	165	PHE	N-CA-CB	-5.66	100.42	110.60
2	E	149	ASP	N-CA-CB	5.65	120.77	110.60
1	G	693	HIS	CA-CB-CG	-5.63	104.02	113.60
4	7	116	ARG	NE-CZ-NH1	5.63	123.11	120.30
4	Z	294	TYR	CB-CG-CD2	-5.63	117.62	121.00
4	X	294	TYR	CB-CG-CD2	-5.62	117.63	121.00
4	X	116	ARG	NE-CZ-NH1	5.62	123.11	120.30
1	J	693	HIS	CA-CB-CG	-5.62	104.05	113.60
4	3	113	LYS	CA-CB-CG	5.62	125.76	113.40
1	G	785	GLU	O-C-N	5.62	131.69	122.70
1	J	780	ASP	CB-CG-OD1	-5.61	113.25	118.30
1	A	781	ASP	CB-CG-OD2	5.61	123.35	118.30
1	J	352	TYR	N-CA-CB	5.61	120.69	110.60
4	0	113	LYS	CA-CB-CG	5.61	125.74	113.40
4	3	356	TRP	CG-CD2-CE3	5.61	138.95	133.90
4	8	356	TRP	CG-CD2-CE3	5.61	138.94	133.90
1	A	352	TYR	N-CA-CB	5.60	120.68	110.60
1	D	693	HIS	CA-CB-CG	-5.60	104.08	113.60
4	5	113	LYS	CA-CB-CG	5.59	125.71	113.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	2	113	LYS	CA-CB-CG	5.59	125.70	113.40
4	5	356	TRP	CG-CD2-CE3	5.59	138.93	133.90
4	5	294	TYR	CB-CG-CD2	-5.59	117.65	121.00
4	V	113	LYS	CA-CB-CG	5.59	125.69	113.40
4	2	356	TRP	CG-CD2-CE3	5.59	138.93	133.90
4	8	113	LYS	CA-CB-CG	5.58	125.69	113.40
4	X	113	LYS	CA-CB-CG	5.58	125.68	113.40
4	1	113	LYS	CA-CB-CG	5.58	125.68	113.40
4	6	294	TYR	CB-CG-CD2	-5.58	117.65	121.00
1	G	320	ILE	CB-CA-C	-5.57	100.45	111.60
4	Y	294	TYR	CB-CG-CD2	-5.57	117.66	121.00
4	Z	113	LYS	CA-CB-CG	5.57	125.66	113.40
4	Y	356	TRP	CG-CD2-CE3	5.57	138.91	133.90
4	1	279	TYR	CB-CG-CD2	-5.57	117.66	121.00
4	W	356	TRP	CG-CD2-CE3	5.57	138.91	133.90
4	7	294	TYR	CB-CG-CD2	-5.57	117.66	121.00
4	8	279	TYR	CB-CG-CD2	-5.57	117.66	121.00
4	W	113	LYS	CA-CB-CG	5.57	125.65	113.40
1	J	33	ASP	CB-CG-OD2	5.57	123.31	118.30
1	G	781	ASP	CB-CG-OD2	5.56	123.31	118.30
4	0	11	ASP	CB-CG-OD1	5.56	123.31	118.30
4	4	294	TYR	CB-CG-CD2	-5.56	117.66	121.00
4	6	113	LYS	CA-CB-CG	5.56	125.63	113.40
4	7	113	LYS	CA-CB-CG	5.56	125.63	113.40
4	Y	113	LYS	CA-CB-CG	5.56	125.63	113.40
4	W	294	TYR	CB-CG-CD2	-5.55	117.67	121.00
1	J	686	MET	N-CA-CB	-5.55	100.61	110.60
1	J	384	ASP	CB-CG-OD1	-5.55	113.30	118.30
4	0	254	ARG	N-CA-CB	-5.55	100.61	110.60
4	6	356	TRP	CG-CD2-CE3	5.55	138.89	133.90
4	4	113	LYS	CA-CB-CG	5.55	125.61	113.40
4	7	254	ARG	N-CA-CB	-5.55	100.61	110.60
1	J	781	ASP	CB-CG-OD2	5.55	123.29	118.30
4	3	254	ARG	N-CA-CB	-5.55	100.62	110.60
1	D	384	ASP	CB-CG-OD1	-5.54	113.31	118.30
1	G	686	MET	N-CA-CB	-5.54	100.62	110.60
4	0	356	TRP	CG-CD2-CE3	5.54	138.89	133.90
4	Y	279	TYR	CB-CG-CD2	-5.54	117.67	121.00
4	Z	254	ARG	N-CA-CB	-5.54	100.62	110.60
1	D	686	MET	N-CA-CB	-5.54	100.63	110.60
1	A	693	HIS	CA-CB-CG	-5.54	104.19	113.60
4	3	279	TYR	CB-CG-CD2	-5.54	117.68	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	0	294	TYR	CB-CG-CD2	-5.54	117.68	121.00
1	D	752	ASP	CB-CA-C	5.54	121.47	110.40
4	V	294	TYR	CB-CG-CD2	-5.54	117.68	121.00
4	W	254	ARG	N-CA-CB	-5.54	100.64	110.60
4	7	279	TYR	CB-CG-CD2	-5.53	117.68	121.00
4	6	254	ARG	N-CA-CB	-5.53	100.65	110.60
1	D	306	THR	CA-CB-CG2	-5.53	104.66	112.40
4	4	254	ARG	N-CA-CB	-5.53	100.65	110.60
1	G	306	THR	CA-CB-CG2	-5.53	104.67	112.40
4	3	294	TYR	CB-CG-CD2	-5.53	117.69	121.00
4	5	254	ARG	N-CA-CB	-5.53	100.66	110.60
4	8	254	ARG	N-CA-CB	-5.52	100.66	110.60
4	8	11	ASP	CB-CG-OD1	5.52	123.27	118.30
4	4	279	TYR	CB-CG-CD2	-5.52	117.69	121.00
4	1	294	TYR	CB-CG-CD2	-5.52	117.69	121.00
4	X	254	ARG	N-CA-CB	-5.52	100.66	110.60
4	1	254	ARG	N-CA-CB	-5.52	100.67	110.60
4	Y	254	ARG	N-CA-CB	-5.52	100.67	110.60
4	2	254	ARG	N-CA-CB	-5.51	100.67	110.60
4	V	254	ARG	N-CA-CB	-5.51	100.67	110.60
1	J	343	PHE	CB-CG-CD2	-5.51	116.94	120.80
1	J	752	ASP	CB-CA-C	5.51	121.42	110.40
1	A	752	ASP	CB-CA-C	5.51	121.41	110.40
4	7	356	TRP	CG-CD2-CE3	5.51	138.86	133.90
1	A	686	MET	N-CA-CB	-5.50	100.69	110.60
4	4	11	ASP	CB-CG-OD1	5.50	123.25	118.30
1	G	752	ASP	CB-CA-C	5.50	121.40	110.40
4	2	294	TYR	CB-CG-CD2	-5.50	117.70	121.00
4	V	11	ASP	CB-CG-OD1	5.49	123.24	118.30
4	4	356	TRP	CG-CD2-CE3	5.49	138.84	133.90
4	6	147	ARG	NE-CZ-NH2	-5.49	117.56	120.30
4	6	279	TYR	CB-CG-CD2	-5.49	117.71	121.00
4	Z	279	TYR	CB-CG-CD2	-5.49	117.71	121.00
4	3	254	ARG	NE-CZ-NH1	5.49	123.04	120.30
1	J	320	ILE	CB-CA-C	-5.48	100.63	111.60
1	D	723	ARG	NE-CZ-NH1	5.48	123.04	120.30
4	0	279	TYR	CB-CG-CD2	-5.48	117.71	121.00
4	1	356	TRP	CG-CD2-CE3	5.48	138.83	133.90
4	2	79	TRP	CB-CG-CD1	-5.48	119.88	127.00
4	3	11	ASP	CB-CG-OD1	5.48	123.23	118.30
4	8	294	TYR	CB-CG-CD2	-5.48	117.71	121.00
4	Z	11	ASP	CB-CG-OD1	5.48	123.23	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	33	ASP	CB-CG-OD2	5.48	123.23	118.30
1	A	33	ASP	CB-CG-OD2	5.47	123.22	118.30
4	X	279	TYR	CB-CG-CD2	-5.47	117.72	121.00
1	A	241	ASP	CB-CG-OD2	5.47	123.22	118.30
4	5	11	ASP	CB-CG-OD1	5.47	123.22	118.30
4	Y	11	ASP	CB-CG-OD1	5.47	123.22	118.30
4	W	11	ASP	CB-CG-OD1	5.47	123.22	118.30
4	X	356	TRP	CG-CD2-CE3	5.47	138.82	133.90
4	Z	356	TRP	CG-CD2-CE3	5.47	138.82	133.90
1	D	320	ILE	CB-CA-C	-5.46	100.68	111.60
4	V	279	TYR	CB-CG-CD2	-5.46	117.72	121.00
4	2	279	TYR	CB-CG-CD2	-5.46	117.73	121.00
4	W	356	TRP	CB-CG-CD1	-5.46	119.91	127.00
1	A	306	THR	CA-CB-CG2	-5.45	104.77	112.40
4	V	356	TRP	CG-CD2-CE3	5.45	138.81	133.90
1	A	320	ILE	CB-CA-C	-5.45	100.70	111.60
4	7	79	TRP	CB-CG-CD1	-5.45	119.92	127.00
1	J	547	ASP	CB-CG-OD2	5.45	123.20	118.30
4	2	147	ARG	NE-CZ-NH2	-5.44	117.58	120.30
1	D	326	ASP	CB-CG-OD2	5.44	123.20	118.30
4	2	11	ASP	CB-CG-OD1	5.44	123.20	118.30
4	4	356	TRP	CB-CG-CD1	-5.44	119.93	127.00
4	5	279	TYR	CB-CG-CD2	-5.44	117.74	121.00
4	W	279	TYR	CB-CG-CD2	-5.44	117.74	121.00
1	J	326	ASP	CB-CG-OD2	5.43	123.19	118.30
4	X	335	ARG	NE-CZ-NH1	5.43	123.02	120.30
1	D	547	ASP	CB-CG-OD2	5.43	123.19	118.30
1	J	306	THR	CA-CB-CG2	-5.43	104.80	112.40
4	4	356	TRP	CG-CD1-NE1	-5.43	104.67	110.10
1	A	343	PHE	CB-CG-CD2	-5.43	117.00	120.80
4	1	79	TRP	CB-CG-CD1	-5.43	119.94	127.00
4	3	79	TRP	CB-CG-CD1	-5.43	119.94	127.00
1	J	218	LEU	O-C-N	5.43	131.38	122.70
4	6	356	TRP	CB-CG-CD1	-5.43	119.95	127.00
4	W	356	TRP	CG-CD1-NE1	-5.43	104.67	110.10
4	W	147	ARG	NE-CZ-NH2	-5.42	117.59	120.30
4	7	11	ASP	CB-CG-OD1	5.42	123.18	118.30
4	1	11	ASP	CB-CG-OD1	5.42	123.18	118.30
4	3	356	TRP	CB-CG-CD1	-5.42	119.95	127.00
1	A	723	ARG	NE-CZ-NH1	5.42	123.01	120.30
4	2	356	TRP	CB-CG-CD1	-5.42	119.96	127.00
4	7	356	TRP	CB-CG-CD1	-5.42	119.96	127.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	2	356	TRP	CG-CD1-NE1	-5.42	104.69	110.10
4	Z	356	TRP	CB-CG-CD1	-5.42	119.96	127.00
4	8	356	TRP	CG-CD1-NE1	-5.41	104.69	110.10
4	Z	79	TRP	CB-CG-CD1	-5.41	119.96	127.00
4	4	79	TRP	CB-CG-CD1	-5.41	119.97	127.00
4	5	79	TRP	CB-CG-CD1	-5.41	119.97	127.00
4	6	356	TRP	CG-CD1-NE1	-5.41	104.69	110.10
4	V	79	TRP	CB-CG-CD1	-5.41	119.97	127.00
4	Y	356	TRP	CG-CD1-NE1	-5.41	104.69	110.10
4	W	79	TRP	CB-CG-CD1	-5.41	119.97	127.00
4	Y	356	TRP	CB-CG-CD1	-5.41	119.97	127.00
1	A	326	ASP	CB-CG-OD2	5.40	123.16	118.30
4	6	11	ASP	CB-CG-OD1	5.40	123.16	118.30
4	V	356	TRP	CB-CG-CD1	-5.40	119.98	127.00
4	X	11	ASP	CB-CG-OD1	5.40	123.16	118.30
4	X	79	TRP	CB-CG-CD1	-5.40	119.98	127.00
4	1	356	TRP	CB-CG-CD1	-5.40	119.98	127.00
4	Y	79	TRP	CB-CG-CD1	-5.40	119.98	127.00
1	A	601	ASP	CB-CG-OD2	5.39	123.16	118.30
4	6	79	TRP	CB-CG-CD1	-5.39	119.99	127.00
4	6	335	ARG	NE-CZ-NH1	5.39	123.00	120.30
4	X	356	TRP	CB-CG-CD1	-5.39	120.00	127.00
1	G	33	ASP	CB-CG-OD2	5.39	123.15	118.30
4	0	79	TRP	CB-CG-CD1	-5.39	120.00	127.00
4	5	335	ARG	NE-CZ-NH1	5.39	122.99	120.30
1	A	384	ASP	CB-CG-OD1	-5.38	113.45	118.30
4	0	356	TRP	CB-CG-CD1	-5.38	120.00	127.00
4	5	356	TRP	CB-CG-CD1	-5.38	120.00	127.00
4	8	356	TRP	CB-CG-CD1	-5.38	120.00	127.00
1	A	686	MET	CG-SD-CE	-5.38	91.60	100.20
4	1	356	TRP	CG-CD1-NE1	-5.38	104.72	110.10
4	5	356	TRP	CG-CD1-NE1	-5.38	104.72	110.10
4	5	251	GLY	CA-C-N	-5.38	105.38	117.20
1	J	241	ASP	CB-CG-OD2	5.37	123.14	118.30
4	V	251	GLY	CA-C-N	-5.37	105.38	117.20
4	Z	356	TRP	CG-CD1-NE1	-5.37	104.73	110.10
4	X	251	GLY	CA-C-N	-5.37	105.40	117.20
1	G	686	MET	CG-SD-CE	-5.36	91.62	100.20
1	G	218	LEU	O-C-N	5.36	131.28	122.70
4	Z	147	ARG	NE-CZ-NH2	-5.36	117.62	120.30
1	J	686	MET	CG-SD-CE	-5.36	91.63	100.20
4	8	79	TRP	CB-CG-CD1	-5.36	120.04	127.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	0	356	TRP	CG-CD1-NE1	-5.35	104.75	110.10
4	7	356	TRP	CG-CD1-NE1	-5.35	104.75	110.10
4	V	147	ARG	NE-CZ-NH2	-5.35	117.62	120.30
4	4	251	GLY	CA-C-N	-5.35	105.43	117.20
1	G	326	ASP	CB-CG-OD2	5.35	123.11	118.30
2	K	136	MET	CG-SD-CE	5.35	108.76	100.20
4	0	251	GLY	CA-C-N	-5.35	105.43	117.20
4	2	251	GLY	CA-C-N	-5.35	105.43	117.20
4	X	356	TRP	CG-CD1-NE1	-5.35	104.75	110.10
4	3	251	GLY	CA-C-N	-5.35	105.44	117.20
4	7	251	GLY	CA-C-N	-5.35	105.44	117.20
1	G	800	ARG	NH1-CZ-NH2	5.34	125.28	119.40
2	B	136	MET	CG-SD-CE	5.34	108.75	100.20
1	D	601	ASP	CB-CG-OD2	5.34	123.11	118.30
4	5	147	ARG	NE-CZ-NH2	-5.34	117.63	120.30
4	W	251	GLY	CA-C-N	-5.34	105.46	117.20
4	4	335	ARG	NE-CZ-NH1	5.34	122.97	120.30
4	7	147	ARG	NE-CZ-NH2	-5.34	117.63	120.30
4	8	251	GLY	CA-C-N	-5.34	105.46	117.20
1	D	241	ASP	CB-CG-OD2	5.33	123.10	118.30
1	D	800	ARG	NH1-CZ-NH2	5.33	125.27	119.40
4	6	251	GLY	CA-C-N	-5.33	105.47	117.20
4	1	251	GLY	CA-C-N	-5.33	105.47	117.20
1	J	601	ASP	CB-CG-OD2	5.33	123.09	118.30
1	J	723	ARG	NE-CZ-NH1	5.33	122.96	120.30
4	W	176	MET	CG-SD-CE	5.33	108.72	100.20
4	Z	251	GLY	CA-C-N	-5.33	105.48	117.20
1	G	241	ASP	CB-CG-OD2	5.32	123.09	118.30
4	Y	251	GLY	CA-C-N	-5.32	105.49	117.20
1	A	125	THR	CA-CB-CG2	-5.32	104.95	112.40
1	G	125	THR	CA-CB-CG2	-5.32	104.95	112.40
1	G	601	ASP	CB-CG-OD2	5.32	123.09	118.30
4	6	176	MET	CG-SD-CE	5.32	108.71	100.20
4	6	337	TYR	CB-CG-CD1	-5.32	117.81	121.00
4	Y	147	ARG	NE-CZ-NH2	-5.32	117.64	120.30
4	V	356	TRP	CG-CD1-NE1	-5.31	104.79	110.10
4	Z	176	MET	CG-SD-CE	5.31	108.70	100.20
4	4	176	MET	CG-SD-CE	5.31	108.70	100.20
1	D	343	PHE	CB-CG-CD2	-5.31	117.08	120.80
4	V	176	MET	CG-SD-CE	5.31	108.69	100.20
4	X	176	MET	CG-SD-CE	5.31	108.69	100.20
1	D	354	LEU	CB-CG-CD2	-5.30	101.98	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	660	LEU	CB-CG-CD2	5.30	120.02	111.00
4	3	356	TRP	CG-CD1-NE1	-5.30	104.80	110.10
4	3	147	ARG	NE-CZ-NH2	-5.30	117.65	120.30
1	A	660	LEU	CB-CG-CD2	5.30	120.01	111.00
1	G	723	ARG	NE-CZ-NH1	5.30	122.95	120.30
4	2	176	MET	CG-SD-CE	5.30	108.67	100.20
4	7	176	MET	CG-SD-CE	5.30	108.67	100.20
1	D	760	PHE	CB-CG-CD1	5.29	124.50	120.80
4	3	176	MET	CG-SD-CE	5.29	108.67	100.20
4	4	147	ARG	NE-CZ-NH2	-5.29	117.65	120.30
1	G	384	ASP	CB-CG-OD1	-5.29	113.54	118.30
4	Y	176	MET	CG-SD-CE	5.29	108.66	100.20
4	1	176	MET	CG-SD-CE	5.29	108.66	100.20
2	E	136	MET	CG-SD-CE	5.29	108.66	100.20
1	J	170	ARG	NE-CZ-NH1	5.29	122.94	120.30
4	0	176	MET	CG-SD-CE	5.28	108.65	100.20
4	X	147	ARG	NE-CZ-NH2	-5.28	117.66	120.30
1	D	125	THR	CA-CB-CG2	-5.28	105.01	112.40
1	D	660	LEU	CB-CG-CD2	5.28	119.97	111.00
2	H	136	MET	CG-SD-CE	5.28	108.65	100.20
1	J	125	THR	CA-CB-CG2	-5.28	105.01	112.40
1	A	354	LEU	CB-CG-CD2	-5.28	102.03	111.00
1	J	800	ARG	NH1-CZ-NH2	5.28	125.20	119.40
4	0	147	ARG	NE-CZ-NH2	-5.27	117.66	120.30
1	D	686	MET	CG-SD-CE	-5.27	91.76	100.20
4	Z	62	ARG	NE-CZ-NH1	5.27	122.94	120.30
4	1	335	ARG	NE-CZ-NH1	5.27	122.94	120.30
1	A	800	ARG	NH1-CZ-NH2	5.26	125.19	119.40
4	8	62	ARG	NE-CZ-NH1	5.26	122.93	120.30
4	8	176	MET	CG-SD-CE	5.26	108.62	100.20
1	G	354	LEU	CB-CG-CD2	-5.26	102.06	111.00
4	5	176	MET	CG-SD-CE	5.25	108.60	100.20
1	J	660	LEU	CB-CG-CD2	5.25	119.93	111.00
4	Z	335	ARG	NE-CZ-NH1	5.24	122.92	120.30
1	A	346	ASP	N-CA-CB	-5.24	101.17	110.60
1	G	547	ASP	CB-CG-OD2	5.23	123.00	118.30
1	G	555	TYR	CB-CG-CD1	5.22	124.14	121.00
4	V	62	ARG	NE-CZ-NH1	5.22	122.91	120.30
1	A	218	LEU	O-C-N	5.22	131.06	122.70
1	D	218	LEU	O-C-N	5.22	131.05	122.70
4	1	62	ARG	NE-CZ-NH1	5.22	122.91	120.30
4	8	147	ARG	NE-CZ-NH2	-5.22	117.69	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	W	335	ARG	NE-CZ-NH1	5.22	122.91	120.30
1	A	760	PHE	CB-CG-CD1	5.21	124.45	120.80
1	J	346	ASP	N-CA-CB	-5.21	101.22	110.60
1	D	346	ASP	N-CA-CB	-5.21	101.22	110.60
1	J	354	LEU	CB-CG-CD2	-5.21	102.14	111.00
4	3	337	TYR	CB-CG-CD1	-5.21	117.87	121.00
1	A	547	ASP	CB-CG-OD2	5.21	122.99	118.30
1	G	343	PHE	CB-CG-CD2	-5.20	117.16	120.80
1	J	760	PHE	CB-CG-CD1	5.20	124.44	120.80
4	3	62	ARG	NE-CZ-NH1	5.20	122.90	120.30
1	D	4	ASP	CB-CG-OD1	-5.20	113.62	118.30
1	J	4	ASP	CB-CG-OD1	-5.19	113.63	118.30
1	A	90	ASP	CB-CG-OD1	-5.19	113.63	118.30
4	8	335	ARG	NE-CZ-NH1	5.19	122.90	120.30
1	G	4	ASP	CB-CG-OD1	-5.19	113.63	118.30
4	0	337	TYR	CB-CG-CD1	-5.19	117.89	121.00
4	0	62	ARG	NE-CZ-NH1	5.18	122.89	120.30
4	V	290	ARG	CA-C-N	5.17	128.59	117.20
4	1	147	ARG	NE-CZ-NH2	-5.17	117.72	120.30
4	V	335	ARG	NE-CZ-NH1	5.17	122.89	120.30
4	X	337	TYR	CB-CG-CD1	-5.17	117.90	121.00
4	4	290	ARG	CA-C-N	5.17	128.56	117.20
4	5	290	ARG	CA-C-N	5.17	128.56	117.20
4	6	290	ARG	CA-C-N	5.16	128.56	117.20
4	X	290	ARG	CA-C-N	5.16	128.56	117.20
4	Y	290	ARG	CA-C-N	5.16	128.56	117.20
4	2	62	ARG	NE-CZ-NH1	5.16	122.88	120.30
4	7	335	ARG	NE-CZ-NH1	5.16	122.88	120.30
4	0	290	ARG	CA-C-N	5.16	128.55	117.20
4	8	290	ARG	CA-C-N	5.16	128.55	117.20
4	3	290	ARG	CA-C-N	5.16	128.54	117.20
4	2	290	ARG	CA-C-N	5.16	128.54	117.20
4	3	335	ARG	NE-CZ-NH1	5.16	122.88	120.30
4	1	290	ARG	CA-C-N	5.15	128.54	117.20
4	V	53	TYR	CB-CG-CD1	-5.15	117.91	121.00
4	Z	290	ARG	CA-C-N	5.15	128.54	117.20
1	A	4	ASP	CB-CG-OD1	-5.15	113.67	118.30
4	2	337	TYR	CB-CG-CD1	-5.15	117.91	121.00
4	6	53	TYR	CB-CG-CD1	-5.15	117.91	121.00
4	7	290	ARG	CA-C-N	5.15	128.53	117.20
4	W	290	ARG	CA-C-N	5.15	128.52	117.20
4	6	62	ARG	NE-CZ-NH1	5.14	122.87	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	Y	335	ARG	NE-CZ-NH1	5.14	122.87	120.30
4	W	91	TYR	CB-CG-CD2	-5.14	117.92	121.00
4	Z	53	TYR	CB-CG-CD1	-5.14	117.92	121.00
4	0	335	ARG	NE-CZ-NH1	5.14	122.87	120.30
4	W	337	TYR	CB-CG-CD1	-5.13	117.92	121.00
4	Y	62	ARG	NE-CZ-NH1	5.13	122.87	120.30
1	G	346	ASP	N-CA-CB	-5.13	101.36	110.60
4	1	91	TYR	CB-CG-CD2	-5.13	117.92	121.00
4	7	62	ARG	NE-CZ-NH1	5.13	122.86	120.30
4	8	91	TYR	CB-CG-CD2	-5.12	117.92	121.00
4	Y	86	TRP	CG-CD1-NE1	-5.12	104.97	110.10
1	A	160	ASP	CB-CG-OD2	-5.12	113.69	118.30
1	D	576	GLU	CA-CB-CG	-5.12	102.13	113.40
1	J	576	GLU	CA-CB-CG	-5.12	102.13	113.40
4	2	335	ARG	NE-CZ-NH1	5.12	122.86	120.30
1	A	576	GLU	CA-CB-CG	-5.12	102.14	113.40
4	Z	62	ARG	CA-CB-CG	5.12	124.66	113.40
1	G	760	PHE	CB-CG-CD1	5.11	124.38	120.80
1	G	160	ASP	CB-CG-OD2	-5.11	113.70	118.30
1	G	576	GLU	CA-CB-CG	-5.11	102.16	113.40
4	0	53	TYR	CB-CG-CD1	-5.11	117.93	121.00
4	5	337	TYR	CB-CG-CD1	-5.11	117.93	121.00
4	7	86	TRP	CG-CD1-NE1	-5.11	104.99	110.10
4	Y	337	TYR	CB-CG-CD1	-5.11	117.93	121.00
1	J	628	GLY	O-C-N	-5.11	114.53	122.70
1	D	628	GLY	O-C-N	-5.11	114.53	122.70
1	J	301	ASP	CB-CG-OD2	5.11	122.90	118.30
4	5	62	ARG	CA-CB-CG	5.11	124.64	113.40
4	8	62	ARG	CA-CB-CG	5.11	124.63	113.40
4	Z	86	TRP	CG-CD1-NE1	-5.10	105.00	110.10
4	7	53	TYR	CB-CG-CD1	-5.10	117.94	121.00
4	1	53	TYR	CB-CG-CD1	-5.10	117.94	121.00
4	8	337	TYR	CB-CG-CD1	-5.10	117.94	121.00
1	G	90	ASP	CB-CG-OD1	-5.10	113.71	118.30
4	6	62	ARG	CA-CB-CG	5.10	124.62	113.40
4	W	62	ARG	CA-CB-CG	5.10	124.61	113.40
4	7	337	TYR	CB-CG-CD1	-5.10	117.94	121.00
4	5	86	TRP	CG-CD1-NE1	-5.09	105.00	110.10
1	A	218	LEU	CA-CB-CG	5.09	127.01	115.30
4	W	62	ARG	NE-CZ-NH1	5.09	122.85	120.30
4	4	62	ARG	CA-CB-CG	5.09	124.59	113.40
4	8	53	TYR	CB-CG-CD1	-5.09	117.95	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	Z	337	TYR	CB-CG-CD1	-5.09	117.95	121.00
4	1	62	ARG	CA-CB-CG	5.09	124.59	113.40
4	2	62	ARG	CA-CB-CG	5.09	124.59	113.40
4	Y	62	ARG	CA-CB-CG	5.08	124.59	113.40
1	D	82	PRO	N-CA-CB	5.08	109.40	103.30
1	D	218	LEU	CA-CB-CG	5.08	126.99	115.30
4	7	62	ARG	CA-CB-CG	5.08	124.58	113.40
1	D	621	LEU	CA-CB-CG	-5.08	103.61	115.30
1	J	555	TYR	CB-CG-CD1	5.08	124.05	121.00
4	4	337	TYR	CB-CG-CD1	-5.08	117.95	121.00
4	X	62	ARG	CA-CB-CG	5.08	124.58	113.40
4	X	91	TYR	CB-CG-CD2	-5.08	117.95	121.00
4	4	191	LYS	CA-C-N	5.08	128.38	117.20
4	V	62	ARG	CA-CB-CG	5.08	124.58	113.40
4	V	91	TYR	CB-CG-CD2	-5.08	117.95	121.00
4	0	91	TYR	CB-CG-CD2	-5.08	117.95	121.00
4	3	53	TYR	CB-CG-CD1	-5.08	117.95	121.00
4	5	191	LYS	CA-C-N	5.08	128.37	117.20
4	Y	191	LYS	CA-C-N	5.08	128.37	117.20
1	G	621	LEU	CA-CB-CG	-5.08	103.62	115.30
4	0	62	ARG	CA-CB-CG	5.08	124.57	113.40
4	3	62	ARG	CA-CB-CG	5.07	124.56	113.40
1	G	170	ARG	NE-CZ-NH1	5.07	122.84	120.30
4	5	91	TYR	CB-CG-CD2	-5.07	117.96	121.00
4	W	191	LYS	CA-C-N	5.07	128.35	117.20
4	X	191	LYS	CA-C-N	5.07	128.35	117.20
1	J	160	ASP	CB-CG-OD2	-5.07	113.74	118.30
4	X	86	TRP	CG-CD1-NE1	-5.07	105.03	110.10
1	A	621	LEU	CA-CB-CG	-5.06	103.66	115.30
4	0	191	LYS	CA-C-N	5.06	128.34	117.20
4	X	62	ARG	NE-CZ-NH1	5.06	122.83	120.30
4	3	191	LYS	CA-C-N	5.06	128.33	117.20
4	6	86	TRP	CG-CD1-NE1	-5.06	105.04	110.10
1	J	621	LEU	CA-CB-CG	-5.06	103.67	115.30
4	8	191	LYS	CA-C-N	5.06	128.33	117.20
4	4	86	TRP	CG-CD1-NE1	-5.05	105.05	110.10
4	V	337	TYR	CB-CG-CD1	-5.05	117.97	121.00
4	Y	53	TYR	CB-CG-CD1	-5.05	117.97	121.00
1	A	628	GLY	O-C-N	-5.05	114.62	122.70
1	D	160	ASP	CB-CG-OD2	-5.05	113.75	118.30
1	J	218	LEU	CA-CB-CG	5.05	126.92	115.30
1	A	739	ASP	CA-CB-CG	-5.05	102.29	113.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	82	PRO	N-CA-CB	5.05	109.36	103.30
4	4	91	TYR	CB-CG-CD2	-5.05	117.97	121.00
4	Z	191	LYS	CA-C-N	5.05	128.30	117.20
4	2	86	TRP	CG-CD1-NE1	-5.04	105.06	110.10
4	1	191	LYS	CA-C-N	5.04	128.29	117.20
4	4	53	TYR	CB-CG-CD1	-5.04	117.97	121.00
4	6	91	TYR	CB-CG-CD2	-5.04	117.97	121.00
4	7	191	LYS	CA-C-N	5.04	128.29	117.20
1	J	82	PRO	N-CA-CB	5.04	109.35	103.30
4	2	191	LYS	CA-C-N	5.04	128.28	117.20
1	A	235	ALA	N-CA-CB	-5.04	103.05	110.10
4	2	91	TYR	CB-CG-CD2	-5.04	117.98	121.00
4	5	62	ARG	NE-CZ-NH1	5.04	122.82	120.30
4	W	53	TYR	CB-CG-CD1	-5.03	117.98	121.00
1	G	218	LEU	CA-CB-CG	5.03	126.87	115.30
4	2	53	TYR	CB-CG-CD1	-5.03	117.98	121.00
1	J	739	ASP	N-CA-CB	5.03	119.65	110.60
1	G	739	ASP	N-CA-CB	5.03	119.64	110.60
1	D	739	ASP	N-CA-CB	5.02	119.64	110.60
1	G	628	GLY	O-C-N	-5.02	114.66	122.70
4	7	91	TYR	CB-CG-CD2	-5.02	117.99	121.00
1	D	90	ASP	CB-CG-OD1	-5.02	113.78	118.30
4	V	191	LYS	CA-C-N	5.02	128.25	117.20
4	6	191	LYS	CA-C-N	5.02	128.24	117.20
4	V	86	TRP	CG-CD1-NE1	-5.02	105.08	110.10
4	0	86	TRP	CG-CD1-NE1	-5.01	105.09	110.10
4	3	91	TYR	CB-CG-CD2	-5.01	117.99	121.00
4	Z	91	TYR	CB-CG-CD2	-5.01	117.99	121.00
1	G	82	PRO	N-CA-CB	5.01	109.32	103.30
1	D	235	ALA	N-CA-CB	-5.01	103.09	110.10

All (5) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	648	THR	CB
1	D	648	THR	CB
1	G	75	ASP	CA
1	G	648	THR	CB
1	J	648	THR	CB

All (52) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	0	62	ARG	Sidechain
4	1	62	ARG	Sidechain
4	2	62	ARG	Sidechain
4	3	62	ARG	Sidechain
4	4	62	ARG	Sidechain
4	5	62	ARG	Sidechain
4	6	62	ARG	Sidechain
4	7	62	ARG	Sidechain
4	8	62	ARG	Sidechain
1	A	623	PHE	Sidechain
1	A	637	LYS	Mainchain
1	A	649	VAL	Mainchain
1	A	98	HIS	Mainchain
2	B	150	TYR	Sidechain
2	B	155	TYR	Mainchain
2	B	22	THR	Mainchain
3	C	75	ALA	Mainchain
3	C	85	GLU	Mainchain
1	D	623	PHE	Sidechain
1	D	637	LYS	Mainchain
1	D	649	VAL	Mainchain
1	D	98	HIS	Mainchain
2	E	150	TYR	Sidechain
2	E	155	TYR	Mainchain
2	E	22	THR	Mainchain
3	F	75	ALA	Mainchain
3	F	85	GLU	Mainchain
1	G	623	PHE	Sidechain
1	G	637	LYS	Mainchain
1	G	649	VAL	Mainchain
1	G	98	HIS	Mainchain
2	H	150	TYR	Sidechain
2	H	155	TYR	Mainchain
2	H	22	THR	Mainchain
3	I	75	ALA	Mainchain
3	I	85	GLU	Mainchain
1	J	623	PHE	Sidechain
1	J	637	LYS	Mainchain
1	J	649	VAL	Mainchain
1	J	709	LYS	Peptide,Mainchain
1	J	98	HIS	Mainchain
2	K	150	TYR	Sidechain
2	K	155	TYR	Mainchain

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Mol	Chain	Res	Type	Group
2	K	22	THR	Mainchain
3	L	75	ALA	Mainchain
3	L	85	GLU	Mainchain
4	V	62	ARG	Sidechain
4	W	62	ARG	Sidechain
4	X	62	ARG	Sidechain
4	Y	62	ARG	Sidechain
4	Z	62	ARG	Sidechain

## 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6797	0	6752	1414	0
1	D	6797	0	6761	1431	0
1	G	6797	0	6754	1380	0
1	J	6797	0	6760	1429	0
2	B	1127	0	1086	252	0
2	E	1127	0	1087	320	0
2	H	1127	0	1087	228	0
2	K	1127	0	1087	227	0
3	C	1123	0	1084	181	0
3	F	1123	0	1082	139	0
3	I	1123	0	1084	169	0
3	L	1123	0	1084	165	0
4	0	2906	0	2866	75	0
4	1	2906	0	2866	77	0
4	2	2906	0	2864	102	0
4	3	2906	0	2864	100	0
4	4	2906	0	2855	345	0
4	5	2906	0	2855	340	0
4	6	2906	0	2852	382	0
4	7	2906	0	2852	377	0
4	8	2906	0	2861	150	0
4	V	2906	0	2861	142	0
4	W	2906	0	2864	107	0
4	X	2906	0	2864	105	0
4	Y	2906	0	2865	78	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	Z	2906	0	2865	78	0
All	All	76872	0	75762	7444	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 49.

All (7444) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:797:PHE:CD1	3:I:149:VAL:HG11	1.20	1.68
2:E:144:VAL:HG13	2:E:153:ILE:CD1	1.22	1.66
1:G:798:LEU:CD1	3:I:126:LEU:HD21	1.20	1.65
1:A:725:ARG:HE	1:A:733:PRO:CB	1.09	1.64
1:D:725:ARG:HE	1:D:733:PRO:CB	1.09	1.64
1:A:757:GLN:CB	1:A:771:LEU:HD11	1.19	1.64
1:J:831:TRP:CZ3	2:K:34:ILE:HD13	1.21	1.64
2:B:144:VAL:HG13	2:B:153:ILE:CG1	1.17	1.64
2:H:144:VAL:HG13	2:H:153:ILE:CD1	1.22	1.62
2:K:144:VAL:HG13	2:K:153:ILE:CG1	1.17	1.62
1:D:831:TRP:HZ2	2:E:47:LEU:CA	1.09	1.61
1:J:510:TRP:CH2	1:J:768:MLY:HH11	1.34	1.61
1:A:206:LYS:CD	1:A:217:THR:HG23	1.28	1.61
1:A:757:GLN:HB3	1:A:771:LEU:CD1	1.26	1.61
2:E:144:VAL:HG13	2:E:153:ILE:CG1	1.17	1.59
1:G:831:TRP:HH2	2:H:47:LEU:CD2	1.06	1.59
1:G:838:ILE:HD11	2:H:54:MET:CE	1.26	1.59
1:G:206:LYS:CD	1:G:217:THR:HG23	1.28	1.59
1:J:84:MLY:CH1	1:J:715:VAL:HG13	1.22	1.59
1:J:206:LYS:CD	1:J:217:THR:HG23	1.28	1.59
1:J:538:GLU:CA	4:7:349:LEU:CD1	1.79	1.59
2:B:144:VAL:HG13	2:B:153:ILE:CD1	1.22	1.59
1:G:769:ALA:CB	1:G:770:GLY:HA2	1.20	1.58
2:K:144:VAL:HG13	2:K:153:ILE:CD1	1.22	1.58
1:A:799:MET:SD	3:C:32:ASP:HB3	1.43	1.58
1:G:725:ARG:HE	1:G:733:PRO:CB	1.09	1.58
1:J:725:ARG:HE	1:J:733:PRO:CB	1.09	1.58
1:D:831:TRP:CZ2	2:E:47:LEU:HA	1.11	1.58
1:D:538:GLU:CA	4:5:349:LEU:CD1	1.78	1.58
1:G:93:MET:CE	1:G:763:THR:HB	1.22	1.57
1:G:538:GLU:CA	4:6:349:LEU:CD1	1.79	1.57
1:G:797:PHE:HD1	3:I:149:VAL:CG1	1.17	1.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:144:VAL:HG13	2:H:153:ILE:CG1	1.17	1.57
1:A:798:LEU:CD1	3:C:126:LEU:HD21	1.27	1.56
1:D:206:LYS:CD	1:D:217:THR:HG23	1.28	1.56
1:J:530:MET:HG2	4:7:354:GLN:CB	1.36	1.56
1:A:736:GLN:HA	1:A:743:ALA:CB	1.35	1.55
1:G:831:TRP:CH2	2:H:47:LEU:HD22	1.39	1.55
1:A:530:MET:HG2	4:4:354:GLN:CB	1.35	1.55
1:D:830:PRO:CG	2:E:67:MET:CE	1.82	1.55
1:G:530:MET:HG2	4:6:354:GLN:CB	1.35	1.54
1:A:836:PHE:CZ	2:B:160:GLY:N	1.71	1.54
1:A:538:GLU:CA	4:4:349:LEU:CD1	1.78	1.54
1:D:530:MET:HG2	4:5:354:GLN:CB	1.35	1.54
1:D:641:LYS:HG3	1:D:647:GLN:CG	1.36	1.53
1:J:768:MLY:CH2	1:J:772:LEU:HD22	1.37	1.53
1:J:641:LYS:HG3	1:J:647:GLN:CG	1.37	1.53
1:J:800:ARG:CD	3:L:149:VAL:CG2	1.81	1.53
1:J:829:TRP:HZ3	2:K:84:PHE:CZ	1.27	1.52
1:D:736:GLN:HA	1:D:743:ALA:CB	1.35	1.52
1:J:829:TRP:CZ3	2:K:84:PHE:CZ	1.96	1.52
1:A:641:LYS:HG3	1:A:647:GLN:CG	1.37	1.52
1:D:799:MET:SD	3:F:32:ASP:HB3	1.48	1.52
1:D:834:LEU:CG	2:E:54:MET:HG3	1.38	1.51
1:G:206:LYS:HD3	1:G:217:THR:CG2	1.40	1.51
1:J:84:MLY:CE	1:J:719:ASP:HB3	1.08	1.51
1:J:757:GLN:CG	1:J:776:GLU:HG3	1.34	1.51
1:G:736:GLN:HA	1:G:743:ALA:CB	1.35	1.51
1:G:641:LYS:HG3	1:G:647:GLN:CG	1.37	1.51
1:J:736:GLN:HA	1:J:743:ALA:CB	1.35	1.51
1:G:93:MET:HE1	1:G:763:THR:CB	1.38	1.50
2:K:117:LEU:HD12	2:K:147:ASN:CB	1.41	1.50
1:J:800:ARG:CD	3:L:149:VAL:HG22	1.39	1.49
1:D:831:TRP:CH2	2:E:47:LEU:HA	1.41	1.49
1:J:768:MLY:HH12	1:J:772:LEU:CD2	1.41	1.49
1:D:206:LYS:HD3	1:D:217:THR:CG2	1.40	1.49
1:A:813:ILE:CG2	2:B:127:ARG:HD2	1.39	1.49
1:G:84:MLY:CH1	1:G:715:VAL:HG13	1.35	1.49
2:E:117:LEU:HD12	2:E:147:ASN:CB	1.41	1.48
1:J:206:LYS:HD3	1:J:217:THR:CG2	1.40	1.48
2:E:111:SER:HB2	2:E:148:VAL:C	1.23	1.48
2:K:111:SER:HB2	2:K:148:VAL:C	1.23	1.48
2:B:117:LEU:HD12	2:B:147:ASN:CB	1.42	1.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:831:TRP:CZ2	2:E:47:LEU:CA	1.82	1.48
1:J:508:ILE:HD11	1:J:759:ALA:CB	1.41	1.48
1:A:206:LYS:HD3	1:A:217:THR:CG2	1.40	1.47
2:E:117:LEU:HD12	2:E:147:ASN:CG	1.30	1.47
2:B:111:SER:HB2	2:B:148:VAL:C	1.23	1.47
1:D:830:PRO:CG	2:E:67:MET:HE3	1.38	1.47
1:J:795:ARG:CD	3:L:35:ARG:HH22	1.28	1.47
1:G:641:LYS:CG	1:G:647:GLN:NE2	1.76	1.47
1:J:768:MLY:HH23	1:J:772:LEU:CD2	1.44	1.47
1:D:831:TRP:CZ3	2:E:34:ILE:HG23	1.48	1.47
2:K:117:LEU:HD12	2:K:147:ASN:CG	1.29	1.47
1:J:800:ARG:HD2	3:L:149:VAL:CG2	1.03	1.46
2:H:117:LEU:HD12	2:H:147:ASN:CB	1.42	1.46
1:J:795:ARG:HD2	3:L:35:ARG:NH2	1.23	1.46
1:A:641:LYS:CG	1:A:647:GLN:NE2	1.76	1.46
1:J:538:GLU:C	4:7:349:LEU:CD1	1.84	1.46
1:J:641:LYS:CG	1:J:647:GLN:NE2	1.77	1.46
1:G:538:GLU:C	4:6:349:LEU:CD1	1.84	1.46
2:H:111:SER:HB2	2:H:148:VAL:C	1.23	1.46
1:A:641:LYS:CD	1:A:647:GLN:CD	1.85	1.45
2:B:117:LEU:HD12	2:B:147:ASN:CG	1.30	1.45
1:J:641:LYS:CD	1:J:647:GLN:CD	1.85	1.45
1:D:830:PRO:HG2	2:E:67:MET:CE	0.99	1.45
1:A:800:ARG:HB3	3:C:149:VAL:CG2	1.44	1.45
1:D:538:GLU:C	4:5:349:LEU:CD1	1.84	1.45
1:G:641:LYS:CD	1:G:647:GLN:CD	1.85	1.45
1:A:836:PHE:CE1	2:B:160:GLY:N	1.82	1.45
1:G:798:LEU:CD1	3:I:126:LEU:CD2	1.93	1.45
1:J:769:ALA:HB3	1:J:770:GLY:CA	1.45	1.45
2:H:117:LEU:HD12	2:H:147:ASN:CG	1.30	1.44
1:D:641:LYS:CG	1:D:647:GLN:NE2	1.76	1.44
1:J:93:MET:CG	1:J:764:MLY:HD3	1.43	1.44
1:A:538:GLU:C	4:4:349:LEU:CD1	1.84	1.44
1:D:814:PHE:CD1	2:E:127:ARG:NH2	1.78	1.44
1:J:721:LYS:HG3	1:J:736:GLN:CG	1.15	1.43
1:D:641:LYS:CD	1:D:647:GLN:CD	1.85	1.42
1:D:768:MLY:C	1:D:771:LEU:HD13	1.34	1.42
1:G:93:MET:CE	1:G:763:THR:CB	1.89	1.42
1:G:721:LYS:HG3	1:G:736:GLN:CG	1.15	1.42
1:G:800:ARG:NH1	3:I:149:VAL:HG22	1.33	1.42
1:A:733:PRO:O	1:A:737:PHE:CD1	1.73	1.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:736:GLN:N	1:D:743:ALA:HB1	1.34	1.42
1:G:733:PRO:O	1:G:737:PHE:CD1	1.74	1.41
1:G:736:GLN:N	1:G:743:ALA:HB1	1.34	1.41
2:H:144:VAL:CG1	2:H:153:ILE:CD1	1.99	1.41
1:A:530:MET:CG	4:4:354:GLN:HB2	1.50	1.41
2:B:144:VAL:CG1	2:B:153:ILE:CD1	1.99	1.41
1:D:530:MET:CG	4:5:354:GLN:HB2	1.50	1.41
1:J:202:SER:HA	1:J:207:LYS:CE	1.51	1.40
1:J:218:LEU:CB	1:J:221:GLN:HG3	1.52	1.40
1:G:730:SER:OG	3:I:109:HIS:CD2	1.72	1.40
1:J:768:MLY:HH23	1:J:772:LEU:CG	1.51	1.40
1:A:202:SER:HA	1:A:207:LYS:CE	1.51	1.40
1:D:218:LEU:CB	1:D:221:GLN:HG3	1.52	1.40
1:D:736:GLN:CA	1:D:743:ALA:CB	2.00	1.39
1:A:149:GLN:CB	1:A:719:ASP:OD1	1.71	1.39
1:A:537:GLU:O	4:4:349:LEU:CD1	1.70	1.39
1:D:537:GLU:O	4:5:349:LEU:CD1	1.70	1.39
2:E:144:VAL:CG1	2:E:153:ILE:CD1	1.99	1.39
1:J:733:PRO:O	1:J:737:PHE:CD1	1.73	1.39
1:D:202:SER:HA	1:D:207:LYS:CE	1.51	1.39
1:G:202:SER:HA	1:G:207:LYS:CE	1.51	1.39
1:G:821:ARG:NH2	2:H:127:ARG:HG2	1.07	1.39
1:D:733:PRO:O	1:D:737:PHE:CD1	1.74	1.39
2:K:144:VAL:CG1	2:K:153:ILE:CD1	1.99	1.39
1:G:819:ASN:CA	2:H:90:GLY:O	1.67	1.38
1:J:530:MET:CG	4:7:354:GLN:HB2	1.51	1.38
1:A:800:ARG:CD	3:C:149:VAL:HG22	1.53	1.38
1:A:831:TRP:NE1	2:B:51:PHE:CZ	1.91	1.38
1:D:831:TRP:HZ2	2:E:47:LEU:CB	1.36	1.38
1:J:736:GLN:CA	1:J:743:ALA:CB	2.00	1.38
1:A:218:LEU:CB	1:A:221:GLN:HG3	1.52	1.38
1:G:795:ARG:CD	3:I:35:ARG:HH22	1.34	1.38
1:G:831:TRP:CH2	2:H:47:LEU:CD2	1.98	1.38
1:J:537:GLU:O	4:7:349:LEU:CD1	1.70	1.38
1:A:736:GLN:CA	1:A:743:ALA:CB	2.00	1.37
1:D:736:GLN:CA	1:D:743:ALA:HB1	1.53	1.38
2:E:144:VAL:CG1	2:E:153:ILE:HG12	1.54	1.37
1:G:534:SER:O	4:6:351:THR:CG2	1.64	1.37
1:J:768:MLY:CH1	1:J:772:LEU:HD22	1.52	1.37
1:A:736:GLN:N	1:A:743:ALA:HB1	1.35	1.37
1:G:218:LEU:CB	1:G:221:GLN:HG3	1.52	1.37

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:736:GLN:CA	1:A:743:ALA:HB1	1.53	1.37
1:D:721:LYS:CG	1:D:736:GLN:CG	1.97	1.37
1:D:641:LYS:CG	1:D:647:GLN:CD	1.93	1.37
1:D:642:LYS:HG3	4:5:23:GLY:N	1.40	1.37
2:H:144:VAL:CG1	2:H:153:ILE:HG12	1.54	1.37
1:J:736:GLN:CA	1:J:743:ALA:HB1	1.53	1.37
2:K:144:VAL:CG1	2:K:153:ILE:CG1	2.03	1.37
1:A:641:LYS:HG3	1:A:647:GLN:CD	1.46	1.36
2:B:117:LEU:HB2	2:B:147:ASN:ND2	1.39	1.36
1:A:721:LYS:HG3	1:A:736:GLN:CG	1.15	1.36
1:G:530:MET:CG	4:6:354:GLN:HB2	1.51	1.36
1:G:537:GLU:O	4:6:349:LEU:CD1	1.71	1.36
2:H:117:LEU:HB2	2:H:147:ASN:ND2	1.40	1.36
1:A:649:VAL:O	1:A:649:VAL:CG1	1.74	1.36
2:B:144:VAL:CG1	2:B:153:ILE:HG12	1.54	1.36
1:J:642:LYS:HG3	4:7:23:GLY:N	1.40	1.36
1:J:641:LYS:CG	1:J:647:GLN:CD	1.93	1.36
1:J:831:TRP:HZ3	2:K:34:ILE:CD1	1.36	1.36
2:K:144:VAL:CG1	2:K:153:ILE:HG12	1.54	1.36
1:G:649:VAL:O	1:G:649:VAL:CG1	1.74	1.36
2:B:117:LEU:CD1	2:B:147:ASN:OD1	1.74	1.35
1:D:800:ARG:HB3	3:F:149:VAL:CG2	1.56	1.35
1:G:538:GLU:CA	4:6:349:LEU:HD12	0.88	1.35
1:D:831:TRP:CE2	2:E:47:LEU:HD22	1.61	1.35
1:G:642:LYS:HG3	4:6:23:GLY:N	1.39	1.35
1:G:736:GLN:CA	1:G:743:ALA:CB	2.00	1.35
1:J:736:GLN:N	1:J:743:ALA:HB1	1.35	1.35
2:K:117:LEU:HB2	2:K:147:ASN:ND2	1.39	1.35
2:B:144:VAL:CG1	2:B:153:ILE:CG1	2.03	1.35
1:G:736:GLN:CA	1:G:743:ALA:HB1	1.53	1.35
1:A:530:MET:HA	4:4:354:GLN:CG	1.56	1.35
1:A:534:SER:O	4:4:351:THR:CG2	1.64	1.35
1:D:721:LYS:HG3	1:D:736:GLN:CG	1.15	1.35
1:G:721:LYS:CG	1:G:736:GLN:CG	1.97	1.35
2:H:144:VAL:CG1	2:H:153:ILE:CG1	2.03	1.35
1:D:534:SER:O	4:5:351:THR:CG2	1.64	1.34
1:J:538:GLU:CA	4:7:349:LEU:HD12	0.88	1.34
1:G:641:LYS:CG	1:G:647:GLN:CD	1.93	1.34
1:G:834:LEU:HD13	2:H:51:PHE:CE1	1.61	1.34
1:D:649:VAL:O	1:D:649:VAL:CG1	1.73	1.34
2:E:144:VAL:CG1	2:E:153:ILE:CG1	2.03	1.34

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:117:LEU:CD1	2:K:147:ASN:OD1	1.74	1.34
1:A:538:GLU:CA	4:4:349:LEU:HD12	0.87	1.34
1:A:641:LYS:CG	1:A:647:GLN:CD	1.93	1.34
1:A:642:LYS:HG3	4:4:23:GLY:N	1.40	1.34
2:E:117:LEU:CD1	2:E:147:ASN:OD1	1.74	1.33
2:H:114:LYS:CA	2:H:146:GLY:O	1.76	1.33
2:H:117:LEU:CD1	2:H:147:ASN:OD1	1.74	1.33
1:D:538:GLU:CA	4:5:349:LEU:HD12	0.87	1.33
1:J:629:GLU:HA	1:J:643:GLY:O	1.17	1.33
1:J:641:LYS:HG3	1:J:647:GLN:CD	1.46	1.33
1:J:795:ARG:HD2	3:L:35:ARG:CZ	1.57	1.33
1:J:821:ARG:NH2	2:K:127:ARG:HG2	1.42	1.33
1:D:530:MET:HA	4:5:354:GLN:CG	1.56	1.33
1:D:635:GLY:CA	4:5:334:GLU:HG2	1.59	1.33
2:E:117:LEU:HB2	2:E:147:ASN:ND2	1.40	1.33
1:J:530:MET:HA	4:7:354:GLN:CG	1.56	1.33
1:J:649:VAL:O	1:J:649:VAL:CG1	1.74	1.33
1:A:813:ILE:CG2	2:B:127:ARG:CD	2.07	1.33
1:G:831:TRP:HE1	2:H:67:MET:CG	1.41	1.33
1:J:635:GLY:CA	4:7:334:GLU:HG2	1.59	1.33
1:J:735:GLY:O	1:J:743:ALA:HB2	1.29	1.33
1:D:629:GLU:HA	1:D:643:GLY:O	1.17	1.32
1:G:530:MET:HA	4:6:354:GLN:CG	1.57	1.32
1:J:534:SER:O	4:7:351:THR:CG2	1.64	1.32
1:J:792:ALA:CB	3:L:40:ASN:HB3	1.59	1.32
1:D:799:MET:SD	3:F:32:ASP:CB	2.18	1.32
1:D:831:TRP:CZ2	2:E:47:LEU:HD23	1.64	1.32
1:J:721:LYS:CG	1:J:736:GLN:CD	1.98	1.32
1:A:725:ARG:NE	1:A:733:PRO:HB3	0.99	1.32
1:G:769:ALA:CB	1:G:770:GLY:CA	2.07	1.32
1:D:831:TRP:NE1	2:E:47:LEU:HD22	1.44	1.32
2:E:114:LYS:CA	2:E:146:GLY:O	1.76	1.32
1:G:757:GLN:OE1	1:G:772:LEU:HB3	1.30	1.32
1:A:538:GLU:O	4:4:349:LEU:CD1	1.78	1.31
1:A:813:ILE:HG22	2:B:127:ARG:CD	1.58	1.31
1:J:831:TRP:CZ3	2:K:34:ILE:CD1	2.11	1.31
2:K:114:LYS:CA	2:K:146:GLY:O	1.76	1.31
2:K:121:LEU:O	2:K:128:PHE:CB	1.78	1.31
1:A:629:GLU:HA	1:A:643:GLY:O	1.17	1.31
2:B:114:LYS:CA	2:B:146:GLY:O	1.76	1.31
1:G:629:GLU:HA	1:G:643:GLY:O	1.17	1.31

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:721:LYS:HG2	1:D:736:GLN:OE1	1.28	1.31
1:D:831:TRP:CE2	2:E:47:LEU:CD2	2.13	1.31
1:J:725:ARG:NE	1:J:733:PRO:HB3	1.00	1.31
1:A:721:LYS:CG	1:A:736:GLN:CD	1.98	1.31
1:G:635:GLY:CA	4:6:334:GLU:HG2	1.59	1.31
1:G:798:LEU:HD11	3:I:126:LEU:CD2	1.55	1.31
1:A:635:GLY:CA	4:4:334:GLU:HG2	1.59	1.30
1:D:599:ASN:HA	1:D:649:VAL:CB	1.60	1.30
1:D:839:MLY:CH1	2:E:159:HIS:CD2	2.15	1.30
1:A:819:ASN:OD1	2:B:91:ALA:CA	1.79	1.30
1:A:834:LEU:HD11	2:B:54:MET:CB	1.60	1.30
1:D:721:LYS:CG	1:D:736:GLN:CD	1.98	1.30
1:D:725:ARG:NE	1:D:733:PRO:HB3	1.00	1.30
2:E:121:LEU:O	2:E:128:PHE:CB	1.79	1.30
1:G:641:LYS:HG3	1:G:647:GLN:CD	1.45	1.30
1:G:789:ALA:HB2	3:I:81:GLN:NE2	1.43	1.30
1:G:538:GLU:O	4:6:349:LEU:CD1	1.78	1.30
1:G:725:ARG:NE	1:G:733:PRO:HB3	0.99	1.30
1:J:599:ASN:HA	1:J:649:VAL:CB	1.60	1.30
1:A:831:TRP:CE2	2:B:51:PHE:CZ	2.20	1.30
1:G:721:LYS:CG	1:G:736:GLN:CD	1.98	1.30
1:D:723:ARG:O	1:D:782:MLY:HD3	1.30	1.29
1:D:735:GLY:C	1:D:743:ALA:CB	2.01	1.29
1:G:800:ARG:HH11	3:I:149:VAL:CG2	1.42	1.29
1:A:735:GLY:O	1:A:743:ALA:HB2	1.29	1.29
2:B:121:LEU:O	2:B:128:PHE:CB	1.79	1.29
1:G:735:GLY:C	1:G:743:ALA:CB	2.01	1.29
1:A:599:ASN:HA	1:A:649:VAL:CB	1.60	1.29
1:D:215:GLN:N	1:D:340:ILE:HG12	1.20	1.29
1:D:641:LYS:HG3	1:D:647:GLN:CD	1.45	1.29
1:G:599:ASN:HA	1:G:649:VAL:CB	1.60	1.29
1:J:537:GLU:C	4:7:349:LEU:HD13	1.52	1.29
1:J:735:GLY:C	1:J:743:ALA:CB	2.01	1.29
1:J:768:MLY:CH1	1:J:772:LEU:CD2	2.10	1.29
1:A:836:PHE:HB2	2:B:161:GLU:OE1	1.32	1.28
1:G:537:GLU:C	4:6:349:LEU:HD13	1.53	1.28
1:J:800:ARG:CB	3:L:149:VAL:HG21	1.62	1.28
1:J:215:GLN:N	1:J:340:ILE:HG12	1.19	1.28
1:G:721:LYS:HG2	1:G:736:GLN:OE1	1.29	1.28
1:G:795:ARG:HD2	3:I:35:ARG:NH2	1.47	1.28
1:J:721:LYS:HG2	1:J:736:GLN:OE1	1.29	1.28

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:819:ASN:HA	2:K:90:GLY:O	1.19	1.28
1:G:752:ASP:O	1:G:779:ARG:NH1	1.66	1.28
2:H:121:LEU:O	2:H:128:PHE:CB	1.78	1.28
1:D:831:TRP:CZ2	2:E:47:LEU:CD2	2.17	1.27
1:G:836:PHE:CE1	2:H:159:HIS:HA	1.67	1.27
1:A:537:GLU:C	4:4:349:LEU:HD13	1.52	1.27
1:A:735:GLY:C	1:A:743:ALA:CB	2.01	1.27
1:J:538:GLU:O	4:7:349:LEU:CD1	1.78	1.27
1:A:534:SER:O	4:4:351:THR:CA	1.81	1.27
1:D:721:LYS:CG	1:D:736:GLN:OE1	1.82	1.27
1:J:733:PRO:O	1:J:737:PHE:HD1	0.93	1.26
1:D:534:SER:O	4:5:351:THR:CA	1.82	1.26
1:J:534:SER:O	4:7:351:THR:CA	1.82	1.26
1:A:836:PHE:CB	2:B:161:GLU:OE1	1.81	1.26
1:D:735:GLY:O	1:D:743:ALA:HB2	1.29	1.26
1:G:721:LYS:CG	1:G:736:GLN:OE1	1.83	1.26
1:J:768:MLY:HH23	1:J:772:LEU:CB	1.65	1.26
1:A:813:ILE:HG22	2:B:127:ARG:NE	1.45	1.26
1:D:537:GLU:C	4:5:349:LEU:HD13	1.52	1.26
1:D:721:LYS:HG3	1:D:736:GLN:CD	1.53	1.26
1:G:790:THR:OG1	3:I:87:PHE:CE2	1.89	1.26
1:A:149:GLN:HB3	1:A:719:ASP:OD1	1.12	1.26
1:A:733:PRO:O	1:A:737:PHE:HD1	0.92	1.25
1:D:538:GLU:O	4:5:349:LEU:CD1	1.78	1.25
1:G:508:ILE:HD11	1:G:759:ALA:CB	1.62	1.25
1:G:821:ARG:NH2	2:H:127:ARG:CG	1.99	1.25
1:J:768:MLY:CH2	1:J:772:LEU:HB2	1.66	1.25
1:A:797:PHE:CD1	3:C:149:VAL:HG11	1.71	1.25
1:G:735:GLY:O	1:G:743:ALA:HB2	1.29	1.25
1:G:721:LYS:HG3	1:G:736:GLN:CD	1.53	1.25
1:J:508:ILE:CD1	1:J:759:ALA:HB2	1.63	1.25
1:J:630:ALA:O	4:7:25:ASP:OD2	1.52	1.25
1:D:641:LYS:CG	1:D:647:GLN:CG	2.15	1.24
1:G:534:SER:O	4:6:351:THR:CA	1.83	1.24
1:G:93:MET:SD	1:G:716:LEU:HD12	1.75	1.24
1:J:641:LYS:CD	1:J:647:GLN:NE2	1.99	1.24
4:5:322:PRO:CB	4:7:244:ASP:OD2	1.86	1.24
1:A:721:LYS:CG	1:A:736:GLN:CG	1.97	1.24
1:G:508:ILE:CD1	1:G:759:ALA:HB2	1.67	1.24
1:G:646:PHE:CE2	1:G:652:LEU:HD11	1.73	1.24
1:G:733:PRO:O	1:G:737:PHE:HD1	0.93	1.24

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:721:LYS:HG3	1:J:736:GLN:CD	1.54	1.24
1:J:792:ALA:HB1	3:L:40:ASN:CB	1.67	1.24
2:K:117:LEU:CD1	2:K:147:ASN:CG	2.05	1.24
4:7:322:PRO:CB	4:V:244:ASP:OD2	1.86	1.24
1:A:795:ARG:HD2	3:C:35:ARG:NH1	1.49	1.24
1:D:646:PHE:CE2	1:D:652:LEU:HD11	1.73	1.24
1:A:646:PHE:CE2	1:A:652:LEU:HD11	1.73	1.24
1:A:834:LEU:HD11	2:B:54:MET:CG	1.67	1.24
1:D:836:PHE:HB3	2:E:161:GLU:OE1	1.35	1.24
1:J:641:LYS:CG	1:J:647:GLN:CG	2.16	1.24
1:A:721:LYS:HG2	1:A:736:GLN:OE1	1.29	1.23
1:J:721:LYS:CG	1:J:736:GLN:OE1	1.83	1.23
1:J:795:ARG:CD	3:L:35:ARG:NH2	1.90	1.23
2:K:117:LEU:HD12	2:K:147:ASN:OD1	1.32	1.23
4:3:322:PRO:CB	4:5:244:ASP:OD2	1.86	1.23
2:B:117:LEU:CD1	2:B:147:ASN:CG	2.05	1.23
1:D:795:ARG:NH2	3:F:116:GLU:OE2	1.67	1.23
4:4:322:PRO:CB	4:6:244:ASP:OD2	1.86	1.23
4:8:322:PRO:CB	4:W:244:ASP:OD2	1.86	1.23
1:A:538:GLU:O	4:4:349:LEU:HD11	1.35	1.23
1:A:630:ALA:O	4:4:25:ASP:OD2	1.53	1.23
1:A:800:ARG:HD2	3:C:149:VAL:CG2	1.68	1.23
2:E:121:LEU:C	2:E:128:PHE:CB	2.07	1.23
4:V:322:PRO:CB	4:X:244:ASP:OD2	1.86	1.23
1:A:629:GLU:CA	1:A:643:GLY:O	1.87	1.23
1:A:721:LYS:CG	1:A:736:GLN:OE1	1.82	1.23
1:A:795:ARG:NH2	3:C:116:GLU:OE2	1.69	1.23
1:A:800:ARG:CB	3:C:149:VAL:CG2	2.17	1.23
1:D:834:LEU:HD11	2:E:54:MET:CG	1.66	1.23
1:J:646:PHE:CE2	1:J:652:LEU:HD11	1.73	1.23
1:A:506:GLU:OE2	1:A:717:TYR:OH	1.57	1.23
1:G:783:LEU:O	1:G:787:ILE:N	1.71	1.23
4:2:322:PRO:CB	4:4:244:ASP:OD2	1.86	1.23
4:W:322:PRO:CB	4:Y:244:ASP:OD2	1.86	1.23
1:D:538:GLU:C	4:5:349:LEU:HD12	1.48	1.22
1:G:538:GLU:C	4:6:349:LEU:HD12	1.48	1.22
1:G:838:ILE:CD1	2:H:54:MET:HE3	1.69	1.22
4:0:322:PRO:CB	4:2:244:ASP:OD2	1.86	1.22
4:X:322:PRO:CB	4:Z:244:ASP:OD2	1.86	1.22
1:A:215:GLN:N	1:A:340:ILE:CG1	2.02	1.22
1:A:534:SER:O	4:4:351:THR:CB	1.87	1.22

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:641:LYS:CD	1:G:647:GLN:NE2	1.99	1.22
1:A:641:LYS:CG	1:A:647:GLN:CG	2.16	1.22
1:A:836:PHE:CZ	2:B:160:GLY:CA	2.20	1.22
2:B:121:LEU:C	2:B:128:PHE:CB	2.07	1.22
1:D:630:ALA:O	4:5:25:ASP:OD2	1.52	1.22
1:D:641:LYS:CD	1:D:647:GLN:NE2	1.99	1.22
1:D:733:PRO:O	1:D:737:PHE:HD1	0.93	1.22
1:G:553:MLY:CE	4:8:45:VAL:HA	1.52	1.22
1:G:757:GLN:OE1	1:G:772:LEU:CB	1.86	1.22
1:J:215:GLN:N	1:J:340:ILE:CG1	2.02	1.22
4:1:322:PRO:CB	4:3:244:ASP:OD2	1.86	1.22
1:D:799:MET:SD	3:F:32:ASP:O	1.97	1.22
2:E:117:LEU:CD1	2:E:147:ASN:CG	2.05	1.22
1:G:215:GLN:N	1:G:340:ILE:CG1	2.02	1.22
2:H:144:VAL:CG1	2:H:153:ILE:HD11	1.64	1.22
1:A:798:LEU:CD1	3:C:126:LEU:CD2	2.16	1.21
1:D:534:SER:O	4:5:351:THR:CB	1.87	1.21
1:D:799:MET:SD	3:F:32:ASP:C	2.18	1.21
1:G:538:GLU:O	4:6:349:LEU:HD11	1.34	1.21
1:G:707:CYS:HB3	1:G:714:ARG:NH1	1.54	1.21
1:J:534:SER:O	4:7:351:THR:CB	1.87	1.21
1:A:641:LYS:CG	1:A:647:GLN:HG3	1.71	1.21
2:B:144:VAL:CG1	2:B:153:ILE:HD11	1.65	1.21
1:D:629:GLU:CA	1:D:643:GLY:O	1.87	1.21
1:G:629:GLU:CA	1:G:643:GLY:O	1.87	1.21
2:H:121:LEU:C	2:H:128:PHE:CB	2.07	1.21
4:6:322:PRO:CB	4:8:244:ASP:OD2	1.86	1.21
1:A:641:LYS:CD	1:A:647:GLN:NE2	1.99	1.21
1:D:215:GLN:N	1:D:340:ILE:CG1	2.02	1.21
1:D:822:SER:OG	2:E:88:LEU:HD23	1.06	1.21
1:J:629:GLU:CA	1:J:643:GLY:O	1.87	1.21
2:K:121:LEU:C	2:K:128:PHE:CB	2.07	1.21
1:D:641:LYS:CG	1:D:647:GLN:HG3	1.71	1.21
2:E:144:VAL:CG1	2:E:153:ILE:HD11	1.65	1.21
1:A:795:ARG:HB3	3:C:35:ARG:NH2	1.56	1.20
1:G:641:LYS:CG	1:G:647:GLN:HG3	1.71	1.20
2:B:117:LEU:CD1	2:B:147:ASN:CB	2.19	1.20
1:G:215:GLN:N	1:G:340:ILE:HG12	1.19	1.20
2:H:117:LEU:CD1	2:H:147:ASN:CB	2.19	1.20
1:J:93:MET:SD	1:J:716:LEU:HD12	1.82	1.20
1:A:797:PHE:HD1	3:C:149:VAL:CG1	1.54	1.20

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:826:VAL:HG21	2:K:88:LEU:HD21	1.21	1.20
4:0:322:PRO:HB2	4:2:244:ASP:OD2	1.39	1.20
1:A:757:GLN:CG	1:A:771:LEU:HD11	1.71	1.20
1:D:553:MLY:CE	4:7:45:VAL:HA	1.52	1.20
4:5:322:PRO:HB2	4:7:244:ASP:OD2	1.39	1.20
1:A:721:LYS:HG3	1:A:736:GLN:CD	1.53	1.19
1:G:534:SER:O	4:6:351:THR:CB	1.88	1.19
4:2:322:PRO:HB2	4:4:244:ASP:OD2	1.39	1.19
1:A:538:GLU:OE2	4:4:355:MET:CE	1.91	1.19
1:G:538:GLU:OE2	4:6:355:MET:CE	1.90	1.19
1:G:769:ALA:HB3	1:G:770:GLY:CA	1.65	1.19
2:H:117:LEU:CD1	2:H:147:ASN:CG	2.05	1.19
1:A:822:SER:OG	2:B:88:LEU:HD23	1.04	1.19
1:G:834:LEU:CD1	2:H:51:PHE:HE1	1.56	1.19
1:G:838:ILE:CD1	2:H:54:MET:CE	2.20	1.19
1:J:538:GLU:OE2	4:7:355:MET:CE	1.90	1.19
1:J:557:GLU:H	4:V:48:GLY:CA	1.56	1.19
1:A:538:GLU:C	4:4:349:LEU:HD11	1.54	1.19
1:A:538:GLU:C	4:4:349:LEU:HD12	1.48	1.19
1:D:538:GLU:OE2	4:5:355:MET:CE	1.90	1.19
1:J:800:ARG:CD	3:L:149:VAL:HG23	1.57	1.19
4:1:322:PRO:HB2	4:3:244:ASP:OD2	1.39	1.19
1:D:735:GLY:O	1:D:743:ALA:CB	1.91	1.19
1:J:90:ASP:CG	1:J:764:MLY:HH11	1.61	1.19
1:A:557:GLU:H	4:6:48:GLY:CA	1.56	1.18
4:4:322:PRO:HB2	4:6:244:ASP:OD2	1.39	1.18
1:D:834:LEU:HG	2:E:54:MET:HG3	1.21	1.18
1:G:510:TRP:CZ3	1:G:768:MLY:HH11	1.77	1.18
1:G:641:LYS:CB	1:G:647:GLN:NE2	2.07	1.18
1:D:557:GLU:H	4:7:48:GLY:CA	1.56	1.18
1:J:641:LYS:CG	1:J:647:GLN:HG3	1.71	1.18
2:K:117:LEU:CD1	2:K:147:ASN:CB	2.19	1.18
1:A:735:GLY:O	1:A:743:ALA:CB	1.91	1.18
1:G:795:ARG:CB	3:I:35:ARG:NH2	2.07	1.18
1:J:721:LYS:HG3	1:J:736:GLN:HG2	1.25	1.18
1:J:817:GLN:CD	2:K:127:ARG:HD2	1.64	1.18
1:G:721:LYS:HA	1:G:736:GLN:NE2	1.58	1.18
1:J:538:GLU:C	4:7:349:LEU:HD12	1.48	1.18
1:J:641:LYS:CB	1:J:647:GLN:NE2	2.07	1.18
4:7:322:PRO:HB2	4:V:244:ASP:OD2	1.39	1.18
2:E:117:LEU:CD1	2:E:147:ASN:CB	2.19	1.17

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:557:GLU:H	4:8:48:GLY:CA	1.56	1.17
1:J:538:GLU:HA	4:7:349:LEU:CD1	1.55	1.17
1:J:768:MLY:HD3	1:J:772:LEU:CB	1.72	1.17
1:J:798:LEU:CD2	3:L:126:LEU:HD11	1.73	1.17
1:J:829:TRP:HZ3	2:K:84:PHE:CE2	1.62	1.17
4:X:322:PRO:HB2	4:Z:244:ASP:OD2	1.39	1.17
1:A:215:GLN:N	1:A:340:ILE:HG12	1.20	1.17
1:A:502:GLU:HG3	1:A:761:GLY:CA	1.75	1.17
1:A:721:LYS:HA	1:A:736:GLN:NE2	1.58	1.17
1:D:725:ARG:N	1:D:782:MLY:HH21	1.57	1.17
1:D:769:ALA:HA	1:D:771:LEU:CA	1.73	1.17
1:G:754:ASP:HB2	1:G:776:GLU:OE2	1.41	1.17
1:G:817:GLN:CG	2:H:127:ARG:HD2	1.72	1.17
4:W:290:ARG:NH2	4:Y:202:THR:HG23	1.59	1.17
1:D:829:TRP:NE1	2:E:67:MET:HG2	1.56	1.17
1:G:201:ALA:O	1:G:202:SER:HB3	1.35	1.17
1:J:530:MET:HE2	4:7:354:GLN:HG2	1.24	1.17
4:4:290:ARG:NH2	4:6:202:THR:HG23	1.59	1.17
1:G:735:GLY:O	1:G:743:ALA:CB	1.91	1.17
1:J:735:GLY:O	1:J:743:ALA:CB	1.91	1.17
1:J:800:ARG:CB	3:L:149:VAL:CG2	2.20	1.17
1:J:829:TRP:CH2	2:K:84:PHE:CE1	2.33	1.17
1:J:829:TRP:HH2	2:K:84:PHE:CE1	1.60	1.17
4:3:322:PRO:HB2	4:5:244:ASP:OD2	1.39	1.17
4:8:322:PRO:HB2	4:W:244:ASP:OD2	1.39	1.17
1:D:538:GLU:HA	4:5:349:LEU:CD1	1.55	1.17
1:D:641:LYS:CE	4:5:348:SER:O	1.93	1.17
1:D:641:LYS:CB	1:D:647:GLN:NE2	2.07	1.17
1:D:830:PRO:HB2	2:E:51:PHE:CZ	1.78	1.17
2:E:117:LEU:CD1	2:E:147:ASN:HB3	1.75	1.17
1:J:641:LYS:CE	4:7:348:SER:O	1.93	1.17
4:6:290:ARG:NH2	4:8:202:THR:HG23	1.59	1.17
4:7:290:ARG:NH2	4:V:202:THR:HG23	1.59	1.17
1:A:553:MLY:CE	4:6:45:VAL:HA	1.52	1.16
1:A:641:LYS:CB	1:A:647:GLN:NE2	2.07	1.16
1:G:201:ALA:O	1:G:202:SER:CB	1.92	1.16
1:A:831:TRP:CD1	2:B:51:PHE:HZ	1.62	1.16
1:D:538:GLU:OE2	4:5:355:MET:HE1	1.44	1.16
4:5:290:ARG:NH2	4:7:202:THR:HG23	1.59	1.16
4:8:290:ARG:NH2	4:W:202:THR:HG23	1.59	1.16
1:A:201:ALA:O	1:A:202:SER:HB3	1.35	1.16

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:822:SER:OG	2:E:88:LEU:CD2	1.92	1.16
1:J:721:LYS:CG	1:J:736:GLN:CG	1.97	1.16
4:V:290:ARG:NH2	4:X:202:THR:HG23	1.59	1.16
1:D:726:VAL:HB	1:D:782:MLY:CH1	1.75	1.16
1:G:215:GLN:HA	1:G:340:ILE:CG2	1.75	1.16
1:G:739:ASP:HB3	1:G:742:LYS:HB3	1.21	1.16
1:J:215:GLN:HA	1:J:340:ILE:CG2	1.75	1.16
1:J:510:TRP:CH2	1:J:768:MLY:CH1	2.28	1.16
1:J:800:ARG:NH1	3:L:149:VAL:HG13	1.59	1.16
1:A:639:GLY:CA	4:4:345:ILE:HA	1.74	1.16
1:D:769:ALA:HB1	1:D:770:GLY:CA	1.74	1.16
1:G:642:LYS:CG	4:6:23:GLY:N	2.08	1.16
1:J:201:ALA:O	1:J:202:SER:CB	1.92	1.16
1:J:510:TRP:CZ2	1:J:768:MLY:HH11	1.80	1.16
1:J:538:GLU:C	4:7:349:LEU:HD11	1.54	1.16
1:J:641:LYS:HD2	1:J:647:GLN:NE2	1.58	1.16
2:K:117:LEU:CD1	2:K:147:ASN:HB3	1.76	1.16
2:K:144:VAL:CG1	2:K:153:ILE:HD11	1.65	1.16
4:3:290:ARG:NH2	4:5:202:THR:HG23	1.59	1.16
4:W:322:PRO:HB2	4:Y:244:ASP:OD2	1.39	1.16
1:A:553:MLY:HB3	4:6:46:GLY:CA	1.51	1.15
1:A:641:LYS:HD2	1:A:647:GLN:NE2	1.59	1.15
1:A:641:LYS:CE	4:4:348:SER:O	1.93	1.15
1:G:93:MET:CE	1:G:763:THR:CG2	2.25	1.15
1:G:93:MET:HE1	1:G:763:THR:CA	1.76	1.15
1:G:553:MLY:HB3	4:8:46:GLY:CA	1.51	1.15
1:G:640:LYS:HB3	1:G:645:SER:OG	1.46	1.15
2:H:117:LEU:CD1	2:H:147:ASN:HB3	1.75	1.15
1:J:538:GLU:OE2	4:7:355:MET:HE1	1.44	1.15
1:D:649:VAL:HA	1:D:649:VAL:CG2	1.76	1.15
1:D:839:MLY:HH11	2:E:159:HIS:CD2	1.79	1.15
2:H:111:SER:CA	2:H:148:VAL:O	1.95	1.15
1:J:640:LYS:HB3	1:J:645:SER:OG	1.45	1.15
4:1:290:ARG:NH2	4:3:202:THR:HG23	1.59	1.15
4:X:290:ARG:NH2	4:Z:202:THR:HG23	1.59	1.15
1:J:749:GLY:O	3:L:114:LEU:HD21	1.45	1.15
4:0:290:ARG:NH2	4:2:202:THR:HG23	1.59	1.15
4:2:290:ARG:NH2	4:4:202:THR:HG23	1.59	1.15
1:A:639:GLY:HA3	4:4:344:SER:O	1.47	1.15
1:D:215:GLN:HA	1:D:340:ILE:CG2	1.75	1.15
1:D:538:GLU:C	4:5:349:LEU:HD11	1.54	1.15

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:542:PHE:HA	4:5:143:TYR:CE1	1.82	1.15
1:D:641:LYS:HD2	1:D:647:GLN:NE2	1.59	1.15
1:D:721:LYS:HA	1:D:736:GLN:NE2	1.58	1.15
1:G:641:LYS:HD2	1:G:647:GLN:NE2	1.59	1.15
1:J:635:GLY:HA2	4:7:334:GLU:HG2	1.16	1.15
1:J:642:LYS:CG	4:7:23:GLY:N	2.08	1.15
1:J:721:LYS:HA	1:J:736:GLN:NE2	1.58	1.15
1:A:215:GLN:HA	1:A:340:ILE:CG2	1.76	1.15
1:A:542:PHE:HA	4:4:143:TYR:CE1	1.82	1.15
1:D:642:LYS:CG	4:5:23:GLY:N	2.08	1.15
2:E:111:SER:CB	2:E:148:VAL:C	1.93	1.15
2:H:121:LEU:CA	2:H:128:PHE:HB3	1.77	1.15
1:J:542:PHE:HA	4:7:143:TYR:CE1	1.82	1.15
1:A:642:LYS:CG	4:4:23:GLY:N	2.09	1.14
1:A:649:VAL:HG13	1:A:649:VAL:HG22	1.21	1.14
2:B:117:LEU:CD1	2:B:147:ASN:HB3	1.76	1.14
1:D:639:GLY:CA	4:5:345:ILE:HA	1.73	1.14
1:D:640:LYS:HB3	1:D:645:SER:OG	1.46	1.14
1:G:639:GLY:HA3	4:6:344:SER:O	1.46	1.14
1:G:639:GLY:HA2	4:6:345:ILE:HA	1.26	1.14
1:J:649:VAL:HA	1:J:649:VAL:CG2	1.76	1.14
1:J:739:ASP:HB3	1:J:742:LYS:HB3	1.21	1.14
1:J:757:GLN:CG	1:J:776:GLU:CG	2.23	1.14
4:1:287:ILE:HG21	4:3:205:GLU:HG2	1.17	1.14
4:3:287:ILE:HG21	4:5:205:GLU:HG2	1.17	1.14
1:A:813:ILE:HG22	2:B:127:ARG:CZ	1.77	1.14
1:D:726:VAL:HG23	1:D:782:MLY:HH22	1.16	1.14
2:E:111:SER:CA	2:E:148:VAL:O	1.95	1.14
1:G:542:PHE:HA	4:6:143:TYR:CE1	1.82	1.14
1:A:149:GLN:CG	1:A:719:ASP:OD1	1.96	1.14
1:A:795:ARG:HE	3:C:118:MET:HE1	1.04	1.14
1:A:836:PHE:CE2	2:B:160:GLY:HA3	1.81	1.14
1:D:201:ALA:O	1:D:202:SER:HB3	1.36	1.14
1:D:641:LYS:NZ	4:5:348:SER:O	1.80	1.14
1:D:839:MLY:HH13	2:E:159:HIS:CD2	1.82	1.14
2:E:121:LEU:CA	2:E:128:PHE:HB3	1.77	1.14
1:G:649:VAL:HA	1:G:649:VAL:CG2	1.76	1.14
1:J:639:GLY:HA3	4:7:344:SER:O	1.46	1.14
1:J:768:MLY:NZ	1:J:772:LEU:HD22	1.62	1.14
1:J:797:PHE:HD1	3:L:149:VAL:CG1	1.59	1.14
2:K:111:SER:CA	2:K:148:VAL:O	1.95	1.14

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:121:LEU:C	2:K:128:PHE:HB2	1.67	1.14
1:A:501:GLU:HG2	1:A:762:HIS:ND1	1.62	1.14
1:A:640:LYS:HB3	1:A:645:SER:OG	1.46	1.14
2:B:111:SER:CA	2:B:148:VAL:O	1.95	1.14
2:B:121:LEU:CA	2:B:128:PHE:HB3	1.78	1.14
1:D:635:GLY:HA2	4:5:334:GLU:HG2	1.16	1.14
1:D:736:GLN:N	1:D:743:ALA:CB	2.05	1.14
2:E:117:LEU:HD12	2:E:147:ASN:OD1	1.32	1.14
1:G:641:LYS:CE	4:6:348:SER:O	1.93	1.14
2:K:121:LEU:CA	2:K:128:PHE:HB3	1.77	1.14
4:6:322:PRO:HB2	4:8:244:ASP:OD2	1.39	1.14
1:A:649:VAL:HA	1:A:649:VAL:CG2	1.76	1.14
2:B:117:LEU:HD12	2:B:147:ASN:OD1	1.32	1.14
1:G:599:ASN:OD1	1:G:649:VAL:CB	1.96	1.14
1:G:831:TRP:NE1	2:H:67:MET:HG2	1.63	1.14
1:J:757:GLN:HG2	1:J:776:GLU:CG	1.76	1.14
4:5:287:ILE:HG21	4:7:205:GLU:HG2	1.17	1.14
1:D:641:LYS:HG3	1:D:647:GLN:HG3	1.20	1.13
1:D:739:ASP:HB3	1:D:742:LYS:HB3	1.21	1.13
1:G:649:VAL:HG22	1:G:649:VAL:HG13	1.21	1.13
2:H:117:LEU:HD12	2:H:147:ASN:OD1	1.32	1.13
2:K:112:ILE:O	2:K:147:ASN:O	1.65	1.13
2:B:121:LEU:C	2:B:128:PHE:HB2	1.67	1.13
1:D:639:GLY:HA3	4:5:344:SER:O	1.46	1.13
1:D:830:PRO:CG	2:E:67:MET:HE1	1.77	1.13
1:G:84:MLY:HH11	1:G:715:VAL:CG1	1.76	1.13
1:G:93:MET:HE1	1:G:763:THR:C	1.67	1.13
1:G:768:MLY:HD3	1:G:772:LEU:HD22	1.19	1.13
1:J:541:MET:C	4:7:143:TYR:OH	1.87	1.13
1:A:599:ASN:OD1	1:A:649:VAL:CB	1.96	1.13
1:A:641:LYS:CE	1:A:647:GLN:OE1	1.97	1.13
1:D:599:ASN:OD1	1:D:649:VAL:CB	1.96	1.13
1:D:834:LEU:CD1	2:E:54:MET:HG3	1.78	1.13
1:G:538:GLU:C	4:6:349:LEU:HD11	1.54	1.13
2:H:112:ILE:O	2:H:147:ASN:O	1.65	1.13
1:A:768:MLY:HB3	1:A:771:LEU:HD13	1.31	1.13
1:A:795:ARG:HH21	3:C:116:GLU:HB3	1.01	1.13
1:G:768:MLY:HD3	1:G:772:LEU:CD2	1.79	1.13
1:J:599:ASN:OD1	1:J:649:VAL:CB	1.96	1.13
1:J:641:LYS:CE	1:J:647:GLN:OE1	1.97	1.13
1:J:831:TRP:HZ2	2:K:47:LEU:HD22	1.08	1.13

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:800:ARG:NH1	3:C:149:VAL:HG13	1.61	1.13
1:A:831:TRP:NE1	2:B:51:PHE:HZ	1.32	1.13
1:A:541:MET:C	4:4:143:TYR:OH	1.87	1.12
1:D:201:ALA:O	1:D:202:SER:CB	1.92	1.12
1:D:541:MET:C	4:5:143:TYR:OH	1.87	1.12
1:D:726:VAL:CB	1:D:782:MLY:HH13	1.77	1.13
1:G:541:MET:C	4:6:143:TYR:OH	1.87	1.12
1:G:639:GLY:CA	4:6:345:ILE:HA	1.73	1.12
1:J:510:TRP:CZ3	1:J:768:MLY:HH11	1.83	1.12
4:W:287:ILE:HG21	4:Y:205:GLU:HG2	1.17	1.12
1:A:641:LYS:NZ	4:4:348:SER:O	1.80	1.12
1:A:839:MLY:HH21	2:B:158:THR:HG22	1.30	1.12
2:B:112:ILE:O	2:B:147:ASN:O	1.65	1.12
1:D:641:LYS:CE	1:D:647:GLN:OE1	1.97	1.12
1:D:724:TYR:CE1	1:D:778:MET:HB3	1.85	1.12
1:D:831:TRP:CZ3	2:E:34:ILE:CG2	2.32	1.12
1:G:641:LYS:NZ	4:6:348:SER:O	1.80	1.12
1:G:834:LEU:CD1	2:H:51:PHE:CE1	2.30	1.12
1:A:201:ALA:O	1:A:202:SER:CB	1.92	1.12
1:D:507:GLY:O	1:D:761:GLY:CA	1.97	1.12
1:D:538:GLU:O	4:5:349:LEU:HD11	1.35	1.12
1:G:641:LYS:CE	1:G:647:GLN:OE1	1.97	1.12
1:G:819:ASN:CG	2:H:92:ASP:HB2	1.62	1.12
2:K:111:SER:HB3	2:K:148:VAL:O	1.50	1.12
4:7:287:ILE:HG21	4:V:205:GLU:HG2	1.17	1.12
1:A:707:CYS:HA	1:A:714:ARG:HH12	1.11	1.12
2:B:121:LEU:O	2:B:128:PHE:HB2	0.94	1.12
1:J:92:ALA:O	1:J:714:ARG:HD2	1.49	1.12
1:J:623:PHE:CG	1:J:623:PHE:CB	2.33	1.12
1:J:821:ARG:NH2	2:K:127:ARG:CG	2.13	1.12
1:J:829:TRP:CH2	2:K:84:PHE:CZ	2.38	1.12
1:A:530:MET:HE2	4:4:354:GLN:HG2	1.30	1.12
1:A:707:CYS:HA	1:A:714:ARG:NH1	1.64	1.12
3:C:48:LYS:C	3:C:52:ASN:ND2	2.03	1.12
2:E:112:ILE:O	2:E:147:ASN:O	1.65	1.12
1:G:538:GLU:OE2	4:6:355:MET:HE1	1.50	1.12
1:J:795:ARG:NH2	3:L:116:GLU:OE2	1.83	1.12
3:I:48:LYS:C	3:I:52:ASN:ND2	2.03	1.11
1:G:649:VAL:O	1:G:649:VAL:HG12	0.94	1.11
1:G:788:THR:C	3:I:42:THR:HG22	1.56	1.11
1:J:641:LYS:NZ	4:7:348:SER:O	1.80	1.11

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:798:LEU:HD11	3:C:126:LEU:HD21	1.29	1.11
2:B:117:LEU:HB2	2:B:147:ASN:CG	1.70	1.11
1:G:819:ASN:CG	2:H:90:GLY:O	1.88	1.11
3:L:24:LYS:CB	3:L:63:ILE:O	1.99	1.11
4:5:290:ARG:CZ	4:7:202:THR:HG21	1.81	1.11
4:7:290:ARG:CZ	4:V:202:THR:HG21	1.81	1.11
4:8:287:ILE:HG21	4:W:205:GLU:HG2	1.17	1.11
4:8:290:ARG:CZ	4:W:202:THR:HG21	1.81	1.11
4:V:322:PRO:HB2	4:X:244:ASP:OD2	1.39	1.11
1:A:649:VAL:O	1:A:649:VAL:HG12	0.94	1.11
1:A:814:PHE:CD1	2:B:127:ARG:NH2	2.16	1.11
3:C:24:LYS:CB	3:C:63:ILE:O	1.99	1.11
1:D:623:PHE:CB	1:D:623:PHE:CG	2.33	1.11
1:D:641:LYS:CE	1:D:647:GLN:CD	2.18	1.11
1:G:736:GLN:N	1:G:743:ALA:CB	2.04	1.11
2:H:111:SER:CB	2:H:148:VAL:C	1.93	1.11
2:H:117:LEU:HB2	2:H:147:ASN:CG	1.70	1.11
4:0:290:ARG:CZ	4:2:202:THR:HG21	1.81	1.11
1:A:623:PHE:CB	1:A:623:PHE:CG	2.33	1.11
1:D:834:LEU:CD1	2:E:54:MET:CG	2.28	1.11
3:F:48:LYS:C	3:F:52:ASN:ND2	2.03	1.11
1:G:798:LEU:HD13	3:I:126:LEU:CD2	1.67	1.11
1:G:817:GLN:CD	2:H:127:ARG:HD2	1.68	1.11
1:J:641:LYS:CE	1:J:647:GLN:CD	2.18	1.11
1:J:798:LEU:HD22	3:L:126:LEU:CD1	1.79	1.11
4:6:290:ARG:CZ	4:8:202:THR:HG21	1.81	1.11
1:D:530:MET:CE	4:5:354:GLN:HG2	1.80	1.10
1:D:530:MET:HE2	4:5:354:GLN:HG2	1.22	1.10
1:D:799:MET:SD	3:F:32:ASP:CA	2.38	1.10
1:G:93:MET:SD	1:G:716:LEU:CD1	2.39	1.10
1:D:798:LEU:HD11	3:F:126:LEU:HD21	1.27	1.10
2:E:117:LEU:HB2	2:E:147:ASN:CG	1.70	1.10
2:E:121:LEU:O	2:E:128:PHE:HB2	0.94	1.10
1:G:623:PHE:CB	1:G:623:PHE:CG	2.33	1.10
1:G:641:LYS:HG3	1:G:647:GLN:HG3	1.21	1.10
1:G:641:LYS:CE	1:G:647:GLN:CD	2.18	1.10
1:J:84:MLY:HH11	1:J:715:VAL:CG1	1.70	1.10
1:J:530:MET:CE	4:7:354:GLN:HG2	1.80	1.10
1:J:538:GLU:O	4:7:349:LEU:HD11	1.35	1.10
4:W:290:ARG:CZ	4:Y:202:THR:HG21	1.81	1.10
1:A:641:LYS:CE	1:A:647:GLN:CD	2.18	1.10

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:649:VAL:HG22	1:D:649:VAL:HG13	1.21	1.10
1:G:730:SER:OG	3:I:109:HIS:CG	2.05	1.10
1:G:838:ILE:HD11	2:H:54:MET:HE1	1.19	1.10
1:J:218:LEU:HB2	1:J:221:GLN:HG3	1.17	1.10
3:L:48:LYS:C	3:L:52:ASN:ND2	2.03	1.10
4:2:290:ARG:CZ	4:4:202:THR:HG21	1.81	1.10
4:V:287:ILE:HG21	4:X:205:GLU:HG2	1.17	1.10
4:V:290:ARG:CZ	4:X:202:THR:HG21	1.81	1.10
1:A:202:SER:CA	1:A:207:LYS:HE2	1.82	1.10
1:A:218:LEU:HB2	1:A:221:GLN:HG3	1.17	1.10
2:H:121:LEU:O	2:H:128:PHE:HB2	0.94	1.10
1:J:553:MLY:CE	4:V:45:VAL:HA	1.52	1.10
1:J:797:PHE:CD1	3:L:149:VAL:CG1	2.34	1.10
1:J:800:ARG:NE	3:L:149:VAL:HG22	1.65	1.10
4:3:290:ARG:CZ	4:5:202:THR:HG21	1.81	1.10
1:A:641:LYS:HE3	1:A:647:GLN:OE1	1.50	1.10
1:A:822:SER:OG	2:B:88:LEU:CD2	2.00	1.10
1:D:817:GLN:CD	2:E:127:ARG:NE	2.04	1.10
1:D:822:SER:CB	2:E:88:LEU:HD23	1.82	1.10
1:D:831:TRP:CZ2	2:E:47:LEU:CB	2.23	1.10
1:D:831:TRP:CD1	2:E:67:MET:SD	2.45	1.10
1:G:202:SER:CA	1:G:207:LYS:HE2	1.82	1.10
1:J:641:LYS:HE3	1:J:647:GLN:OE1	1.50	1.10
1:A:721:LYS:HA	1:A:736:GLN:CD	1.73	1.09
1:A:739:ASP:HB3	1:A:742:LYS:HB3	1.21	1.09
1:A:799:MET:SD	3:C:32:ASP:CB	2.38	1.09
1:D:639:GLY:HA2	4:5:345:ILE:HA	1.26	1.09
1:D:734:GLU:O	1:D:738:MET:HG2	1.51	1.09
1:D:817:GLN:HE21	2:E:127:ARG:HG2	1.12	1.09
3:I:24:LYS:CB	3:I:63:ILE:O	1.99	1.09
1:J:641:LYS:HD2	1:J:647:GLN:CD	1.70	1.09
1:J:768:MLY:HD3	1:J:772:LEU:HB3	1.30	1.09
4:6:287:ILE:HG21	4:8:205:GLU:HG2	1.17	1.09
1:A:530:MET:CE	4:4:354:GLN:HG2	1.80	1.09
1:A:538:GLU:HA	4:4:349:LEU:CD1	1.54	1.09
1:D:218:LEU:HB2	1:D:221:GLN:HG3	1.17	1.09
1:D:768:MLY:O	1:D:771:LEU:HD11	1.29	1.09
2:E:121:LEU:C	2:E:128:PHE:HB2	1.67	1.09
1:G:530:MET:CE	4:6:354:GLN:HG2	1.80	1.09
1:J:571:ALA:O	1:J:572:LYS:HG3	1.52	1.09
1:J:649:VAL:O	1:J:649:VAL:HG12	0.94	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:4:290:ARG:CZ	4:6:202:THR:HG21	1.81	1.09
1:D:571:ALA:O	1:D:572:LYS:HG3	1.52	1.09
3:F:24:LYS:CB	3:F:63:ILE:O	1.99	1.09
1:G:218:LEU:HB2	1:G:221:GLN:HG3	1.17	1.09
1:J:93:MET:O	1:J:714:ARG:O	1.71	1.09
1:J:641:LYS:HG3	1:J:647:GLN:HG3	1.20	1.09
1:J:721:LYS:HA	1:J:736:GLN:CD	1.73	1.09
1:J:754:ASP:OD2	1:J:776:GLU:CA	1.99	1.09
2:K:121:LEU:O	2:K:128:PHE:HB2	0.94	1.09
4:X:290:ARG:CZ	4:Z:202:THR:HG21	1.81	1.09
1:D:641:LYS:HE3	1:D:647:GLN:OE1	1.50	1.09
1:D:649:VAL:O	1:D:649:VAL:HG12	0.94	1.09
1:D:809:ARG:NH1	2:E:124:GLY:HA2	1.68	1.09
1:G:84:MLY:HH12	1:G:715:VAL:HG13	1.32	1.09
1:G:707:CYS:CB	1:G:714:ARG:HH12	1.65	1.09
1:G:831:TRP:HE1	2:H:67:MET:HG2	0.92	1.09
1:G:831:TRP:NE1	2:H:67:MET:CG	2.13	1.09
2:H:121:LEU:C	2:H:128:PHE:HB2	1.67	1.09
1:J:201:ALA:O	1:J:202:SER:HB3	1.36	1.09
1:J:649:VAL:HG22	1:J:649:VAL:HG13	1.21	1.09
1:J:734:GLU:O	1:J:738:MET:HG2	1.51	1.09
2:K:121:LEU:C	2:K:128:PHE:HB3	1.71	1.09
4:0:287:ILE:HG21	4:2:205:GLU:HG2	1.17	1.09
4:1:290:ARG:CZ	4:3:202:THR:HG21	1.81	1.09
1:A:734:GLU:O	1:A:738:MET:HG2	1.51	1.09
1:D:202:SER:CA	1:D:207:LYS:HE2	1.82	1.09
1:G:84:MLY:HH13	1:G:715:VAL:HG13	1.17	1.09
1:G:791:GLN:OE1	3:I:116:GLU:HB2	1.52	1.09
1:G:821:ARG:HH22	2:H:127:ARG:CG	1.63	1.09
2:H:111:SER:OG	2:H:148:VAL:O	1.71	1.09
1:J:643:GLY:O	1:J:644:SER:OG	1.70	1.09
2:K:117:LEU:HB2	2:K:147:ASN:CG	1.70	1.09
1:A:798:LEU:HD13	3:C:126:LEU:HD21	1.09	1.08
1:D:530:MET:HE2	4:5:354:GLN:CG	1.82	1.08
1:D:721:LYS:HA	1:D:736:GLN:CD	1.73	1.08
1:D:829:TRP:HE1	2:E:67:MET:CG	1.64	1.08
1:G:538:GLU:HA	4:6:349:LEU:CD1	1.55	1.08
2:K:111:SER:OG	2:K:148:VAL:O	1.71	1.08
4:X:287:ILE:HG21	4:Z:205:GLU:HG2	1.17	1.08
2:B:111:SER:CB	2:B:148:VAL:C	1.93	1.08
1:D:721:LYS:HG3	1:D:736:GLN:HG2	1.25	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:800:ARG:CB	3:F:149:VAL:HG22	1.83	1.08
1:J:95:THR:OG1	1:J:713:SER:HB3	1.50	1.08
1:J:769:ALA:CB	1:J:770:GLY:CA	2.31	1.08
1:A:635:GLY:HA2	4:4:334:GLU:HG2	1.16	1.08
1:D:834:LEU:CD2	2:E:54:MET:HG3	1.82	1.08
1:J:84:MLY:HH13	1:J:715:VAL:HG13	1.28	1.08
1:J:639:GLY:CA	4:7:345:ILE:HA	1.73	1.08
1:J:797:PHE:CD1	3:L:149:VAL:HG11	1.88	1.08
4:4:287:ILE:HG21	4:6:205:GLU:HG2	1.17	1.08
1:A:639:GLY:HA2	4:4:345:ILE:HA	1.26	1.08
2:E:111:SER:HB3	2:E:148:VAL:O	1.50	1.08
1:G:530:MET:HE2	4:6:354:GLN:HG2	1.27	1.08
1:G:734:GLU:O	1:G:738:MET:HG2	1.51	1.08
1:J:202:SER:CA	1:J:207:LYS:HE2	1.82	1.08
1:J:736:GLN:HA	1:J:743:ALA:HB3	1.35	1.08
1:A:798:LEU:HD11	3:C:126:LEU:CD2	1.79	1.08
2:E:111:SER:OG	2:E:148:VAL:O	1.71	1.08
1:J:639:GLY:HA2	4:7:345:ILE:HA	1.26	1.08
2:B:111:SER:CB	2:B:148:VAL:O	0.78	1.07
2:B:121:LEU:C	2:B:128:PHE:HB3	1.72	1.07
1:D:643:GLY:O	1:D:644:SER:OG	1.70	1.07
2:E:111:SER:CB	2:E:148:VAL:O	0.78	1.07
2:E:121:LEU:C	2:E:128:PHE:HB3	1.72	1.07
1:G:641:LYS:HE3	1:G:647:GLN:OE1	1.50	1.07
1:G:643:GLY:O	1:G:644:SER:OG	1.70	1.07
1:G:721:LYS:HG3	1:G:736:GLN:HG2	1.25	1.07
1:J:529:PRO:HB3	4:7:353:GLN:OE1	1.53	1.07
1:J:768:MLY:HH22	1:J:772:LEU:HB2	1.36	1.07
4:2:287:ILE:HG21	4:4:205:GLU:HG2	1.17	1.07
1:A:409:GLY:N	1:A:636:LYS:HG3	1.69	1.07
1:A:501:GLU:O	1:A:762:HIS:NE2	1.87	1.07
1:D:409:GLY:N	1:D:636:LYS:HG3	1.69	1.07
1:D:529:PRO:HB3	4:5:353:GLN:OE1	1.53	1.07
1:D:638:GLY:CA	4:5:341:ILE:O	2.01	1.07
1:G:721:LYS:HA	1:G:736:GLN:CD	1.73	1.07
2:H:111:SER:CB	2:H:148:VAL:O	0.77	1.07
1:J:530:MET:HE2	4:7:354:GLN:CG	1.84	1.07
1:D:769:ALA:HB1	1:D:770:GLY:C	1.72	1.07
1:G:72:VAL:HG13	1:G:76:GLN:HB3	1.36	1.07
1:G:529:PRO:HB3	4:6:353:GLN:OE1	1.53	1.07
1:G:641:LYS:CG	1:G:647:GLN:CG	2.16	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:641:LYS:HB2	1:G:647:GLN:NE2	1.68	1.07
1:J:831:TRP:CZ2	2:K:47:LEU:HD22	1.88	1.07
2:K:111:SER:CB	2:K:148:VAL:O	0.78	1.07
1:A:529:PRO:HB3	4:4:353:GLN:OE1	1.53	1.07
1:A:641:LYS:HB2	1:A:647:GLN:NE2	1.68	1.07
1:A:839:MLY:HD2	2:B:159:HIS:CG	1.88	1.07
1:D:541:MET:SD	4:5:345:ILE:O	2.12	1.07
1:G:409:GLY:N	1:G:636:LYS:HG3	1.69	1.07
1:J:541:MET:SD	4:7:345:ILE:O	2.13	1.07
1:J:638:GLY:CA	4:7:341:ILE:O	2.01	1.07
2:K:111:SER:CB	2:K:148:VAL:C	1.93	1.07
1:A:541:MET:SD	4:4:345:ILE:O	2.12	1.07
1:A:638:GLY:CA	4:4:341:ILE:O	2.01	1.07
1:G:638:GLY:CA	4:6:341:ILE:O	2.02	1.07
1:J:793:ARG:HE	3:L:147:MET:HA	0.93	1.07
1:J:795:ARG:HD3	3:L:35:ARG:HH22	1.14	1.07
1:A:502:GLU:HG3	1:A:761:GLY:HA3	1.34	1.06
1:D:834:LEU:CG	2:E:54:MET:CG	2.32	1.06
1:J:409:GLY:N	1:J:636:LYS:HG3	1.69	1.06
1:A:643:GLY:O	1:A:644:SER:OG	1.69	1.06
1:G:635:GLY:HA2	4:6:334:GLU:HG2	1.16	1.06
1:G:831:TRP:HH2	2:H:47:LEU:HD21	1.13	1.06
1:J:768:MLY:CH2	1:J:772:LEU:CD2	2.12	1.06
1:A:72:VAL:HG13	1:A:76:GLN:HB3	1.36	1.06
1:A:571:ALA:O	1:A:572:LYS:HG3	1.52	1.06
1:D:542:PHE:CG	4:5:143:TYR:HE1	1.73	1.06
1:D:736:GLN:HA	1:D:743:ALA:HB3	1.34	1.06
2:E:114:LYS:HA	2:E:146:GLY:O	0.89	1.06
1:G:541:MET:SD	4:6:345:ILE:O	2.13	1.06
2:H:111:SER:HB3	2:H:148:VAL:O	1.49	1.06
2:K:114:LYS:HA	2:K:146:GLY:O	0.89	1.06
1:D:576:GLU:HG2	1:D:577:ALA:N	1.66	1.06
1:G:797:PHE:CD1	3:I:149:VAL:CG1	2.03	1.06
1:J:510:TRP:CZ3	1:J:768:MLY:CH1	2.39	1.06
1:A:736:GLN:HA	1:A:743:ALA:HB3	1.35	1.06
1:A:793:ARG:NE	3:C:147:MET:HG2	1.70	1.06
1:A:795:ARG:CD	3:C:35:ARG:HH22	1.68	1.06
2:B:111:SER:OG	2:B:148:VAL:O	1.71	1.06
2:B:114:LYS:HA	2:B:146:GLY:O	0.89	1.06
1:D:641:LYS:HE3	4:5:348:SER:O	1.55	1.06
1:D:768:MLY:O	1:D:771:LEU:CD1	0.76	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:571:ALA:O	1:G:572:LYS:HG3	1.52	1.06
1:A:800:ARG:NH1	3:C:149:VAL:C	2.08	1.05
1:D:641:LYS:HB2	1:D:647:GLN:NE2	1.68	1.05
2:E:140:PHE:O	2:E:141:PRO:O	1.74	1.05
1:G:635:GLY:HA3	4:6:341:ILE:HD13	1.36	1.05
1:J:769:ALA:CB	1:J:770:GLY:HA2	1.86	1.05
2:K:140:PHE:O	2:K:141:PRO:O	1.75	1.05
1:A:530:MET:CA	4:4:354:GLN:HG3	1.86	1.05
1:A:721:LYS:HG3	1:A:736:GLN:HG2	1.25	1.05
1:D:831:TRP:CH2	2:E:34:ILE:HG23	1.89	1.05
1:J:530:MET:CA	4:7:354:GLN:HG3	1.87	1.05
4:1:3:ASP:HA	4:1:6:THR:HB	1.36	1.05
1:A:542:PHE:CG	4:4:143:TYR:HE1	1.73	1.05
1:D:72:VAL:HG13	1:D:76:GLN:HB3	1.36	1.05
1:D:795:ARG:HH21	3:F:116:GLU:CD	1.59	1.05
1:G:819:ASN:HA	2:H:90:GLY:O	0.87	1.05
1:J:638:GLY:HA2	4:7:341:ILE:O	1.57	1.05
1:J:641:LYS:HE3	4:7:348:SER:O	1.55	1.05
1:J:641:LYS:HB2	1:J:647:GLN:NE2	1.68	1.05
4:Y:3:ASP:HA	4:Y:6:THR:HB	1.36	1.05
1:A:797:PHE:CD1	3:C:149:VAL:CG1	2.33	1.05
1:G:542:PHE:CG	4:6:143:TYR:HE1	1.74	1.05
1:J:793:ARG:NE	3:L:147:MET:HA	1.71	1.05
1:J:795:ARG:HD2	3:L:35:ARG:NH1	1.72	1.05
1:J:797:PHE:HD1	3:L:149:VAL:HG12	1.21	1.05
1:J:819:ASN:CA	2:K:90:GLY:O	2.04	1.05
1:A:800:ARG:CB	3:C:149:VAL:HG22	1.83	1.05
1:J:72:VAL:HG13	1:J:76:GLN:HB3	1.36	1.05
1:J:641:LYS:HE3	1:J:647:GLN:CD	1.77	1.05
1:J:800:ARG:HB3	3:L:149:VAL:HG21	1.35	1.05
1:A:505:MLY:CB	1:A:762:HIS:H	1.68	1.04
1:A:635:GLY:HA3	4:4:341:ILE:HD13	1.37	1.04
1:D:530:MET:CA	4:5:354:GLN:HG3	1.87	1.04
1:D:829:TRP:HE1	2:E:67:MET:HG2	0.88	1.04
1:G:829:TRP:CH2	2:H:87:LYS:HE2	1.91	1.04
2:H:114:LYS:HA	2:H:146:GLY:O	0.88	1.04
1:A:599:ASN:HA	1:A:649:VAL:HB	1.06	1.04
1:A:641:LYS:HE3	1:A:647:GLN:CD	1.77	1.04
1:A:834:LEU:CD1	2:B:54:MET:HG3	1.86	1.04
3:C:49:ILE:CA	3:C:52:ASN:HD22	1.70	1.04
1:D:638:GLY:HA2	4:5:341:ILE:O	1.57	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:830:PRO:CD	2:E:67:MET:HE1	1.86	1.04
1:G:530:MET:HE2	4:6:354:GLN:CG	1.87	1.04
1:J:542:PHE:CG	4:7:143:TYR:HE1	1.73	1.04
1:J:576:GLU:HG2	1:J:577:ALA:N	1.66	1.04
1:J:736:GLN:N	1:J:743:ALA:CB	2.05	1.04
1:J:800:ARG:CZ	3:L:149:VAL:HG22	1.86	1.04
1:A:641:LYS:HD2	1:A:647:GLN:CD	1.70	1.04
1:G:641:LYS:HE3	1:G:647:GLN:CD	1.77	1.04
1:G:757:GLN:OE1	1:G:772:LEU:CG	2.03	1.04
1:G:769:ALA:HB1	1:G:770:GLY:HA2	1.37	1.04
1:G:817:GLN:HB3	2:H:127:ARG:CD	1.86	1.04
1:J:795:ARG:NH1	3:L:35:ARG:HH12	1.56	1.04
4:0:290:ARG:CZ	4:2:202:THR:CG2	2.36	1.04
4:W:3:ASP:HA	4:W:6:THR:HB	1.36	1.04
1:A:529:PRO:C	4:4:354:GLN:HB3	1.78	1.04
1:A:757:GLN:HB3	1:A:771:LEU:HD13	1.32	1.04
1:A:795:ARG:NH2	3:C:116:GLU:HB3	1.70	1.04
2:B:111:SER:HB3	2:B:148:VAL:O	1.49	1.04
1:G:93:MET:O	1:G:714:ARG:O	1.76	1.04
1:G:789:ALA:CB	3:I:81:GLN:HE21	1.68	1.04
4:2:3:ASP:HA	4:2:6:THR:HB	1.36	1.04
4:8:290:ARG:CZ	4:W:202:THR:CG2	2.36	1.04
1:J:56:GLU:HB2	1:J:59:MLY:HB3	1.40	1.04
1:A:538:GLU:OE2	4:4:355:MET:HE1	1.55	1.03
1:D:202:SER:CA	1:D:207:LYS:CE	2.36	1.03
1:D:641:LYS:HE3	1:D:647:GLN:CD	1.77	1.03
1:G:639:GLY:N	4:6:345:ILE:N	1.94	1.03
1:G:641:LYS:HD2	1:G:647:GLN:CD	1.70	1.03
2:K:149:ASP:OD2	2:K:150:TYR:N	1.91	1.03
4:2:290:ARG:CZ	4:4:202:THR:CG2	2.36	1.03
4:V:290:ARG:CZ	4:X:202:THR:CG2	2.36	1.03
1:A:502:GLU:OE1	1:A:763:THR:N	1.89	1.03
1:A:795:ARG:HH21	3:C:116:GLU:CB	1.71	1.03
1:A:800:ARG:HH11	3:C:149:VAL:C	1.61	1.03
1:G:56:GLU:HB2	1:G:59:MLY:HB3	1.40	1.03
1:G:599:ASN:HA	1:G:649:VAL:HB	1.05	1.03
4:4:3:ASP:HA	4:4:6:THR:HB	1.36	1.03
4:6:290:ARG:CZ	4:8:202:THR:CG2	2.36	1.03
4:W:290:ARG:CZ	4:Y:202:THR:CG2	2.36	1.03
4:X:290:ARG:CZ	4:Z:202:THR:CG2	2.36	1.03
1:A:642:LYS:HG3	4:4:23:GLY:H	0.87	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:49:ILE:CA	3:F:52:ASN:HD22	1.70	1.03
1:G:639:GLY:HA3	4:6:344:SER:C	1.78	1.03
3:L:49:ILE:CA	3:L:52:ASN:HD22	1.71	1.03
1:A:639:GLY:HA3	4:4:344:SER:C	1.78	1.03
1:A:795:ARG:HD2	3:C:35:ARG:HH12	0.88	1.03
1:A:836:PHE:CE2	2:B:160:GLY:CA	2.40	1.03
2:B:140:PHE:O	2:B:141:PRO:O	1.75	1.03
1:D:553:MLY:CB	4:7:46:GLY:CA	2.32	1.03
2:H:149:ASP:OD2	2:H:150:TYR:N	1.91	1.03
3:I:49:ILE:CA	3:I:52:ASN:HD22	1.70	1.03
1:J:202:SER:CA	1:J:207:LYS:CE	2.36	1.03
1:J:553:MLY:HB3	4:V:46:GLY:CA	1.51	1.03
4:3:3:ASP:HA	4:3:6:THR:HB	1.36	1.03
1:A:638:GLY:HA2	4:4:341:ILE:O	1.56	1.03
1:G:93:MET:HE3	1:G:763:THR:HB	1.03	1.03
1:G:557:GLU:N	4:8:48:GLY:CA	2.12	1.03
1:J:93:MET:HG3	1:J:764:MLY:NZ	1.72	1.03
1:J:795:ARG:HE	3:L:118:MET:HE1	1.16	1.03
4:4:290:ARG:CZ	4:6:202:THR:CG2	2.36	1.03
4:7:290:ARG:CZ	4:V:202:THR:CG2	2.36	1.03
4:V:3:ASP:HA	4:V:6:THR:HB	1.36	1.03
4:X:3:ASP:HA	4:X:6:THR:HB	1.36	1.03
1:A:202:SER:CA	1:A:207:LYS:CE	2.36	1.02
1:A:501:GLU:O	1:A:762:HIS:CD2	2.12	1.02
1:A:502:GLU:O	1:A:761:GLY:HA2	1.58	1.02
1:A:541:MET:HB3	4:4:143:TYR:OH	1.60	1.02
1:A:641:LYS:HG3	1:A:647:GLN:HG3	1.21	1.02
1:A:641:LYS:HE3	4:4:348:SER:O	1.56	1.02
1:A:646:PHE:HE2	1:A:652:LEU:HD21	1.24	1.02
1:A:813:ILE:HG23	2:B:127:ARG:HD2	1.05	1.02
1:A:834:LEU:HD11	2:B:54:MET:HB3	1.32	1.02
2:E:144:VAL:HG13	2:E:153:ILE:HD11	1.21	1.02
1:G:529:PRO:C	4:6:354:GLN:HB3	1.79	1.02
1:G:642:LYS:HG3	4:6:23:GLY:H	0.85	1.02
1:G:817:GLN:CB	2:H:127:ARG:HD2	1.89	1.02
1:G:836:PHE:CE2	2:H:160:GLY:N	2.26	1.02
2:H:140:PHE:O	2:H:141:PRO:O	1.75	1.02
1:J:541:MET:HB3	4:7:143:TYR:OH	1.59	1.02
4:0:3:ASP:HA	4:0:6:THR:HB	1.36	1.02
4:8:3:ASP:HA	4:8:6:THR:HB	1.36	1.02
1:D:642:LYS:HG3	4:5:23:GLY:H	0.86	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:150:TYR:O	2:E:151:LYS:CB	2.06	1.02
1:G:530:MET:CA	4:6:354:GLN:HG3	1.88	1.02
1:G:638:GLY:HA2	4:6:341:ILE:O	1.58	1.02
4:5:290:ARG:CZ	4:7:202:THR:CG2	2.36	1.02
4:6:3:ASP:HA	4:6:6:THR:HB	1.36	1.02
1:A:800:ARG:CG	3:C:149:VAL:HG22	1.88	1.02
2:B:149:ASP:OD2	2:B:150:TYR:N	1.91	1.02
1:D:639:GLY:HA3	4:5:344:SER:C	1.78	1.02
1:D:817:GLN:NE2	2:E:127:ARG:HG2	1.74	1.02
1:J:553:MLY:CB	4:V:46:GLY:CA	2.33	1.02
1:J:599:ASN:CA	1:J:649:VAL:HB	1.89	1.02
1:J:639:GLY:HA3	4:7:344:SER:C	1.78	1.02
1:J:800:ARG:HB2	3:L:149:VAL:HG21	1.36	1.02
2:K:144:VAL:HG13	2:K:153:ILE:HD11	1.21	1.02
2:K:144:VAL:HG11	2:K:153:ILE:HG12	1.37	1.02
3:L:24:LYS:CG	3:L:63:ILE:O	2.08	1.02
4:3:290:ARG:CZ	4:5:202:THR:CG2	2.36	1.02
1:A:800:ARG:HB3	3:C:149:VAL:HG21	1.05	1.02
1:D:800:ARG:HD2	3:F:149:VAL:C	1.79	1.02
1:D:839:MLY:HH13	2:E:159:HIS:CG	1.94	1.02
3:F:24:LYS:HG2	3:F:63:ILE:O	1.59	1.02
4:1:290:ARG:CZ	4:3:202:THR:CG2	2.36	1.02
4:6:287:ILE:HB	4:8:204:ALA:H	1.25	1.02
4:7:3:ASP:HA	4:7:6:THR:HB	1.36	1.02
4:Z:3:ASP:HA	4:Z:6:THR:HB	1.36	1.02
1:A:642:LYS:HD3	4:4:340:TRP:CH2	1.95	1.02
1:A:642:LYS:HD3	4:4:340:TRP:CZ3	1.95	1.02
2:B:121:LEU:HG	2:B:128:PHE:CA	1.59	1.02
1:D:507:GLY:HA3	1:D:762:HIS:CG	1.95	1.02
1:G:736:GLN:HA	1:G:743:ALA:HB3	1.35	1.02
1:J:754:ASP:HB2	1:J:776:GLU:HB3	1.38	1.02
3:C:24:LYS:HG2	3:C:63:ILE:O	1.59	1.01
1:D:557:GLU:N	4:7:48:GLY:CA	2.12	1.01
1:D:814:PHE:CE1	2:E:127:ARG:NH2	2.26	1.01
1:G:576:GLU:HG2	1:G:577:ALA:H	0.85	1.01
3:I:24:LYS:CG	3:I:63:ILE:O	2.08	1.01
1:J:98:HIS:HB3	1:J:100:PRO:HD2	1.42	1.01
4:1:290:ARG:NH2	4:3:202:THR:CG2	2.23	1.01
4:3:290:ARG:NH2	4:5:202:THR:CG2	2.23	1.01
4:8:290:ARG:NH2	4:W:202:THR:CG2	2.23	1.01
4:W:290:ARG:NH2	4:Y:202:THR:CG2	2.23	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:599:ASN:CA	1:D:649:VAL:HB	1.89	1.01
1:D:830:PRO:CD	2:E:67:MET:CE	2.37	1.01
1:G:751:GLY:HA2	3:I:114:LEU:HD13	1.40	1.01
2:H:144:VAL:HG13	2:H:153:ILE:HD11	1.21	1.01
3:I:49:ILE:HA	3:I:52:ASN:HD22	1.22	1.01
1:J:757:GLN:NE2	1:J:776:GLU:HG2	1.75	1.01
4:1:287:ILE:HB	4:3:204:ALA:H	1.25	1.01
4:2:287:ILE:HB	4:4:204:ALA:H	1.25	1.01
4:6:290:ARG:NH2	4:8:202:THR:CG2	2.23	1.01
1:A:599:ASN:CA	1:A:649:VAL:HB	1.89	1.01
1:A:639:GLY:N	4:4:345:ILE:N	1.94	1.01
1:A:822:SER:CB	2:B:88:LEU:HD23	1.91	1.01
2:B:144:VAL:HG11	2:B:153:ILE:HG12	1.38	1.01
2:E:144:VAL:HG11	2:E:153:ILE:HG12	1.38	1.01
2:E:149:ASP:OD2	2:E:150:TYR:N	1.91	1.01
1:G:797:PHE:CG	3:I:149:VAL:HG11	1.95	1.01
1:J:599:ASN:HA	1:J:649:VAL:HB	1.05	1.01
1:J:635:GLY:HA3	4:7:341:ILE:HD13	1.36	1.01
4:5:290:ARG:NH2	4:7:202:THR:CG2	2.23	1.01
4:W:287:ILE:HB	4:Y:204:ALA:H	1.26	1.01
2:B:150:TYR:O	2:B:151:LYS:CB	2.07	1.01
1:D:541:MET:HB3	4:5:143:TYR:OH	1.60	1.01
1:D:553:MLY:HG2	4:7:44:MET:O	1.59	1.01
1:G:202:SER:CA	1:G:207:LYS:CE	2.36	1.01
1:G:641:LYS:HE3	1:G:647:GLN:HB2	1.42	1.01
2:H:144:VAL:HG11	2:H:153:ILE:HG12	1.38	1.01
1:A:793:ARG:HE	3:C:147:MET:HG2	1.24	1.01
3:C:48:LYS:O	3:C:52:ASN:ND2	1.94	1.01
1:D:635:GLY:HA3	4:5:341:ILE:HD13	1.37	1.01
1:D:788:THR:HG23	3:F:42:THR:HG21	1.42	1.01
2:E:163:ALA:O	2:K:22:THR:N	1.94	1.01
1:G:84:MLY:HH12	1:G:715:VAL:CG1	1.83	1.01
1:G:553:MLY:HG2	4:8:44:MET:O	1.60	1.01
3:I:48:LYS:O	3:I:52:ASN:ND2	1.94	1.01
1:J:641:LYS:HE3	1:J:647:GLN:HB2	1.43	1.01
1:J:642:LYS:HG3	4:7:23:GLY:H	0.86	1.01
2:K:121:LEU:CB	2:K:128:PHE:HB3	1.69	1.01
3:L:48:LYS:O	3:L:52:ASN:ND2	1.94	1.01
4:4:290:ARG:NH2	4:6:202:THR:CG2	2.23	1.01
4:7:290:ARG:NH2	4:V:202:THR:CG2	2.23	1.01
1:A:502:GLU:CA	1:A:761:GLY:HA3	1.91	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:206:LYS:HD2	1:D:217:THR:HG23	1.41	1.00
1:D:553:MLY:HB3	4:7:46:GLY:CA	1.51	1.00
1:G:599:ASN:CA	1:G:649:VAL:HB	1.89	1.00
1:G:646:PHE:HE2	1:G:652:LEU:HD21	1.24	1.00
3:I:24:LYS:HG2	3:I:63:ILE:O	1.59	1.00
1:J:84:MLY:HH12	1:J:715:VAL:HG13	1.03	1.00
1:J:553:MLY:HG2	4:V:44:MET:O	1.59	1.00
1:J:557:GLU:N	4:V:48:GLY:CA	2.12	1.00
1:J:642:LYS:HD3	4:7:340:TRP:CH2	1.96	1.00
1:J:646:PHE:HE2	1:J:652:LEU:HD21	1.24	1.00
1:J:707:CYS:SG	1:J:714:ARG:NH1	2.31	1.00
4:5:3:ASP:HA	4:5:6:THR:HB	1.36	1.00
1:A:149:GLN:HG2	1:A:719:ASP:OD1	1.57	1.00
1:A:206:LYS:HD2	1:A:217:THR:HG23	1.41	1.00
1:A:501:GLU:O	1:A:762:HIS:CE1	2.14	1.00
1:A:530:MET:HE2	4:4:354:GLN:CG	1.91	1.00
1:A:534:SER:O	4:4:351:THR:HA	1.60	1.00
1:A:800:ARG:HD2	3:C:149:VAL:C	1.81	1.00
1:D:599:ASN:HA	1:D:649:VAL:HB	1.05	1.00
1:D:769:ALA:HA	1:D:771:LEU:HA	1.42	1.00
1:D:800:ARG:HB3	3:F:149:VAL:HG22	1.38	1.00
1:G:93:MET:HE1	1:G:763:THR:CG2	1.86	1.00
1:G:642:LYS:HD3	4:6:340:TRP:CH2	1.96	1.00
1:G:800:ARG:HD2	3:I:149:VAL:CG2	1.90	1.00
1:J:800:ARG:CG	3:L:149:VAL:CG2	2.38	1.00
3:L:24:LYS:HG2	3:L:63:ILE:O	1.59	1.00
4:5:287:ILE:HB	4:7:204:ALA:H	1.25	1.00
4:X:287:ILE:HB	4:Z:204:ALA:H	1.25	1.00
1:A:576:GLU:HG2	1:A:577:ALA:H	0.85	1.00
1:A:641:LYS:HE3	1:A:647:GLN:CB	1.91	1.00
1:D:174:SER:HB3	1:D:667:THR:HG21	1.44	1.00
1:D:809:ARG:NH1	2:E:124:GLY:CA	2.23	1.00
3:F:24:LYS:CG	3:F:63:ILE:O	2.08	1.00
3:F:49:ILE:HA	3:F:52:ASN:HD22	1.22	1.00
1:G:215:GLN:CA	1:G:340:ILE:HG23	1.92	1.00
1:G:534:SER:O	4:6:351:THR:HA	1.60	1.00
1:G:534:SER:C	4:6:351:THR:HA	1.82	1.00
1:J:90:ASP:CB	1:J:764:MLY:HH21	1.89	1.00
1:J:529:PRO:C	4:7:354:GLN:HB3	1.77	1.00
1:J:534:SER:C	4:7:351:THR:HA	1.81	1.00
4:2:290:ARG:NH2	4:4:202:THR:CG2	2.23	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:736:GLN:N	1:A:743:ALA:CB	2.05	1.00
3:C:24:LYS:CG	3:C:63:ILE:O	2.08	1.00
1:D:642:LYS:HD3	4:5:340:TRP:CZ3	1.95	1.00
1:G:576:GLU:CG	1:G:577:ALA:H	1.75	1.00
1:G:641:LYS:HE3	1:G:647:GLN:CB	1.91	1.00
1:G:642:LYS:HD3	4:6:340:TRP:CZ3	1.96	1.00
2:H:150:TYR:O	2:H:151:LYS:CB	2.06	1.00
1:J:174:SER:HB3	1:J:667:THR:HG21	1.44	1.00
1:J:642:LYS:HD3	4:7:340:TRP:CZ3	1.96	1.00
4:0:286:ASP:OD1	4:2:203:THR:HG22	1.62	1.00
1:A:641:LYS:HE3	1:A:647:GLN:HB2	1.42	1.00
1:D:218:LEU:CA	1:D:221:GLN:HG3	1.91	1.00
1:D:534:SER:O	4:5:351:THR:HA	1.60	1.00
1:D:641:LYS:HE3	1:D:647:GLN:HB2	1.42	1.00
1:D:809:ARG:HH12	2:E:124:GLY:HA2	1.27	1.00
1:G:541:MET:HB3	4:6:143:TYR:OH	1.59	1.00
1:J:93:MET:HG2	1:J:764:MLY:CD	1.78	1.00
1:J:757:GLN:OE1	1:J:772:LEU:C	2.00	1.00
1:A:56:GLU:HB2	1:A:59:MLY:HB3	1.40	1.00
1:D:642:LYS:HD3	4:5:340:TRP:CH2	1.95	1.00
1:D:831:TRP:HD1	2:E:67:MET:SD	1.81	1.00
1:G:206:LYS:HD2	1:G:217:THR:HG23	1.41	1.00
1:A:576:GLU:CG	1:A:577:ALA:H	1.75	1.00
1:G:98:HIS:HB3	1:G:100:PRO:HD2	1.42	1.00
4:6:286:ASP:OD1	4:8:203:THR:HG22	1.62	1.00
4:7:286:ASP:OD1	4:V:203:THR:HG22	1.62	1.00
4:V:290:ARG:NH2	4:X:202:THR:CG2	2.24	1.00
4:W:286:ASP:OD1	4:Y:203:THR:HG22	1.62	1.00
1:D:98:HIS:HB3	1:D:100:PRO:HD2	1.42	0.99
1:A:576:GLU:HG2	1:A:577:ALA:N	1.66	0.99
1:A:795:ARG:HD3	3:C:35:ARG:HH22	1.25	0.99
1:J:206:LYS:HD2	1:J:217:THR:HG23	1.41	0.99
2:K:141:PRO:HB2	2:K:142:PRO:HD2	1.44	0.99
4:0:290:ARG:NH2	4:2:202:THR:CG2	2.23	0.99
4:V:286:ASP:OD1	4:X:203:THR:HG22	1.62	0.99
1:A:501:GLU:CG	1:A:762:HIS:HD1	1.74	0.99
1:A:612:GLN:HE22	1:A:627:GLY:CA	1.75	0.99
2:B:139:ALA:O	2:B:141:PRO:HD3	1.62	0.99
1:D:56:GLU:HB2	1:D:59:MLY:HB3	1.40	0.99
1:D:800:ARG:CB	3:F:149:VAL:CG2	2.37	0.99
3:F:48:LYS:O	3:F:52:ASN:ND2	1.94	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:218:LEU:CA	1:J:221:GLN:HG3	1.91	0.99
4:2:322:PRO:HB3	4:4:244:ASP:OD2	1.62	0.99
4:V:287:ILE:HB	4:X:204:ALA:H	1.25	0.99
4:X:290:ARG:NH2	4:Z:202:THR:CG2	2.23	0.99
1:A:797:PHE:HD1	3:C:149:VAL:HG12	1.27	0.99
4:4:286:ASP:OD1	4:6:203:THR:HG22	1.62	0.99
4:4:322:PRO:HB3	4:6:244:ASP:OD2	1.62	0.99
1:A:502:GLU:CG	1:A:761:GLY:HA3	1.92	0.99
1:A:534:SER:C	4:4:351:THR:HA	1.81	0.99
1:D:534:SER:C	4:5:351:THR:HA	1.81	0.99
1:D:639:GLY:CA	4:5:345:ILE:CA	2.41	0.99
1:D:792:ALA:HB1	3:F:40:ASN:CB	1.92	0.99
2:E:139:ALA:O	2:E:141:PRO:HD3	1.62	0.99
1:G:649:VAL:CG1	1:G:649:VAL:HG22	1.92	0.99
2:H:121:LEU:HG	2:H:128:PHE:CA	1.59	0.99
1:J:641:LYS:HE3	1:J:647:GLN:CB	1.91	0.99
2:K:149:ASP:OD2	2:K:150:TYR:O	1.80	0.99
1:A:553:MLY:HG2	4:6:44:MET:O	1.59	0.99
1:A:834:LEU:HD11	2:B:54:MET:HG3	1.35	0.99
1:D:612:GLN:HE22	1:D:627:GLY:CA	1.75	0.99
4:1:286:ASP:OD1	4:3:203:THR:HG22	1.62	0.99
4:6:322:PRO:HB3	4:8:244:ASP:OD2	1.62	0.99
1:D:834:LEU:HD11	2:E:54:MET:CB	1.92	0.99
1:J:639:GLY:CA	4:7:345:ILE:CA	2.40	0.99
4:5:286:ASP:OD1	4:7:203:THR:HG22	1.62	0.99
4:8:287:ILE:HB	4:W:204:ALA:H	1.25	0.99
1:A:836:PHE:HB3	2:B:161:GLU:CD	1.83	0.99
1:D:529:PRO:C	4:5:354:GLN:HB3	1.78	0.99
2:E:149:ASP:OD2	2:E:150:TYR:O	1.80	0.99
1:G:218:LEU:CA	1:G:221:GLN:HG3	1.91	0.99
1:J:215:GLN:CA	1:J:340:ILE:HG23	1.91	0.99
1:J:798:LEU:CD2	3:L:126:LEU:CD1	2.36	0.99
1:A:98:HIS:HB3	1:A:100:PRO:HD2	1.42	0.99
1:A:215:GLN:CA	1:A:340:ILE:HG23	1.92	0.99
1:A:218:LEU:CA	1:A:221:GLN:HG3	1.91	0.99
1:A:797:PHE:CE2	3:C:126:LEU:CD2	2.45	0.99
1:D:576:GLU:HG2	1:D:577:ALA:H	0.85	0.99
1:D:639:GLY:N	4:5:345:ILE:N	1.94	0.99
1:J:534:SER:O	4:7:351:THR:HG23	1.13	0.99
4:0:322:PRO:HB3	4:2:244:ASP:OD2	1.62	0.99
4:X:286:ASP:OD1	4:Z:203:THR:HG22	1.62	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:797:PHE:HE2	3:C:126:LEU:HD23	1.26	0.99
2:B:149:ASP:OD2	2:B:150:TYR:O	1.80	0.99
1:D:641:LYS:CG	4:5:348:SER:HB2	1.87	0.99
1:G:530:MET:CE	4:6:354:GLN:CG	2.39	0.99
1:D:768:MLY:C	1:D:771:LEU:HD12	1.61	0.98
1:G:831:TRP:CZ2	2:H:67:MET:SD	2.56	0.98
2:K:121:LEU:HG	2:K:128:PHE:CA	1.60	0.98
4:3:287:ILE:HB	4:5:204:ALA:H	1.26	0.98
4:8:322:PRO:HB3	4:W:244:ASP:OD2	1.62	0.98
1:A:639:GLY:CA	4:4:345:ILE:CA	2.41	0.98
1:D:649:VAL:CG1	1:D:649:VAL:HG22	1.92	0.98
2:E:112:ILE:O	2:E:147:ASN:C	2.01	0.98
1:G:798:LEU:HD23	3:I:122:GLU:HB3	1.45	0.98
1:J:508:ILE:CD1	1:J:759:ALA:CB	2.31	0.98
1:J:649:VAL:CG1	1:J:649:VAL:HG22	1.92	0.98
1:J:831:TRP:CZ2	2:K:47:LEU:CD2	2.47	0.98
4:1:322:PRO:HB3	4:3:244:ASP:OD2	1.62	0.98
4:W:322:PRO:HB3	4:Y:244:ASP:OD2	1.62	0.98
1:A:649:VAL:CG1	1:A:649:VAL:HG22	1.92	0.98
1:A:819:ASN:H	2:B:90:GLY:HA3	1.28	0.98
2:B:141:PRO:HB2	2:B:142:PRO:HD2	1.44	0.98
1:G:639:GLY:CA	4:6:345:ILE:CA	2.40	0.98
1:G:788:THR:O	3:I:42:THR:HG22	1.62	0.98
1:J:757:GLN:CD	1:J:776:GLU:CG	2.32	0.98
1:A:530:MET:CE	4:4:354:GLN:CG	2.41	0.98
2:B:112:ILE:O	2:B:147:ASN:C	2.01	0.98
1:D:215:GLN:CA	1:D:340:ILE:HG23	1.92	0.98
1:G:641:LYS:HE3	4:6:348:SER:O	1.56	0.98
2:K:150:TYR:O	2:K:151:LYS:CB	2.06	0.98
4:2:286:ASP:OD1	4:4:203:THR:HG22	1.62	0.98
1:A:836:PHE:HB3	2:B:161:GLU:OE1	1.60	0.98
3:C:52:ASN:HB2	3:C:53:PRO:HD3	1.45	0.98
1:D:530:MET:CE	4:5:354:GLN:CG	2.40	0.98
1:D:641:LYS:HE3	1:D:647:GLN:CB	1.91	0.98
1:G:612:GLN:HE22	1:G:627:GLY:CA	1.75	0.98
2:H:112:ILE:O	2:H:147:ASN:C	2.01	0.98
1:J:641:LYS:HG3	1:J:647:GLN:NE2	1.59	0.98
1:J:800:ARG:NH1	3:L:149:VAL:CG1	2.17	0.98
1:A:206:LYS:CD	1:A:217:THR:CG2	2.16	0.98
2:E:121:LEU:HG	2:E:128:PHE:CA	1.59	0.98
1:G:817:GLN:HG2	2:H:127:ARG:HB2	1.40	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:121:LEU:C	2:H:128:PHE:HB3	1.71	0.98
2:K:112:ILE:O	2:K:147:ASN:C	2.02	0.98
1:A:505:MLY:HB2	1:A:762:HIS:N	1.76	0.98
1:A:641:LYS:CG	4:4:348:SER:HB2	1.87	0.98
2:B:117:LEU:CB	2:B:147:ASN:CG	2.32	0.98
1:D:576:GLU:CG	1:D:577:ALA:H	1.75	0.98
1:D:642:LYS:HD2	4:5:24:ASP:O	1.64	0.98
1:D:646:PHE:HE2	1:D:652:LEU:HD21	1.24	0.98
2:E:130:PRO:O	2:E:133:ILE:N	1.96	0.98
1:G:576:GLU:HG2	1:G:577:ALA:N	1.66	0.98
1:J:534:SER:O	4:7:351:THR:HA	1.60	0.98
3:C:49:ILE:HA	3:C:52:ASN:HD22	1.22	0.98
2:E:117:LEU:CB	2:E:147:ASN:CG	2.32	0.98
2:E:150:TYR:C	2:E:151:LYS:HG3	1.83	0.98
4:4:287:ILE:HB	4:6:204:ALA:H	1.25	0.98
2:E:141:PRO:HB2	2:E:142:PRO:HD2	1.44	0.98
2:H:141:PRO:HB2	2:H:142:PRO:HD2	1.44	0.98
1:J:612:GLN:HE22	1:J:627:GLY:CA	1.76	0.98
3:L:52:ASN:HB2	3:L:53:PRO:HD3	1.46	0.98
1:A:831:TRP:HH2	2:B:50:THR:HB	1.25	0.97
2:K:139:ALA:O	2:K:141:PRO:HD3	1.62	0.97
3:L:49:ILE:HA	3:L:52:ASN:HD22	1.23	0.97
4:3:322:PRO:HB3	4:5:244:ASP:OD2	1.62	0.97
2:B:130:PRO:O	2:B:133:ILE:N	1.96	0.97
1:D:218:LEU:CA	1:D:221:GLN:CG	2.42	0.97
1:D:795:ARG:HB3	3:F:35:ARG:NE	1.35	0.97
2:H:149:ASP:OD2	2:H:150:TYR:O	1.80	0.97
1:J:576:GLU:HG2	1:J:577:ALA:H	0.85	0.97
1:A:174:SER:HB3	1:A:667:THR:HG21	1.44	0.97
2:B:150:TYR:C	2:B:151:LYS:HG3	1.83	0.97
3:F:46:ILE:O	3:F:50:LEU:HG	1.65	0.97
2:H:117:LEU:CB	2:H:147:ASN:CG	2.32	0.97
4:3:286:ASP:OD1	4:5:203:THR:HG22	1.62	0.97
4:X:322:PRO:HB3	4:Z:244:ASP:OD2	1.62	0.97
1:A:795:ARG:CD	3:C:35:ARG:HH12	1.77	0.97
4:8:286:ASP:OD1	4:W:203:THR:HG22	1.62	0.97
1:A:215:GLN:H	1:A:340:ILE:CG1	1.73	0.97
1:A:218:LEU:CA	1:A:221:GLN:CG	2.42	0.97
1:A:542:PHE:CG	4:4:143:TYR:CE1	2.52	0.97
1:A:642:LYS:HG2	4:4:21:PHE:O	1.65	0.97
1:G:829:TRP:CZ3	2:H:87:LYS:NZ	2.30	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:139:ALA:O	2:H:141:PRO:HD3	1.62	0.97
1:J:642:LYS:HG2	4:7:21:PHE:O	1.65	0.97
2:K:130:PRO:O	2:K:133:ILE:N	1.96	0.97
4:7:287:ILE:HB	4:V:204:ALA:H	1.25	0.97
1:A:502:GLU:C	1:A:761:GLY:HA3	1.84	0.97
2:H:121:LEU:HG	2:H:128:PHE:HA	1.46	0.97
2:K:117:LEU:CB	2:K:147:ASN:CG	2.32	0.97
4:0:287:ILE:HB	4:2:204:ALA:H	1.25	0.97
1:G:174:SER:HB3	1:G:667:THR:HG21	1.44	0.97
1:G:784:ALA:O	1:G:788:THR:N	1.96	0.97
1:J:639:GLY:N	4:7:345:ILE:N	1.94	0.97
1:J:754:ASP:OD2	1:J:776:GLU:C	2.03	0.97
2:K:150:TYR:C	2:K:151:LYS:HG3	1.83	0.97
2:E:121:LEU:HG	2:E:128:PHE:HA	1.46	0.97
1:G:736:GLN:CA	1:G:743:ALA:HB2	1.95	0.97
1:J:649:VAL:CG2	1:J:649:VAL:CA	2.42	0.97
1:D:724:TYR:HE1	1:D:778:MET:HB3	1.24	0.97
1:G:642:LYS:HG2	4:6:21:PHE:O	1.65	0.97
1:J:218:LEU:CA	1:J:221:GLN:CG	2.42	0.97
1:J:576:GLU:CG	1:J:577:ALA:H	1.75	0.97
1:J:797:PHE:CB	3:L:149:VAL:HG11	1.94	0.97
1:D:542:PHE:CG	4:5:143:TYR:CE1	2.52	0.97
1:G:218:LEU:CA	1:G:221:GLN:CG	2.42	0.97
2:H:130:PRO:O	2:H:133:ILE:N	1.96	0.97
1:A:501:GLU:HG2	1:A:762:HIS:HD1	0.83	0.96
1:A:502:GLU:O	1:A:761:GLY:CA	2.13	0.96
1:A:795:ARG:NH2	3:C:116:GLU:CD	2.18	0.96
1:D:724:TYR:C	1:D:782:MLY:HH21	1.85	0.96
1:G:819:ASN:HA	2:H:90:GLY:C	1.85	0.96
3:L:46:ILE:O	3:L:50:LEU:HG	1.64	0.96
2:E:150:TYR:O	2:E:151:LYS:HG3	1.65	0.96
1:J:642:LYS:HD2	4:7:24:ASP:O	1.64	0.96
1:J:768:MLY:HH12	1:J:772:LEU:HD23	1.44	0.96
1:A:534:SER:O	4:4:351:THR:HG23	1.13	0.96
1:A:795:ARG:NE	3:C:118:MET:HE1	1.80	0.96
1:D:215:GLN:H	1:D:340:ILE:CG1	1.73	0.96
1:D:553:MLY:HB3	4:7:46:GLY:HA2	1.47	0.96
1:G:637:LYS:NZ	4:6:141:SER:O	1.99	0.96
4:V:322:PRO:HB3	4:X:244:ASP:OD2	1.62	0.96
2:B:144:VAL:HG13	2:B:153:ILE:HD11	1.22	0.96
1:D:649:VAL:CG2	1:D:649:VAL:CA	2.42	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:736:GLN:CA	1:D:743:ALA:HB2	1.95	0.96
2:H:117:LEU:HD13	2:H:147:ASN:OD1	1.64	0.96
1:A:642:LYS:HD2	4:4:24:ASP:O	1.64	0.96
2:B:150:TYR:O	2:B:151:LYS:HG3	1.65	0.96
1:A:538:GLU:N	4:4:349:LEU:CD1	2.28	0.96
1:A:649:VAL:CG1	1:A:649:VAL:CG2	2.43	0.96
1:G:635:GLY:HA3	4:6:334:GLU:HG2	1.47	0.96
1:G:649:VAL:CG2	1:G:649:VAL:CA	2.42	0.96
1:J:821:ARG:HH21	2:K:127:ARG:HG2	1.21	0.96
1:A:649:VAL:CG2	1:A:649:VAL:CA	2.43	0.96
1:D:642:LYS:HG2	4:5:21:PHE:O	1.65	0.96
1:G:642:LYS:HD2	4:6:24:ASP:O	1.64	0.96
1:J:543:PRO:CG	4:7:143:TYR:O	2.14	0.96
1:J:793:ARG:HE	3:L:147:MET:CA	1.77	0.96
4:5:322:PRO:HB3	4:7:244:ASP:OD2	1.62	0.96
4:V:288:ASP:HA	4:X:204:ALA:HB2	1.48	0.96
4:W:288:ASP:HA	4:Y:204:ALA:HB2	1.48	0.96
1:D:206:LYS:CD	1:D:217:THR:CG2	2.16	0.96
4:6:288:ASP:HA	4:8:204:ALA:HB2	1.48	0.96
4:7:288:ASP:HA	4:V:204:ALA:HB2	1.48	0.96
4:8:288:ASP:HA	4:W:204:ALA:HB2	1.48	0.96
1:G:641:LYS:HG3	1:G:647:GLN:NE2	1.58	0.96
1:G:735:GLY:C	1:G:743:ALA:CA	2.34	0.96
3:I:46:ILE:O	3:I:50:LEU:HG	1.64	0.96
1:J:542:PHE:CG	4:7:143:TYR:CE1	2.53	0.96
4:X:288:ASP:HA	4:Z:204:ALA:HB2	1.48	0.96
1:A:795:ARG:HH22	3:C:116:GLU:CD	1.69	0.96
2:B:121:LEU:HG	2:B:128:PHE:HA	1.47	0.96
3:C:46:ILE:O	3:C:50:LEU:HG	1.65	0.96
2:H:150:TYR:C	2:H:151:LYS:HG3	1.83	0.96
2:K:121:LEU:HG	2:K:128:PHE:HA	1.47	0.96
4:4:288:ASP:HA	4:6:204:ALA:HB2	1.48	0.96
4:5:288:ASP:HA	4:7:204:ALA:HB2	1.48	0.96
1:D:538:GLU:N	4:5:349:LEU:CD1	2.28	0.95
1:D:735:GLY:C	1:D:743:ALA:CA	2.34	0.95
1:D:792:ALA:C	3:F:40:ASN:HB3	1.85	0.95
1:G:206:LYS:CD	1:G:217:THR:CG2	2.16	0.95
4:0:288:ASP:HA	4:2:204:ALA:HB2	1.48	0.95
4:2:288:ASP:HA	4:4:204:ALA:HB2	1.48	0.95
1:D:726:VAL:CG2	1:D:782:MLY:HH22	1.96	0.95
1:J:649:VAL:CG1	1:J:649:VAL:CG2	2.43	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:736:GLN:CA	1:J:743:ALA:HB2	1.95	0.95
1:D:649:VAL:CG1	1:D:649:VAL:CG2	2.43	0.95
1:G:538:GLU:HG3	4:6:352:PHE:N	1.81	0.95
1:G:754:ASP:CB	1:G:776:GLU:OE2	2.14	0.95
1:J:817:GLN:CG	2:K:127:ARG:HD2	1.95	0.95
1:A:635:GLY:HA3	4:4:334:GLU:HG2	1.47	0.95
1:A:721:LYS:CA	1:A:736:GLN:CD	2.34	0.95
1:A:735:GLY:C	1:A:743:ALA:CA	2.34	0.95
1:D:839:MLY:HH11	2:E:159:HIS:HD2	1.18	0.95
1:G:530:MET:HA	4:6:354:GLN:HG3	0.97	0.95
1:G:649:VAL:CG1	1:G:649:VAL:CG2	2.44	0.95
1:G:790:THR:OG1	3:I:87:PHE:CD2	2.18	0.95
1:J:84:MLY:HE2	1:J:719:ASP:HB3	0.99	0.95
1:J:735:GLY:C	1:J:743:ALA:CA	2.34	0.95
4:3:288:ASP:HA	4:5:204:ALA:HB2	1.48	0.95
1:A:505:MLY:HG3	1:A:741:LYS:NZ	1.81	0.95
1:A:834:LEU:CD1	2:B:54:MET:CB	2.45	0.95
1:D:721:LYS:CA	1:D:736:GLN:CD	2.34	0.95
1:G:542:PHE:CG	4:6:143:TYR:CE1	2.53	0.95
1:J:553:MLY:HB3	4:V:46:GLY:HA2	1.48	0.95
4:1:288:ASP:HA	4:3:204:ALA:HB2	1.48	0.95
1:A:637:LYS:NZ	4:4:141:SER:O	1.99	0.95
1:D:641:LYS:HD2	1:D:647:GLN:CD	1.70	0.95
1:G:538:GLU:N	4:6:349:LEU:CD1	2.29	0.95
2:H:150:TYR:O	2:H:151:LYS:HB2	1.67	0.95
4:7:322:PRO:HB3	4:V:244:ASP:OD2	1.62	0.95
1:A:541:MET:N	4:4:349:LEU:HD21	1.80	0.95
1:D:724:TYR:HA	1:D:782:MLY:NZ	1.81	0.95
1:G:546:THR:HG22	1:G:548:THR:H	1.32	0.95
2:K:117:LEU:HD13	2:K:147:ASN:OD1	1.64	0.95
1:A:502:GLU:CD	1:A:764:MLY:N	2.20	0.95
2:B:117:LEU:HD13	2:B:147:ASN:OD1	1.64	0.95
1:D:543:PRO:CG	4:5:143:TYR:O	2.14	0.95
1:D:818:TYR:HB2	2:E:90:GLY:N	1.81	0.95
2:H:150:TYR:O	2:H:151:LYS:HG3	1.65	0.95
1:J:538:GLU:N	4:7:349:LEU:CD1	2.28	0.95
1:J:795:ARG:NH1	3:L:35:ARG:NH1	2.15	0.95
2:K:150:TYR:O	2:K:151:LYS:HG3	1.65	0.95
1:A:813:ILE:CG2	2:B:127:ARG:NE	2.26	0.95
1:A:819:ASN:N	2:B:90:GLY:HA3	1.81	0.95
2:E:150:TYR:O	2:E:151:LYS:CG	2.15	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:93:MET:CG	1:J:764:MLY:NZ	2.22	0.95
1:J:637:LYS:NZ	4:7:141:SER:O	1.98	0.95
1:A:543:PRO:CG	4:4:143:TYR:O	2.14	0.95
1:A:768:MLY:C	1:A:771:LEU:HB2	1.96	0.95
2:B:121:LEU:CB	2:B:128:PHE:HB3	1.69	0.95
1:D:215:GLN:HA	1:D:340:ILE:HG23	0.95	0.95
1:D:537:GLU:C	4:5:349:LEU:CD1	2.20	0.95
1:D:635:GLY:HA3	4:5:334:GLU:HG2	1.47	0.95
3:F:52:ASN:HB2	3:F:53:PRO:HD3	1.45	0.95
1:G:721:LYS:CA	1:G:736:GLN:CD	2.34	0.95
1:A:530:MET:HA	4:4:354:GLN:HG3	0.96	0.94
1:A:538:GLU:HG3	4:4:352:PHE:N	1.82	0.94
1:A:800:ARG:HH11	3:C:149:VAL:HG13	1.21	0.94
1:J:721:LYS:CA	1:J:736:GLN:CD	2.34	0.94
1:J:749:GLY:O	3:L:114:LEU:CD2	2.14	0.94
1:J:783:LEU:O	1:J:787:ILE:N	1.99	0.94
1:A:709:LYS:C	1:A:710:GLY:HA3	1.88	0.94
1:A:757:GLN:CB	1:A:771:LEU:CD1	2.05	0.94
1:D:637:LYS:NZ	4:5:141:SER:O	1.99	0.94
2:H:121:LEU:CB	2:H:128:PHE:HB3	1.69	0.94
1:A:530:MET:CA	4:4:354:GLN:CG	2.44	0.94
1:A:768:MLY:HB3	1:A:771:LEU:HB2	1.46	0.94
1:D:541:MET:N	4:5:349:LEU:HD21	1.80	0.94
1:J:538:GLU:HG3	4:7:352:PHE:N	1.82	0.94
1:J:635:GLY:HA3	4:7:334:GLU:HG2	1.47	0.94
2:K:150:TYR:O	2:K:151:LYS:CG	2.15	0.94
2:B:150:TYR:O	2:B:151:LYS:HB2	1.67	0.94
2:E:150:TYR:O	2:E:151:LYS:HB2	1.67	0.94
1:J:795:ARG:HH11	3:L:35:ARG:NH1	1.65	0.94
1:A:800:ARG:CD	3:C:149:VAL:C	2.35	0.94
1:G:84:MLY:CH2	1:G:716:LEU:O	2.14	0.94
1:G:642:LYS:CG	4:6:23:GLY:H	1.76	0.94
2:H:150:TYR:O	2:H:151:LYS:CG	2.15	0.94
1:A:502:GLU:CG	1:A:761:GLY:CA	2.45	0.94
1:D:538:GLU:HG3	4:5:352:PHE:N	1.82	0.94
1:G:93:MET:HE2	1:G:764:MLY:HG3	1.49	0.94
1:G:218:LEU:CB	1:G:221:GLN:CG	2.46	0.94
1:G:831:TRP:CE2	2:H:67:MET:SD	2.60	0.94
2:H:144:VAL:HG13	2:H:153:ILE:HG12	1.14	0.94
1:A:553:MLY:HB3	4:6:46:GLY:HA2	1.47	0.94
1:A:612:GLN:NE2	1:A:627:GLY:HA3	1.83	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:642:LYS:CG	4:4:23:GLY:H	1.77	0.94
1:D:530:MET:HA	4:5:354:GLN:HG3	0.96	0.94
1:D:546:THR:HG22	1:D:548:THR:H	1.32	0.94
1:D:839:MLY:NZ	2:E:159:HIS:HB3	1.83	0.94
1:G:834:LEU:HD13	2:H:51:PHE:HE1	0.79	0.94
3:I:52:ASN:HB2	3:I:53:PRO:HD3	1.46	0.94
1:J:530:MET:HA	4:7:354:GLN:HG3	0.96	0.94
1:J:612:GLN:NE2	1:J:627:GLY:CA	2.31	0.94
1:J:797:PHE:CA	3:L:149:VAL:HG11	1.98	0.94
1:J:823:PHE:CE1	2:K:156:VAL:O	2.21	0.94
1:A:218:LEU:CB	1:A:221:GLN:CG	2.46	0.94
1:A:736:GLN:CA	1:A:743:ALA:HB2	1.95	0.94
2:E:163:ALA:C	2:K:22:THR:H	1.69	0.94
1:A:768:MLY:HB3	1:A:771:LEU:CD1	1.97	0.93
1:D:218:LEU:CB	1:D:221:GLN:CG	2.46	0.93
1:J:798:LEU:HD22	3:L:126:LEU:HD11	0.94	0.93
1:J:800:ARG:NH1	3:L:149:VAL:HG22	1.84	0.93
2:B:150:TYR:O	2:B:151:LYS:CG	2.15	0.93
1:G:541:MET:N	4:6:349:LEU:HD21	1.80	0.93
1:G:543:PRO:CG	4:6:143:TYR:O	2.14	0.93
1:G:612:GLN:NE2	1:G:627:GLY:HA3	1.83	0.93
1:G:817:GLN:HG2	2:H:127:ARG:CB	1.97	0.93
1:D:507:GLY:O	1:D:761:GLY:HA3	1.69	0.93
1:D:798:LEU:CD1	3:F:126:LEU:HD21	1.97	0.93
1:D:839:MLY:CH1	2:E:159:HIS:HB3	1.97	0.93
1:G:707:CYS:C	1:G:714:ARG:HH22	1.70	0.93
1:J:557:GLU:H	4:V:48:GLY:HA2	1.32	0.93
1:D:817:GLN:HG3	2:E:127:ARG:HD3	1.49	0.93
1:D:830:PRO:HG2	2:E:67:MET:HE2	1.46	0.93
2:E:117:LEU:HD13	2:E:147:ASN:OD1	1.64	0.93
1:J:530:MET:CE	4:7:354:GLN:CG	2.40	0.93
1:J:537:GLU:C	4:7:349:LEU:CD1	2.20	0.93
1:J:612:GLN:NE2	1:J:627:GLY:HA3	1.83	0.93
1:A:557:GLU:N	4:6:48:GLY:CA	2.12	0.93
1:A:836:PHE:CE1	2:B:159:HIS:C	2.42	0.93
1:D:834:LEU:CD1	2:E:54:MET:HB2	1.98	0.93
1:J:508:ILE:HD11	1:J:759:ALA:HB1	1.48	0.93
1:J:530:MET:CA	4:7:354:GLN:CG	2.44	0.93
1:A:836:PHE:CZ	2:B:160:GLY:HA3	1.94	0.93
1:G:553:MLY:HB3	4:8:46:GLY:HA2	1.48	0.93
1:J:786:ILE:HG12	3:L:86:ASP:HB3	1.51	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:612:GLN:NE2	1:D:627:GLY:CA	2.31	0.93
1:J:538:GLU:N	4:7:351:THR:H	1.67	0.93
1:A:502:GLU:HG3	1:A:761:GLY:N	1.84	0.93
1:A:629:GLU:CB	1:A:643:GLY:O	2.17	0.93
1:A:753:VAL:HA	1:A:778:MET:SD	2.09	0.93
1:G:789:ALA:HB2	3:I:81:GLN:HE21	0.77	0.93
1:G:798:LEU:HD11	3:I:126:LEU:HD23	1.49	0.93
1:A:648:THR:HG21	1:A:651:ALA:HB2	1.50	0.93
1:D:831:TRP:CE2	2:E:47:LEU:HD23	1.94	0.93
1:G:612:GLN:NE2	1:G:627:GLY:CA	2.31	0.93
1:G:819:ASN:CB	2:H:90:GLY:O	2.16	0.93
1:J:206:LYS:CD	1:J:217:THR:CG2	2.16	0.93
1:J:739:ASP:HB3	1:J:742:LYS:CB	1.98	0.93
1:A:549:SER:C	4:6:46:GLY:HA3	1.90	0.92
1:A:215:GLN:HA	1:A:340:ILE:HG23	0.96	0.92
1:A:505:MLY:NZ	1:A:762:HIS:C	2.16	0.92
1:A:612:GLN:NE2	1:A:627:GLY:CA	2.31	0.92
1:A:793:ARG:HH21	3:C:147:MET:HB3	1.33	0.92
1:G:215:GLN:HA	1:G:340:ILE:HG23	0.95	0.92
1:G:530:MET:CA	4:6:354:GLN:CG	2.45	0.92
1:G:795:ARG:HB3	3:I:35:ARG:NH2	1.82	0.92
1:J:90:ASP:CG	1:J:764:MLY:CH1	2.37	0.92
1:J:215:GLN:HA	1:J:340:ILE:HG23	0.95	0.92
1:J:768:MLY:HD3	1:J:772:LEU:HB2	1.49	0.92
1:D:549:SER:C	4:7:46:GLY:HA3	1.90	0.92
1:G:642:LYS:CB	4:6:21:PHE:O	2.17	0.92
1:J:541:MET:N	4:7:349:LEU:HD21	1.80	0.92
1:J:549:SER:C	4:V:46:GLY:HA3	1.90	0.92
1:J:648:THR:HG21	1:J:651:ALA:HB2	1.50	0.92
1:J:768:MLY:HH12	1:J:772:LEU:HD21	1.49	0.92
1:A:641:LYS:HE3	1:A:647:GLN:CG	2.00	0.92
1:D:213:LYS:HA	1:D:220:ASP:CG	1.90	0.92
1:D:530:MET:CA	4:5:354:GLN:CG	2.44	0.92
1:D:834:LEU:CD1	2:E:54:MET:CB	2.47	0.92
1:G:537:GLU:C	4:6:349:LEU:CD1	2.21	0.92
1:A:739:ASP:HB3	1:A:742:LYS:CB	1.98	0.92
1:A:800:ARG:CB	3:C:149:VAL:HG21	1.89	0.92
1:D:557:GLU:H	4:7:48:GLY:HA2	1.32	0.92
1:J:546:THR:HG22	1:J:548:THR:H	1.32	0.92
1:J:636:LYS:HD2	4:7:332:PRO:HB3	1.52	0.92
1:J:818:TYR:HB3	2:K:90:GLY:HA3	1.51	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:821:ARG:HH22	2:K:127:ARG:HG2	1.31	0.92
1:A:642:LYS:CB	4:4:21:PHE:O	2.17	0.92
1:D:550:PHE:HA	4:7:46:GLY:CA	2.00	0.92
1:D:612:GLN:NE2	1:D:627:GLY:HA3	1.83	0.92
1:D:629:GLU:CB	1:D:643:GLY:O	2.17	0.92
1:D:790:THR:HA	3:F:87:PHE:CE2	2.04	0.92
1:J:213:LYS:HA	1:J:220:ASP:CG	1.90	0.92
1:J:629:GLU:CB	1:J:643:GLY:O	2.17	0.92
1:D:278:GLN:HG2	1:D:317:GLU:HB2	1.52	0.92
1:D:790:THR:N	3:F:87:PHE:HE2	1.67	0.92
1:G:629:GLU:CB	1:G:643:GLY:O	2.17	0.92
1:G:783:LEU:O	1:G:787:ILE:HB	1.70	0.92
1:A:795:ARG:HD2	3:C:35:ARG:CZ	1.99	0.92
1:A:546:THR:HG22	1:A:548:THR:H	1.32	0.92
1:A:636:LYS:HD2	4:4:332:PRO:HB3	1.51	0.92
1:D:790:THR:CA	3:F:87:PHE:CE2	2.47	0.92
1:G:648:THR:HG21	1:G:651:ALA:HB2	1.51	0.92
1:J:92:ALA:O	1:J:714:ARG:CD	2.18	0.92
1:A:831:TRP:CE2	2:B:51:PHE:CE1	2.58	0.92
1:D:537:GLU:O	4:5:349:LEU:HD13	0.74	0.92
1:G:641:LYS:HE3	1:G:647:GLN:CG	2.00	0.92
1:G:757:GLN:OE1	1:G:772:LEU:HG	1.70	0.92
1:G:831:TRP:CH2	2:H:47:LEU:HD21	1.93	0.92
1:J:550:PHE:HA	4:V:46:GLY:CA	2.00	0.92
1:D:636:LYS:HD2	4:5:332:PRO:HB3	1.52	0.91
1:D:648:THR:HG21	1:D:651:ALA:HB2	1.50	0.91
1:D:739:ASP:HB3	1:D:742:LYS:CB	1.98	0.91
1:G:549:SER:C	4:8:46:GLY:HA3	1.90	0.91
1:G:795:ARG:CG	3:I:35:ARG:HH22	1.82	0.91
1:J:537:GLU:O	4:7:349:LEU:HD13	0.73	0.91
1:J:642:LYS:CB	4:7:21:PHE:O	2.17	0.91
1:A:735:GLY:C	1:A:743:ALA:HA	1.90	0.91
1:D:642:LYS:CB	4:5:21:PHE:O	2.17	0.91
1:G:795:ARG:HB3	3:I:35:ARG:HH21	1.33	0.91
1:G:821:ARG:HH21	2:H:127:ARG:HG2	1.34	0.91
1:J:538:GLU:N	4:7:349:LEU:HD12	1.86	0.91
1:J:797:PHE:CG	3:L:149:VAL:HG11	2.05	0.91
1:A:218:LEU:HA	1:A:221:GLN:CG	2.01	0.91
1:G:537:GLU:O	4:6:349:LEU:HD13	0.74	0.91
1:J:641:LYS:HE3	1:J:647:GLN:CG	2.00	0.91
1:A:649:VAL:CG1	1:A:649:VAL:C	2.38	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:538:GLU:N	4:5:351:THR:H	1.68	0.91
1:G:550:PHE:HA	4:8:46:GLY:CA	2.00	0.91
1:G:838:ILE:HD11	2:H:54:MET:HE3	0.92	0.91
1:J:278:GLN:HG2	1:J:317:GLU:HB2	1.52	0.91
1:A:544:LYS:HD2	4:4:147:ARG:HB3	1.53	0.91
1:D:834:LEU:HD11	2:E:54:MET:HG2	1.53	0.91
1:G:218:LEU:HA	1:G:221:GLN:CG	2.01	0.91
1:J:218:LEU:CB	1:J:221:GLN:CG	2.46	0.91
1:J:735:GLY:C	1:J:743:ALA:HA	1.90	0.91
1:A:557:GLU:H	4:6:48:GLY:HA2	1.32	0.91
3:F:62:ALA:O	3:F:63:ILE:CG1	2.19	0.91
1:G:544:LYS:HD2	4:6:147:ARG:HB3	1.53	0.91
1:J:736:GLN:HA	1:J:743:ALA:HB2	1.50	0.91
1:D:649:VAL:CG1	1:D:649:VAL:C	2.38	0.91
1:G:410:ASN:OD1	4:6:334:GLU:C	2.10	0.91
1:G:557:GLU:H	4:8:48:GLY:HA2	1.33	0.91
1:A:819:ASN:ND2	2:B:91:ALA:C	2.23	0.91
2:B:149:ASP:CG	2:B:150:TYR:H	1.73	0.91
3:C:62:ALA:O	3:C:63:ILE:CG1	2.19	0.91
1:D:735:GLY:C	1:D:743:ALA:HA	1.91	0.91
3:F:62:ALA:O	3:F:63:ILE:HG12	1.71	0.91
1:G:538:GLU:N	4:6:351:THR:H	1.68	0.91
1:G:768:MLY:HH23	1:G:772:LEU:HD22	1.53	0.91
1:J:93:MET:HG2	1:J:764:MLY:HD3	0.92	0.91
1:A:537:GLU:O	4:4:349:LEU:HD13	0.74	0.91
1:A:537:GLU:C	4:4:349:LEU:CD1	2.20	0.91
1:A:550:PHE:HA	4:6:46:GLY:CA	2.00	0.91
1:D:724:TYR:CE1	1:D:778:MET:SD	2.64	0.91
1:G:638:GLY:HA3	4:6:341:ILE:O	1.70	0.91
1:G:739:ASP:HB3	1:G:742:LYS:CB	1.99	0.91
3:I:62:ALA:O	3:I:63:ILE:HG12	1.71	0.91
1:A:538:GLU:N	4:4:349:LEU:HD12	1.86	0.90
1:A:836:PHE:HB3	2:B:161:GLU:CG	2.01	0.90
1:D:553:MLY:HE2	4:7:45:VAL:HA	1.53	0.90
1:D:735:GLY:O	1:D:743:ALA:CA	2.19	0.90
1:D:790:THR:N	3:F:87:PHE:CE2	2.39	0.90
1:G:649:VAL:CG1	1:G:649:VAL:C	2.38	0.90
1:J:800:ARG:HB3	3:L:149:VAL:CG2	1.94	0.90
1:A:538:GLU:N	4:4:351:THR:H	1.68	0.90
1:A:649:VAL:CB	1:A:649:VAL:CG2	2.50	0.90
1:G:213:LYS:HA	1:G:220:ASP:CG	1.90	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:636:LYS:HD2	4:6:332:PRO:HB3	1.52	0.90
1:G:649:VAL:CB	1:G:649:VAL:CG2	2.49	0.90
2:H:149:ASP:CG	2:H:150:TYR:H	1.73	0.90
1:J:544:LYS:HD2	4:7:147:ARG:HB3	1.53	0.90
1:A:638:GLY:HA3	4:4:341:ILE:O	1.70	0.90
1:A:768:MLY:CB	1:A:771:LEU:HB2	2.00	0.90
1:D:649:VAL:CG2	1:D:649:VAL:HG13	2.02	0.90
1:G:278:GLN:HG2	1:G:317:GLU:HB2	1.52	0.90
1:J:649:VAL:CG1	1:J:649:VAL:C	2.38	0.90
1:J:798:LEU:HD21	3:L:126:LEU:HG	1.51	0.90
2:K:150:TYR:O	2:K:151:LYS:HB2	1.67	0.90
1:A:213:LYS:HA	1:A:220:ASP:CG	1.90	0.90
1:A:505:MLY:CH2	1:A:762:HIS:O	2.19	0.90
1:A:757:GLN:CG	1:A:771:LEU:CD1	2.44	0.90
1:D:218:LEU:HA	1:D:221:GLN:CG	2.01	0.90
1:D:538:GLU:O	4:5:349:LEU:CG	2.20	0.90
1:D:641:LYS:HE3	1:D:647:GLN:CG	2.00	0.90
1:D:796:GLY:HA3	3:F:40:ASN:OD1	1.71	0.90
1:G:538:GLU:N	4:6:349:LEU:HD12	1.87	0.90
1:G:721:LYS:CB	1:G:736:GLN:OE1	2.20	0.90
1:G:735:GLY:C	1:G:743:ALA:HA	1.90	0.90
1:J:553:MLY:HE2	4:V:45:VAL:HA	1.53	0.90
1:J:649:VAL:CG2	1:J:649:VAL:HG13	2.02	0.90
1:D:544:LYS:HD2	4:5:147:ARG:HB3	1.53	0.90
1:G:557:GLU:H	4:8:48:GLY:HA3	1.28	0.90
1:G:754:ASP:OD2	1:G:776:GLU:OE2	1.89	0.90
3:I:62:ALA:O	3:I:63:ILE:CG1	2.19	0.90
1:J:735:GLY:O	1:J:743:ALA:CA	2.19	0.90
1:D:534:SER:O	4:5:351:THR:HG23	1.13	0.90
1:D:839:MLY:CH1	2:E:159:HIS:CG	2.50	0.90
2:E:121:LEU:CB	2:E:128:PHE:HB3	1.69	0.90
1:J:553:MLY:CG	4:V:44:MET:O	2.20	0.90
2:H:137:TRP:HA	2:H:145:ALA:HB2	1.54	0.90
1:J:818:TYR:HB3	2:K:90:GLY:CA	2.01	0.90
1:A:278:GLN:HG2	1:A:317:GLU:HB2	1.52	0.90
1:D:550:PHE:CA	4:7:46:GLY:HA3	2.02	0.90
2:E:137:TRP:HA	2:E:145:ALA:HB2	1.53	0.90
1:J:757:GLN:CD	1:J:776:GLU:HG2	1.90	0.90
1:A:410:ASN:OD1	4:4:334:GLU:C	2.10	0.90
1:A:629:GLU:HG2	1:A:643:GLY:O	1.72	0.90
1:D:538:GLU:N	4:5:349:LEU:HD12	1.86	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:795:ARG:CB	3:F:35:ARG:NE	2.26	0.90
1:D:836:PHE:CB	2:E:161:GLU:OE1	2.20	0.90
2:E:163:ALA:C	2:K:22:THR:OG1	2.10	0.90
1:G:629:GLU:HG2	1:G:643:GLY:O	1.72	0.90
1:J:218:LEU:HA	1:J:221:GLN:CG	2.01	0.90
1:J:410:ASN:OD1	4:7:334:GLU:C	2.10	0.90
1:J:530:MET:N	4:7:354:GLN:HB3	1.87	0.90
1:A:817:GLN:HB2	2:B:127:ARG:CZ	2.02	0.90
1:G:215:GLN:H	1:G:340:ILE:CG1	1.72	0.90
1:G:817:GLN:OE1	2:H:127:ARG:HD2	1.71	0.90
1:J:538:GLU:O	4:7:349:LEU:CG	2.20	0.90
1:J:550:PHE:CA	4:V:46:GLY:HA3	2.02	0.90
1:A:735:GLY:O	1:A:743:ALA:CA	2.19	0.89
1:D:799:MET:CE	3:F:32:ASP:HB3	2.02	0.89
2:E:163:ALA:C	2:K:22:THR:N	2.24	0.89
1:J:635:GLY:CA	4:7:341:ILE:HD13	2.02	0.89
1:D:638:GLY:HA3	4:5:341:ILE:O	1.70	0.89
1:G:735:GLY:O	1:G:743:ALA:CA	2.19	0.89
1:J:84:MLY:HE2	1:J:719:ASP:CG	1.92	0.89
1:J:821:ARG:NH2	2:K:127:ARG:CD	2.35	0.89
3:C:24:LYS:HB3	3:C:63:ILE:O	1.72	0.89
3:C:62:ALA:O	3:C:63:ILE:HG12	1.71	0.89
1:D:553:MLY:CG	4:7:44:MET:O	2.20	0.89
1:D:649:VAL:CB	1:D:649:VAL:CG2	2.49	0.89
1:A:795:ARG:CZ	3:C:116:GLU:OE2	2.19	0.89
1:A:800:ARG:HD2	3:C:149:VAL:HG22	0.92	0.89
1:D:815:CYS:O	2:E:90:GLY:O	1.89	0.89
1:G:599:ASN:OD1	1:G:649:VAL:HB	1.72	0.89
1:J:534:SER:HA	4:7:350:SER:O	1.71	0.89
3:L:62:ALA:O	3:L:63:ILE:CG1	2.19	0.89
1:A:530:MET:N	4:4:354:GLN:HB3	1.87	0.89
1:D:629:GLU:HG2	1:D:643:GLY:O	1.72	0.89
1:D:721:LYS:CB	1:D:736:GLN:OE1	2.20	0.89
1:J:557:GLU:H	4:V:48:GLY:HA3	1.28	0.89
1:J:649:VAL:CB	1:J:649:VAL:CG2	2.49	0.89
1:J:721:LYS:CB	1:J:736:GLN:OE1	2.20	0.89
1:D:410:ASN:OD1	4:5:334:GLU:C	2.10	0.89
1:D:630:ALA:O	4:5:25:ASP:CG	2.09	0.89
1:D:635:GLY:CA	4:5:341:ILE:HD13	2.03	0.89
1:G:538:GLU:O	4:6:349:LEU:CG	2.20	0.89
1:J:630:ALA:O	4:7:25:ASP:CG	2.09	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:137:TRP:HA	2:K:145:ALA:HB2	1.53	0.89
1:D:534:SER:HA	4:5:350:SER:O	1.71	0.89
1:J:503:TYR:OH	1:J:711:PHE:HD2	1.55	0.89
1:A:553:MLY:CG	4:6:44:MET:O	2.20	0.89
1:A:721:LYS:CB	1:A:736:GLN:OE1	2.20	0.89
1:D:507:GLY:CA	1:D:762:HIS:CG	2.56	0.89
1:D:530:MET:N	4:5:354:GLN:HB3	1.87	0.89
1:D:641:LYS:HD2	4:5:348:SER:CB	2.02	0.89
1:G:93:MET:HE3	1:G:763:THR:CB	1.74	0.89
1:J:215:GLN:H	1:J:340:ILE:CG1	1.72	0.89
1:G:816:ILE:HD11	2:H:100:ALA:CB	2.02	0.89
1:A:505:MLY:HG3	1:A:741:LYS:HZ3	1.37	0.89
1:A:538:GLU:O	4:4:349:LEU:CG	2.20	0.89
1:A:630:ALA:O	4:4:25:ASP:CG	2.10	0.89
1:J:638:GLY:HA3	4:7:341:ILE:O	1.70	0.89
1:J:641:LYS:HD2	4:7:348:SER:CB	2.02	0.89
1:J:826:VAL:HG21	2:K:88:LEU:CD2	2.03	0.89
1:A:534:SER:HA	4:4:350:SER:O	1.71	0.88
1:A:769:ALA:C	1:A:772:LEU:H	1.76	0.88
1:A:795:ARG:CD	3:C:35:ARG:NH2	2.36	0.88
1:G:534:SER:HA	4:6:350:SER:O	1.71	0.88
1:G:838:ILE:CD1	2:H:54:MET:HE1	1.96	0.88
2:H:121:LEU:CA	2:H:128:PHE:CB	2.46	0.88
1:A:550:PHE:CA	4:6:46:GLY:HA3	2.02	0.88
1:G:530:MET:N	4:6:354:GLN:HB3	1.88	0.88
1:J:829:TRP:CZ3	2:K:84:PHE:HZ	1.85	0.88
1:D:541:MET:CB	4:5:143:TYR:OH	2.21	0.88
1:D:800:ARG:HD2	3:F:149:VAL:HG22	1.53	0.88
2:E:137:TRP:HA	2:E:145:ALA:CB	2.03	0.88
1:J:769:ALA:HB3	1:J:770:GLY:HA2	0.90	0.88
3:L:62:ALA:O	3:L:63:ILE:HG12	1.71	0.88
4:X:322:PRO:HB2	4:Z:244:ASP:CG	1.94	0.88
1:A:836:PHE:HE1	2:B:159:HIS:HA	1.37	0.88
1:D:215:GLN:H	1:D:340:ILE:HG12	1.06	0.88
1:D:641:LYS:CD	1:D:647:GLN:OE1	2.17	0.88
1:G:541:MET:CB	4:6:143:TYR:OH	2.21	0.88
1:G:795:ARG:CG	3:I:35:ARG:NH2	2.35	0.88
1:D:599:ASN:OD1	1:D:649:VAL:HB	1.73	0.88
1:G:553:MLY:HE2	4:8:45:VAL:HA	1.53	0.88
1:J:629:GLU:HG2	1:J:643:GLY:O	1.72	0.88
1:J:757:GLN:OE1	1:J:772:LEU:O	1.92	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:818:TYR:CE1	2:K:127:ARG:NH2	2.42	0.88
1:A:541:MET:CB	4:4:143:TYR:OH	2.20	0.88
1:G:553:MLY:CG	4:8:44:MET:O	2.20	0.88
1:G:641:LYS:CD	1:G:647:GLN:OE1	2.17	0.88
1:G:728:ASN:HD21	3:I:110:VAL:HA	1.38	0.88
1:J:215:GLN:H	1:J:340:ILE:HG12	1.05	0.88
1:J:642:LYS:HG2	4:7:22:ALA:CA	2.03	0.88
1:J:838:ILE:HD11	2:K:54:MET:CE	2.04	0.88
3:L:24:LYS:HB3	3:L:63:ILE:O	1.72	0.88
4:0:322:PRO:HB2	4:2:244:ASP:CG	1.94	0.88
1:A:642:LYS:HG2	4:4:22:ALA:CA	2.04	0.88
1:A:707:CYS:SG	1:A:714:ARG:NH1	2.47	0.88
1:G:93:MET:CB	1:G:764:MLY:NZ	2.27	0.88
1:G:642:LYS:HG2	4:6:22:ALA:CA	2.03	0.88
1:J:831:TRP:HZ2	2:K:47:LEU:CD2	1.83	0.88
1:A:641:LYS:HD2	4:4:348:SER:CB	2.02	0.88
1:A:795:ARG:HB3	3:C:35:ARG:CZ	2.04	0.88
1:J:642:LYS:CG	4:7:21:PHE:O	2.22	0.88
1:A:553:MLY:HE2	4:6:45:VAL:HA	1.53	0.88
2:B:137:TRP:HA	2:B:145:ALA:HB2	1.54	0.88
1:D:635:GLY:HA2	4:5:334:GLU:CG	2.03	0.88
3:F:139:TYR:HA	3:F:142:PHE:HB3	1.56	0.88
1:G:510:TRP:CZ3	1:G:768:MLY:CH1	2.57	0.88
1:G:542:PHE:HA	4:6:143:TYR:HE1	1.34	0.88
1:G:642:LYS:CG	4:6:21:PHE:O	2.22	0.88
4:2:322:PRO:HB2	4:4:244:ASP:CG	1.94	0.88
4:V:322:PRO:HB2	4:X:244:ASP:CG	1.94	0.88
1:A:789:ALA:HB1	3:C:87:PHE:HE2	1.39	0.88
1:A:817:GLN:OE1	2:B:127:ARG:NH2	1.81	0.88
1:A:839:MLY:NZ	2:B:159:HIS:HB3	1.89	0.88
1:D:646:PHE:CE2	1:D:652:LEU:CD1	2.57	0.88
1:G:550:PHE:CA	4:8:46:GLY:HA3	2.03	0.88
1:G:707:CYS:O	1:G:714:ARG:NH2	2.06	0.88
3:C:139:TYR:HA	3:C:142:PHE:HB3	1.56	0.87
1:G:646:PHE:CE2	1:G:652:LEU:CD1	2.58	0.87
1:G:649:VAL:CG2	1:G:649:VAL:HG13	2.02	0.87
1:G:817:GLN:HB3	2:H:127:ARG:HH11	1.39	0.87
1:J:541:MET:CB	4:7:143:TYR:OH	2.20	0.87
1:J:795:ARG:HE	3:L:118:MET:CE	1.87	0.87
1:D:795:ARG:HB3	3:F:35:ARG:CD	2.04	0.87
1:G:817:GLN:CG	2:H:127:ARG:CD	2.52	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:84:MLY:HE2	1:J:719:ASP:OD2	1.73	0.87
1:J:735:GLY:C	1:J:743:ALA:HB2	1.82	0.87
1:J:754:ASP:CB	1:J:776:GLU:HB3	2.03	0.87
1:A:72:VAL:CG1	1:A:76:GLN:HB3	2.05	0.87
1:A:641:LYS:HG3	1:A:647:GLN:NE2	1.58	0.87
2:B:137:TRP:HA	2:B:145:ALA:CB	2.04	0.87
1:J:92:ALA:O	1:J:714:ARG:HG3	1.74	0.87
4:8:322:PRO:HB2	4:W:244:ASP:CG	1.94	0.87
1:D:642:LYS:CG	4:5:21:PHE:O	2.22	0.87
1:G:534:SER:O	4:6:351:THR:HG23	1.12	0.87
1:G:635:GLY:CA	4:6:341:ILE:HD13	2.02	0.87
3:I:24:LYS:HB3	3:I:63:ILE:O	1.72	0.87
1:J:768:MLY:CH2	1:J:772:LEU:CG	2.45	0.87
3:L:139:TYR:HA	3:L:142:PHE:HB3	1.56	0.87
1:A:642:LYS:CG	4:4:21:PHE:O	2.22	0.87
1:G:752:ASP:OD2	1:G:783:LEU:CB	2.22	0.87
1:G:816:ILE:HD11	2:H:100:ALA:HB1	1.56	0.87
4:4:322:PRO:HB2	4:6:244:ASP:CG	1.94	0.87
4:5:322:PRO:HB2	4:7:244:ASP:CG	1.94	0.87
1:A:635:GLY:CA	4:4:341:ILE:HD13	2.02	0.87
1:D:636:LYS:H	4:5:334:GLU:CD	1.77	0.87
1:D:792:ALA:HB1	3:F:40:ASN:O	1.74	0.87
1:D:795:ARG:NH2	3:F:116:GLU:CD	2.20	0.87
1:G:649:VAL:CG1	1:G:649:VAL:CA	2.53	0.87
1:J:635:GLY:HA2	4:7:334:GLU:CG	2.03	0.87
1:J:646:PHE:CE2	1:J:652:LEU:CD1	2.58	0.87
1:A:649:VAL:HG13	1:A:649:VAL:CG2	2.02	0.87
1:D:642:LYS:HG2	4:5:22:ALA:CA	2.04	0.87
2:K:149:ASP:CG	2:K:150:TYR:H	1.73	0.87
1:A:215:GLN:H	1:A:340:ILE:HG12	1.06	0.87
1:A:649:VAL:CG1	1:A:649:VAL:CA	2.53	0.87
1:A:819:ASN:OD1	2:B:91:ALA:HA	0.87	0.87
1:D:649:VAL:CG1	1:D:649:VAL:CA	2.53	0.87
1:G:93:MET:CE	1:G:763:THR:HG22	2.03	0.87
1:G:823:PHE:CE1	2:H:156:VAL:O	2.28	0.87
1:J:93:MET:HG3	1:J:764:MLY:CH1	2.04	0.87
1:J:754:ASP:OD2	1:J:776:GLU:O	1.91	0.87
4:3:322:PRO:HB2	4:5:244:ASP:CG	1.94	0.87
4:W:322:PRO:HB2	4:Y:244:ASP:CG	1.94	0.87
1:A:831:TRP:CH2	2:B:50:THR:HB	2.08	0.87
1:J:636:LYS:H	4:7:334:GLU:CD	1.78	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:641:LYS:CD	1:J:647:GLN:OE1	2.18	0.87
1:J:649:VAL:CG1	1:J:649:VAL:CA	2.53	0.87
1:A:798:LEU:CD2	3:C:122:GLU:HB3	2.05	0.86
1:G:72:VAL:CG1	1:G:76:GLN:HB3	2.05	0.86
1:G:795:ARG:HD2	3:I:35:ARG:HH22	0.71	0.86
1:G:831:TRP:HE1	2:H:67:MET:CB	1.87	0.86
1:J:84:MLY:HH12	1:J:715:VAL:CG1	1.75	0.86
4:7:322:PRO:HB2	4:V:244:ASP:CG	1.94	0.86
1:D:755:HIS:HA	1:D:758:TYR:CE1	2.10	0.86
1:G:817:GLN:HB3	2:H:127:ARG:HD3	1.56	0.86
4:0:287:ILE:CG2	4:2:205:GLU:HG2	2.05	0.86
4:1:322:PRO:HB2	4:3:244:ASP:CG	1.94	0.86
1:A:530:MET:HG2	4:4:354:GLN:CG	2.05	0.86
1:D:646:PHE:CD2	1:D:652:LEU:HD11	2.09	0.86
1:G:636:LYS:H	4:6:334:GLU:CD	1.78	0.86
1:G:641:LYS:HD2	4:6:348:SER:CB	2.03	0.86
2:H:137:TRP:HA	2:H:145:ALA:CB	2.04	0.86
1:J:508:ILE:HD11	1:J:759:ALA:HB2	0.87	0.86
1:J:757:GLN:CD	1:J:776:GLU:HG3	1.93	0.86
1:J:797:PHE:CD1	3:L:149:VAL:HG12	2.06	0.86
1:A:95:THR:OG1	1:A:769:ALA:HA	1.74	0.86
1:D:310:TYR:CZ	1:D:320:ILE:HD11	2.11	0.86
1:D:735:GLY:C	1:D:743:ALA:HB2	1.82	0.86
1:D:800:ARG:HB3	3:F:149:VAL:HG21	1.57	0.86
1:G:646:PHE:CD2	1:G:652:LEU:HD11	2.09	0.86
2:K:137:TRP:HA	2:K:145:ALA:CB	2.04	0.86
1:A:542:PHE:HA	4:4:143:TYR:HE1	1.34	0.86
1:D:530:MET:HG2	4:5:354:GLN:CG	2.05	0.86
1:G:107:MLY:HB3	1:G:686:MET:HE2	1.58	0.86
1:J:72:VAL:CG1	1:J:76:GLN:HB3	2.05	0.86
1:J:599:ASN:OD1	1:J:649:VAL:HB	1.73	0.86
1:A:502:GLU:HA	1:A:762:HIS:N	1.90	0.86
1:A:636:LYS:H	4:4:334:GLU:CD	1.77	0.86
2:E:149:ASP:CG	2:E:150:TYR:H	1.73	0.86
3:F:24:LYS:HB3	3:F:63:ILE:O	1.72	0.86
1:G:530:MET:HG2	4:6:354:GLN:CG	2.05	0.86
1:J:310:TYR:CZ	1:J:320:ILE:HD11	2.11	0.86
1:J:530:MET:HG2	4:7:354:GLN:CG	2.06	0.86
1:D:72:VAL:CG1	1:D:76:GLN:HB3	2.05	0.86
1:D:206:LYS:HD3	1:D:217:THR:CB	2.06	0.86
1:D:769:ALA:C	1:D:770:GLY:O	2.14	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:4:287:ILE:CG2	4:6:205:GLU:HG2	2.05	0.86
4:6:322:PRO:HB2	4:8:244:ASP:CG	1.94	0.86
1:G:84:MLY:CH1	1:G:715:VAL:HG12	2.05	0.86
1:G:206:LYS:HD3	1:G:217:THR:CB	2.06	0.86
1:G:755:HIS:HA	1:G:758:TYR:CE1	2.10	0.86
4:V:287:ILE:CG2	4:X:205:GLU:HG2	2.05	0.86
1:D:814:PHE:HD1	2:E:127:ARG:NH2	1.70	0.86
1:A:538:GLU:N	4:4:351:THR:N	2.24	0.86
1:A:793:ARG:HG3	3:C:146:ILE:HG22	1.58	0.86
1:D:724:TYR:HE1	1:D:778:MET:CB	1.89	0.86
1:J:755:HIS:HA	1:J:758:TYR:CE1	2.10	0.86
1:A:538:GLU:OE2	4:4:355:MET:HE3	1.73	0.85
1:A:641:LYS:CD	1:A:647:GLN:OE1	2.17	0.85
1:A:755:HIS:HA	1:A:758:TYR:CE1	2.10	0.85
2:E:163:ALA:HA	2:K:21:GLU:HB3	1.55	0.85
1:G:798:LEU:HD11	3:I:126:LEU:CG	2.06	0.85
1:J:206:LYS:HD3	1:J:217:THR:CB	2.06	0.85
1:A:599:ASN:OD1	1:A:649:VAL:CA	2.25	0.85
2:B:117:LEU:CG	2:B:147:ASN:CG	2.44	0.85
1:G:215:GLN:H	1:G:340:ILE:HG12	1.06	0.85
1:J:410:ASN:OD1	4:7:334:GLU:CA	2.24	0.85
1:A:97:LEU:HD22	1:A:712:PRO:HB3	1.58	0.85
1:A:831:TRP:CD1	2:B:51:PHE:CZ	2.49	0.85
2:E:117:LEU:CG	2:E:147:ASN:CG	2.44	0.85
1:G:204:GLU:H	1:G:207:LYS:HE3	1.42	0.85
2:H:117:LEU:CG	2:H:147:ASN:CG	2.45	0.85
1:J:646:PHE:CD2	1:J:652:LEU:HD11	2.09	0.85
1:J:797:PHE:HA	3:L:149:VAL:HG11	1.58	0.85
3:I:139:TYR:HA	3:I:142:PHE:HB3	1.56	0.85
1:J:630:ALA:C	4:7:25:ASP:OD2	2.15	0.85
1:D:507:GLY:O	1:D:761:GLY:HA2	1.75	0.85
1:D:732:ILE:HG23	1:D:747:LEU:HB2	1.57	0.85
1:G:202:SER:HA	1:G:207:LYS:HE2	0.85	0.85
1:G:599:ASN:OD1	1:G:649:VAL:CA	2.25	0.85
1:G:725:ARG:CZ	1:G:733:PRO:HB3	2.05	0.85
4:7:287:ILE:CG2	4:V:205:GLU:HG2	2.05	0.85
1:A:204:GLU:H	1:A:207:LYS:HE3	1.42	0.85
4:6:287:ILE:CG2	4:8:205:GLU:HG2	2.05	0.85
1:A:206:LYS:HD3	1:A:217:THR:CB	2.06	0.85
1:A:410:ASN:OD1	4:4:334:GLU:CA	2.25	0.85
1:G:752:ASP:OD2	1:G:783:LEU:HB2	1.77	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:640:LYS:CB	1:J:645:SER:OG	2.25	0.85
2:K:117:LEU:CG	2:K:147:ASN:CG	2.44	0.85
4:X:287:ILE:CG2	4:Z:205:GLU:HG2	2.05	0.85
1:A:202:SER:HA	1:A:207:LYS:HE2	0.85	0.85
1:A:800:ARG:HH11	3:C:149:VAL:CG1	1.90	0.85
1:D:599:ASN:OD1	1:D:649:VAL:CA	2.25	0.85
1:D:630:ALA:C	4:5:25:ASP:OD2	2.15	0.85
1:G:310:TYR:CZ	1:G:320:ILE:HD11	2.11	0.85
1:G:707:CYS:HB3	1:G:714:ARG:HH12	0.75	0.85
1:A:630:ALA:C	4:4:25:ASP:OD2	2.15	0.85
1:A:646:PHE:CD2	1:A:652:LEU:HD11	2.09	0.85
1:A:797:PHE:CD2	3:C:126:LEU:CD2	2.59	0.85
1:D:204:GLU:H	1:D:207:LYS:HE3	1.42	0.85
1:D:418:THR:HB	1:D:421:GLU:HG3	1.59	0.85
1:D:769:ALA:CB	1:D:770:GLY:C	2.45	0.85
1:G:410:ASN:OD1	4:6:334:GLU:CA	2.24	0.85
1:J:797:PHE:CB	3:L:149:VAL:CG1	2.54	0.85
1:A:725:ARG:CD	1:A:733:PRO:HB3	2.07	0.85
1:D:410:ASN:OD1	4:5:334:GLU:CA	2.24	0.85
1:D:792:ALA:HB1	3:F:40:ASN:HB2	1.55	0.85
1:J:725:ARG:CZ	1:J:733:PRO:HB3	2.06	0.85
4:2:287:ILE:CG2	4:4:205:GLU:HG2	2.05	0.85
1:A:530:MET:HE1	4:4:355:MET:SD	2.17	0.84
1:A:640:LYS:C	4:4:23:GLY:O	2.15	0.84
1:G:725:ARG:CD	1:G:733:PRO:HB3	2.07	0.84
1:G:732:ILE:HG23	1:G:747:LEU:HB2	1.57	0.84
1:J:410:ASN:ND2	4:7:336:LYS:HG2	1.92	0.84
1:J:529:PRO:CB	4:7:353:GLN:OE1	2.25	0.84
2:K:121:LEU:CA	2:K:128:PHE:CB	2.46	0.84
4:5:287:ILE:CG2	4:7:205:GLU:HG2	2.05	0.84
4:8:287:ILE:CG2	4:W:205:GLU:HG2	2.05	0.84
1:A:836:PHE:HB3	2:B:161:GLU:HG2	1.57	0.84
1:D:202:SER:HA	1:D:207:LYS:HE2	0.85	0.84
1:J:543:PRO:HG3	4:7:143:TYR:O	1.77	0.84
1:J:800:ARG:HD2	3:L:149:VAL:HG23	0.85	0.84
1:J:821:ARG:HH22	2:K:127:ARG:CD	1.89	0.84
1:A:795:ARG:NH2	3:C:116:GLU:CB	2.36	0.84
1:A:822:SER:OG	2:B:88:LEU:HA	1.77	0.84
1:G:410:ASN:ND2	4:6:336:LYS:HG2	1.92	0.84
1:G:538:GLU:N	4:6:351:THR:N	2.24	0.84
1:G:553:MLY:HG2	4:8:47:MET:H	1.43	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:418:THR:HB	1:J:421:GLU:HG3	1.60	0.84
1:J:510:TRP:CZ3	1:J:772:LEU:HD21	2.11	0.84
1:J:757:GLN:NE2	1:J:776:GLU:CG	2.39	0.84
4:3:287:ILE:CG2	4:5:205:GLU:HG2	2.05	0.84
2:B:121:LEU:CA	2:B:128:PHE:CB	2.46	0.84
1:J:202:SER:HA	1:J:207:LYS:HE2	0.85	0.84
1:J:640:LYS:C	4:7:23:GLY:O	2.15	0.84
1:J:732:ILE:HG23	1:J:747:LEU:CB	1.85	0.84
1:A:635:GLY:HA2	4:4:334:GLU:CG	2.03	0.84
1:A:800:ARG:NH1	3:C:149:VAL:O	2.10	0.84
1:D:732:ILE:HG21	1:D:747:LEU:HD13	0.91	0.84
1:D:769:ALA:HA	1:D:771:LEU:CB	2.07	0.84
1:D:817:GLN:NE2	2:E:127:ARG:CG	2.40	0.84
1:G:730:SER:OG	3:I:109:HIS:NE2	2.09	0.84
1:G:735:GLY:C	1:G:743:ALA:HB2	1.82	0.84
1:G:768:MLY:CD	1:G:772:LEU:HD22	2.06	0.84
1:J:732:ILE:HG23	1:J:747:LEU:HB2	1.57	0.84
1:J:754:ASP:OD2	1:J:776:GLU:HA	1.77	0.84
1:A:310:TYR:CZ	1:A:320:ILE:HD11	2.11	0.84
1:A:732:ILE:HG23	1:A:747:LEU:HB2	1.57	0.84
1:D:529:PRO:CB	4:5:353:GLN:OE1	2.25	0.84
1:D:557:GLU:H	4:7:48:GLY:HA3	1.28	0.84
1:D:640:LYS:C	4:5:23:GLY:O	2.15	0.84
1:J:735:GLY:C	1:J:743:ALA:HB1	1.84	0.84
4:W:287:ILE:CG2	4:Y:205:GLU:HG2	2.05	0.84
1:J:649:VAL:HG12	1:J:649:VAL:C	1.98	0.84
1:A:814:PHE:HA	2:B:127:ARG:NH2	1.93	0.84
1:D:641:LYS:HG3	1:D:647:GLN:NE2	1.59	0.84
1:D:649:VAL:HG12	1:D:649:VAL:C	1.98	0.84
1:G:557:GLU:N	4:8:48:GLY:HA2	1.91	0.84
1:G:648:THR:CG2	1:G:651:ALA:HB2	2.08	0.84
1:J:204:GLU:H	1:J:207:LYS:HE3	1.41	0.84
1:J:753:VAL:HA	1:J:780:ASP:OD2	1.78	0.84
4:5:237:GLU:HA	4:5:251:GLY:HA2	1.60	0.84
1:A:410:ASN:ND2	4:4:336:LYS:HG2	1.93	0.84
1:D:629:GLU:CG	1:D:643:GLY:O	2.26	0.84
1:D:640:LYS:CB	1:D:645:SER:OG	2.25	0.84
1:G:788:THR:C	3:I:42:THR:CG2	2.34	0.84
1:J:629:GLU:CG	1:J:643:GLY:O	2.26	0.84
4:3:237:GLU:HA	4:3:251:GLY:HA2	1.60	0.84
4:7:237:GLU:HA	4:7:251:GLY:HA2	1.60	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:X:286:ASP:OD1	4:Z:203:THR:CG2	2.26	0.84
1:A:542:PHE:CA	4:4:143:TYR:CE1	2.61	0.84
2:H:141:PRO:CB	2:H:142:PRO:CD	2.56	0.84
4:0:286:ASP:OD1	4:2:203:THR:CG2	2.26	0.84
4:1:286:ASP:OD1	4:3:203:THR:CG2	2.26	0.84
1:A:797:PHE:CE2	3:C:126:LEU:HD23	2.07	0.83
1:D:538:GLU:N	4:5:351:THR:N	2.25	0.83
1:D:730:SER:O	1:D:734:GLU:HG3	1.78	0.83
1:G:635:GLY:HA2	4:6:334:GLU:CG	2.03	0.83
1:J:95:THR:OG1	1:J:713:SER:CB	2.25	0.83
1:J:599:ASN:OD1	1:J:649:VAL:CA	2.25	0.83
4:1:237:GLU:HA	4:1:251:GLY:HA2	1.60	0.83
1:A:543:PRO:HG3	4:4:143:TYR:O	1.77	0.83
1:A:648:THR:CG2	1:A:651:ALA:HB2	2.08	0.83
1:A:798:LEU:HD13	3:C:126:LEU:CD2	1.95	0.83
1:D:410:ASN:ND2	4:5:336:LYS:HG2	1.92	0.83
1:D:648:THR:CG2	1:D:651:ALA:HB2	2.08	0.83
1:D:725:ARG:CD	1:D:733:PRO:HB3	2.07	0.83
1:J:783:LEU:O	1:J:787:ILE:HB	1.79	0.83
2:K:141:PRO:CB	2:K:142:PRO:CD	2.56	0.83
4:3:286:ASP:OD1	4:5:203:THR:CG2	2.26	0.83
4:V:237:GLU:HA	4:V:251:GLY:HA2	1.60	0.83
1:A:768:MLY:CB	1:A:771:LEU:HD13	2.08	0.83
1:D:724:TYR:CE1	1:D:778:MET:CB	2.61	0.83
1:G:549:SER:O	4:8:46:GLY:HA3	1.78	0.83
1:G:640:LYS:C	4:6:23:GLY:O	2.16	0.83
1:G:736:GLN:HA	1:G:743:ALA:HB2	1.51	0.83
1:G:819:ASN:CG	2:H:92:ASP:CB	2.47	0.83
1:J:542:PHE:CA	4:7:143:TYR:CE1	2.61	0.83
4:V:286:ASP:OD1	4:X:203:THR:CG2	2.26	0.83
1:A:599:ASN:OD1	1:A:649:VAL:HB	1.72	0.83
1:G:529:PRO:CB	4:6:353:GLN:OE1	2.25	0.83
1:G:795:ARG:HB2	3:I:35:ARG:NH2	1.91	0.83
1:D:732:ILE:CG2	1:D:747:LEU:HD13	1.34	0.83
1:G:542:PHE:CA	4:6:143:TYR:CE1	2.61	0.83
1:G:640:LYS:CB	1:G:645:SER:OG	2.25	0.83
1:J:795:ARG:CZ	3:L:35:ARG:HH12	1.92	0.83
4:2:286:ASP:OD1	4:4:203:THR:CG2	2.26	0.83
1:A:549:SER:O	4:6:46:GLY:HA3	1.77	0.83
1:A:553:MLY:HG2	4:6:47:MET:H	1.44	0.83
1:A:646:PHE:CE2	1:A:652:LEU:CD1	2.58	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:831:TRP:HZ3	2:B:50:THR:HG21	1.44	0.83
1:J:218:LEU:HB3	1:J:221:GLN:HG3	1.60	0.83
1:J:549:SER:O	4:V:46:GLY:HA3	1.78	0.83
1:J:817:GLN:HB3	2:K:127:ARG:HH11	1.44	0.83
4:1:287:ILE:CG2	4:3:205:GLU:HG2	2.05	0.83
4:X:237:GLU:HA	4:X:251:GLY:HA2	1.60	0.83
1:A:629:GLU:CG	1:A:643:GLY:O	2.26	0.83
2:B:141:PRO:CB	2:B:142:PRO:CD	2.56	0.83
1:D:549:SER:O	4:7:46:GLY:HA3	1.77	0.83
1:D:725:ARG:CZ	1:D:733:PRO:HB3	2.05	0.83
1:D:834:LEU:HD11	2:E:54:MET:HB2	1.56	0.83
1:J:730:SER:O	1:J:734:GLU:HG3	1.79	0.83
4:Z:237:GLU:HA	4:Z:251:GLY:HA2	1.60	0.83
1:A:506:GLU:H	1:A:761:GLY:HA2	1.43	0.83
1:A:529:PRO:CB	4:4:353:GLN:OE1	2.25	0.83
2:E:141:PRO:CB	2:E:142:PRO:CD	2.56	0.83
2:H:144:VAL:HG12	2:H:153:ILE:CD1	2.09	0.83
1:J:538:GLU:N	4:7:351:THR:N	2.24	0.83
4:5:286:ASP:OD1	4:7:203:THR:CG2	2.26	0.83
4:6:286:ASP:OD1	4:8:203:THR:CG2	2.26	0.83
1:A:732:ILE:CG2	1:A:747:LEU:HD13	1.34	0.83
1:G:418:THR:HB	1:G:421:GLU:HG3	1.59	0.83
1:G:791:GLN:OE1	3:I:116:GLU:CB	2.27	0.83
1:J:279:LEU:HB2	1:J:282:GLU:HG3	1.60	0.83
1:A:836:PHE:HE1	2:B:159:HIS:CA	1.92	0.83
1:D:279:LEU:HB2	1:D:282:GLU:HG3	1.60	0.83
1:D:553:MLY:HG2	4:7:47:MET:H	1.44	0.83
2:E:121:LEU:CA	2:E:128:PHE:CB	2.46	0.83
4:0:237:GLU:HA	4:0:251:GLY:HA2	1.60	0.83
4:7:286:ASP:OD1	4:V:203:THR:CG2	2.26	0.83
4:8:286:ASP:OD1	4:W:203:THR:CG2	2.26	0.83
4:X:290:ARG:NH1	4:Z:202:THR:HG21	1.94	0.83
1:D:641:LYS:HG2	1:D:647:GLN:HG3	1.61	0.82
1:G:543:PRO:HG3	4:6:143:TYR:O	1.78	0.82
1:J:831:TRP:CH2	2:K:34:ILE:HG21	2.14	0.82
4:0:290:ARG:NH1	4:2:202:THR:HG21	1.94	0.82
1:A:499:GLU:OE1	1:A:766:PHE:HZ	1.61	0.82
1:A:814:PHE:HD1	2:B:127:ARG:HH22	1.14	0.82
1:D:542:PHE:CA	4:5:143:TYR:CE1	2.61	0.82
1:G:538:GLU:OE2	4:6:355:MET:HE3	1.78	0.82
1:J:549:SER:O	4:V:46:GLY:CA	2.27	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:111:SER:OG	2:K:148:VAL:C	2.15	0.82
4:1:290:ARG:NH1	4:3:202:THR:HG21	1.95	0.82
4:2:290:ARG:NH1	4:4:202:THR:HG21	1.94	0.82
4:4:290:ARG:NH1	4:6:202:THR:HG21	1.94	0.82
4:8:290:ARG:NH1	4:W:202:THR:HG21	1.94	0.82
4:W:286:ASP:OD1	4:Y:203:THR:CG2	2.26	0.82
1:A:418:THR:HB	1:A:421:GLU:HG3	1.60	0.82
1:D:831:TRP:HH2	2:E:47:LEU:HA	1.43	0.82
1:J:542:PHE:CA	4:7:143:TYR:HE1	1.92	0.82
1:A:557:GLU:H	4:6:48:GLY:HA3	1.28	0.82
1:A:578:HIS:HB3	1:A:592:ILE:HD12	1.62	0.82
1:A:795:ARG:NH1	3:C:43:ASN:H	1.78	0.82
1:J:641:LYS:HG2	1:J:647:GLN:HG3	1.61	0.82
4:2:237:GLU:HA	4:2:251:GLY:HA2	1.60	0.82
4:6:290:ARG:NH1	4:8:202:THR:HG21	1.94	0.82
1:A:735:GLY:C	1:A:743:ALA:HB2	1.82	0.82
1:G:556:ASP:HA	4:8:49:GLN:O	1.69	0.82
1:G:629:GLU:CG	1:G:643:GLY:O	2.26	0.82
1:G:769:ALA:HB3	1:G:770:GLY:HA2	0.83	0.82
1:J:90:ASP:OD2	1:J:764:MLY:CH1	2.27	0.82
1:J:648:THR:CG2	1:J:651:ALA:HB2	2.08	0.82
4:W:290:ARG:NH1	4:Y:202:THR:HG21	1.94	0.82
1:A:107:MLY:HB3	1:A:686:MET:HE2	1.61	0.82
1:D:218:LEU:HD22	1:D:222:ILE:CG1	2.10	0.82
1:G:218:LEU:HD22	1:G:222:ILE:CG1	2.09	0.82
1:G:549:SER:O	4:8:46:GLY:C	2.18	0.82
1:G:549:SER:O	4:8:46:GLY:CA	2.27	0.82
1:J:127:ASN:HD22	1:J:128:PRO:HD2	1.44	0.82
1:J:218:LEU:HD22	1:J:222:ILE:CG1	2.10	0.82
1:J:549:SER:O	4:V:46:GLY:C	2.18	0.82
4:V:290:ARG:NH1	4:X:202:THR:HG21	1.95	0.82
4:Y:237:GLU:HA	4:Y:251:GLY:HA2	1.60	0.82
1:D:543:PRO:HG3	4:5:143:TYR:O	1.77	0.82
1:D:817:GLN:NE2	2:E:127:ARG:HE	1.77	0.82
1:G:279:LEU:HB2	1:G:282:GLU:HG3	1.60	0.82
1:G:578:HIS:HB3	1:G:592:ILE:HD12	1.62	0.82
1:G:643:GLY:N	4:6:24:ASP:HA	1.94	0.82
1:J:218:LEU:HA	1:J:221:GLN:HG2	1.62	0.82
1:J:643:GLY:N	4:7:24:ASP:HA	1.93	0.82
4:3:290:ARG:NH1	4:5:202:THR:HG21	1.95	0.82
4:4:286:ASP:OD1	4:6:203:THR:CG2	2.26	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:127:ASN:HD22	1:A:128:PRO:HD2	1.45	0.82
1:A:279:LEU:HB2	1:A:282:GLU:HG3	1.60	0.82
1:A:542:PHE:CA	4:4:143:TYR:HE1	1.92	0.82
1:D:817:GLN:OE1	2:E:127:ARG:CZ	2.28	0.82
1:D:834:LEU:HD21	2:E:54:MET:CG	2.09	0.82
1:J:725:ARG:CD	1:J:733:PRO:HB3	2.07	0.82
1:J:816:ILE:HD11	2:K:100:ALA:HB1	1.59	0.82
1:A:641:LYS:HG2	1:A:647:GLN:HG3	1.61	0.82
1:A:768:MLY:C	1:A:771:LEU:CB	2.57	0.82
1:G:95:THR:OG1	1:G:713:SER:HB3	1.79	0.82
1:J:599:ASN:CA	1:J:649:VAL:CB	2.53	0.82
1:J:721:LYS:CA	1:J:736:GLN:NE2	2.43	0.82
1:J:757:GLN:HG2	1:J:776:GLU:HG3	0.82	0.82
1:A:218:LEU:HD22	1:A:222:ILE:CG1	2.10	0.82
1:D:218:LEU:HB3	1:D:221:GLN:HG3	1.60	0.82
1:D:809:ARG:CZ	2:E:124:GLY:HA3	2.10	0.82
1:D:817:GLN:NE2	2:E:127:ARG:NE	2.28	0.82
1:G:730:SER:O	1:G:734:GLU:HG3	1.78	0.82
1:A:639:GLY:CA	4:4:344:SER:C	2.48	0.81
1:D:549:SER:O	4:7:46:GLY:C	2.18	0.81
1:J:734:GLU:O	1:J:738:MET:CG	2.28	0.81
1:J:821:ARG:HH22	2:K:127:ARG:CG	1.84	0.81
1:A:640:LYS:CB	1:A:645:SER:OG	2.25	0.81
1:A:730:SER:O	1:A:734:GLU:HG3	1.78	0.81
1:D:549:SER:O	4:7:46:GLY:CA	2.27	0.81
1:D:734:GLU:O	1:D:738:MET:CG	2.28	0.81
4:4:237:GLU:HA	4:4:251:GLY:HA2	1.60	0.81
4:7:290:ARG:NH1	4:V:202:THR:HG21	1.94	0.81
4:W:237:GLU:HA	4:W:251:GLY:HA2	1.60	0.81
1:A:549:SER:O	4:6:46:GLY:CA	2.28	0.81
1:A:553:MLY:CB	4:6:46:GLY:CA	2.32	0.81
1:A:798:LEU:HD12	3:C:126:LEU:HD21	1.58	0.81
1:A:831:TRP:CZ3	2:B:50:THR:HG21	2.15	0.81
2:B:111:SER:OG	2:B:148:VAL:C	2.15	0.81
1:D:571:ALA:O	1:D:572:LYS:CG	2.28	0.81
1:D:639:GLY:CA	4:5:344:SER:C	2.48	0.81
1:D:643:GLY:N	4:5:24:ASP:HA	1.93	0.81
1:D:830:PRO:HD2	2:E:67:MET:HE1	1.63	0.81
1:D:834:LEU:HD21	2:E:54:MET:HG3	1.62	0.81
1:G:232:PHE:CZ	1:G:287:ILE:HD13	2.16	0.81
1:G:734:GLU:O	1:G:738:MET:CG	2.28	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:480:ILE:HG22	1:J:481:ASN:HD22	1.45	0.81
1:J:578:HIS:HB3	1:J:592:ILE:HD12	1.62	0.81
2:K:121:LEU:CG	2:K:128:PHE:CA	2.48	0.81
4:6:237:GLU:HA	4:6:251:GLY:HA2	1.60	0.81
4:8:237:GLU:HA	4:8:251:GLY:HA2	1.60	0.81
1:A:549:SER:O	4:6:46:GLY:C	2.19	0.81
1:D:127:ASN:HD22	1:D:128:PRO:HD2	1.45	0.81
1:D:557:GLU:N	4:7:48:GLY:HA2	1.90	0.81
1:D:792:ALA:HB1	3:F:40:ASN:HB3	1.62	0.81
1:G:641:LYS:HG2	1:G:647:GLN:HG3	1.61	0.81
1:G:800:ARG:HD2	3:I:149:VAL:HG22	1.61	0.81
1:J:510:TRP:CZ2	1:J:768:MLY:CH1	2.58	0.81
1:J:639:GLY:CA	4:7:344:SER:C	2.48	0.81
1:J:768:MLY:CH2	1:J:772:LEU:CB	2.35	0.81
1:A:218:LEU:HA	1:A:221:GLN:HG2	1.62	0.81
1:A:789:ALA:CB	3:C:87:PHE:HE2	1.94	0.81
1:A:834:LEU:CD1	2:B:54:MET:HB3	2.08	0.81
1:D:550:PHE:CA	4:7:46:GLY:CA	2.59	0.81
1:D:578:HIS:HD2	1:D:591:ASN:HA	1.45	0.81
1:G:127:ASN:HD22	1:G:128:PRO:HD2	1.45	0.81
1:J:550:PHE:CA	4:V:46:GLY:CA	2.59	0.81
1:A:643:GLY:N	4:4:24:ASP:HA	1.93	0.81
1:D:538:GLU:CA	4:5:351:THR:H	1.93	0.81
1:D:542:PHE:CA	4:5:143:TYR:HE1	1.92	0.81
1:J:553:MLY:HG2	4:V:47:MET:H	1.44	0.81
4:5:290:ARG:NH1	4:7:202:THR:HG21	1.94	0.81
1:A:538:GLU:CA	4:4:351:THR:H	1.93	0.81
1:A:721:LYS:CA	1:A:736:GLN:NE2	2.43	0.81
1:D:641:LYS:HD2	4:5:348:SER:CA	2.09	0.81
1:G:480:ILE:HG22	1:G:481:ASN:HD22	1.45	0.81
4:5:223:PHE:HE1	4:5:255:PHE:HB2	1.46	0.81
1:A:793:ARG:HE	3:C:147:MET:CG	1.94	0.81
2:B:121:LEU:CG	2:B:128:PHE:CA	2.48	0.81
1:D:107:MLY:HB3	1:D:686:MET:HE2	1.63	0.81
1:D:218:LEU:CA	1:D:221:GLN:HG2	2.10	0.81
1:D:723:ARG:O	1:D:782:MLY:NZ	2.13	0.81
1:G:530:MET:HE1	4:6:355:MET:SD	2.20	0.81
1:G:721:LYS:CA	1:G:736:GLN:NE2	2.43	0.81
2:K:144:VAL:HG12	2:K:153:ILE:CD1	2.10	0.81
4:2:223:PHE:HE1	4:2:255:PHE:HB2	1.46	0.81
4:4:223:PHE:HE1	4:4:255:PHE:HB2	1.46	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:7:223:PHE:HE1	4:7:255:PHE:HB2	1.46	0.81
1:A:734:GLU:O	1:A:738:MET:CG	2.28	0.81
1:D:507:GLY:HA2	1:D:762:HIS:CE1	2.16	0.81
1:D:724:TYR:CZ	1:D:778:MET:SD	2.73	0.81
1:D:792:ALA:CB	3:F:40:ASN:O	2.29	0.81
1:D:831:TRP:CZ2	2:E:47:LEU:CG	2.63	0.81
1:G:639:GLY:CA	4:6:344:SER:C	2.48	0.81
1:J:641:LYS:HD2	4:7:348:SER:CA	2.09	0.81
4:3:223:PHE:HE1	4:3:255:PHE:HB2	1.46	0.81
1:A:232:PHE:CZ	1:A:287:ILE:HD13	2.16	0.81
1:A:709:LYS:O	1:A:710:GLY:HA3	1.81	0.81
1:D:218:LEU:HA	1:D:221:GLN:HG2	1.62	0.81
1:D:724:TYR:O	1:D:782:MLY:HH11	1.80	0.81
4:V:223:PHE:HE1	4:V:255:PHE:HB2	1.46	0.81
1:A:646:PHE:CE2	1:A:652:LEU:HD21	2.14	0.80
1:G:641:LYS:HD2	4:6:348:SER:CA	2.10	0.80
1:G:646:PHE:CE2	1:G:652:LEU:HD21	2.14	0.80
1:J:218:LEU:CA	1:J:221:GLN:HG2	2.10	0.80
1:J:538:GLU:CA	4:7:351:THR:H	1.93	0.80
1:J:578:HIS:HD2	1:J:591:ASN:HA	1.45	0.80
4:0:223:PHE:HE1	4:0:255:PHE:HB2	1.46	0.80
4:X:223:PHE:HE1	4:X:255:PHE:HB2	1.46	0.80
1:A:550:PHE:CA	4:6:46:GLY:CA	2.59	0.80
1:A:641:LYS:HD2	4:4:348:SER:CA	2.09	0.80
1:A:725:ARG:CZ	1:A:733:PRO:HB3	2.06	0.80
1:A:813:ILE:HG23	2:B:127:ARG:CD	1.94	0.80
1:D:374:GLN:HG3	1:D:375:ALA:N	1.96	0.80
1:D:721:LYS:CA	1:D:736:GLN:NE2	2.43	0.80
1:G:571:ALA:O	1:G:572:LYS:CG	2.28	0.80
1:G:836:PHE:CZ	2:H:159:HIS:HA	2.15	0.80
1:J:800:ARG:HD2	3:L:149:VAL:CB	2.10	0.80
4:Y:223:PHE:HE1	4:Y:255:PHE:HB2	1.46	0.80
1:D:215:GLN:N	1:D:340:ILE:CD1	2.44	0.80
1:D:723:ARG:O	1:D:782:MLY:CE	2.30	0.80
1:J:798:LEU:CD2	3:L:126:LEU:CG	2.59	0.80
2:K:141:PRO:CB	2:K:142:PRO:HD2	2.11	0.80
2:B:144:VAL:CA	2:B:153:ILE:HD11	2.11	0.80
1:D:818:TYR:CB	2:E:90:GLY:N	2.45	0.80
1:G:93:MET:CE	1:G:763:THR:C	2.48	0.80
1:G:553:MLY:NZ	4:8:45:VAL:HA	1.84	0.80
1:J:215:GLN:N	1:J:340:ILE:CD1	2.44	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:374:GLN:HG3	1:J:375:ALA:N	1.96	0.80
4:Z:223:PHE:HE1	4:Z:255:PHE:HB2	1.46	0.80
2:B:141:PRO:CB	2:B:142:PRO:HD2	2.11	0.80
1:D:732:ILE:HG22	1:D:747:LEU:HD12	0.81	0.80
1:D:797:PHE:HE2	3:F:126:LEU:CD2	1.93	0.80
1:D:831:TRP:HA	2:E:51:PHE:HE1	1.45	0.80
1:G:538:GLU:CA	4:6:351:THR:H	1.93	0.80
1:G:538:GLU:HG3	4:6:351:THR:C	2.02	0.80
1:A:215:GLN:N	1:A:340:ILE:CD1	2.44	0.80
1:A:732:ILE:HG21	1:A:747:LEU:HD13	0.91	0.80
1:D:578:HIS:HB3	1:D:592:ILE:HD12	1.62	0.80
1:D:822:SER:CB	2:E:88:LEU:CD2	2.52	0.80
2:E:111:SER:OG	2:E:148:VAL:C	2.15	0.80
1:G:829:TRP:CH2	2:H:87:LYS:CE	2.63	0.80
2:K:141:PRO:HB2	2:K:142:PRO:CD	2.11	0.80
1:A:480:ILE:HG22	1:A:481:ASN:HD22	1.45	0.80
1:J:93:MET:SD	1:J:716:LEU:CD1	2.67	0.80
1:J:93:MET:HG3	1:J:764:MLY:CD	2.11	0.80
1:G:542:PHE:CA	4:6:143:TYR:HE1	1.93	0.80
1:G:578:HIS:HD2	1:G:591:ASN:HA	1.44	0.80
1:G:599:ASN:CA	1:G:649:VAL:CB	2.53	0.80
1:G:732:ILE:HG22	1:G:747:LEU:HD12	0.81	0.80
3:L:49:ILE:N	3:L:52:ASN:ND2	2.29	0.80
4:6:223:PHE:HE1	4:6:255:PHE:HB2	1.46	0.80
1:A:374:GLN:HG3	1:A:375:ALA:N	1.96	0.80
1:A:578:HIS:HD2	1:A:591:ASN:HA	1.45	0.80
1:D:232:PHE:CZ	1:D:287:ILE:HD13	2.16	0.80
1:G:215:GLN:N	1:G:340:ILE:CD1	2.44	0.80
1:G:798:LEU:CD2	3:I:122:GLU:HB3	2.10	0.80
1:J:571:ALA:O	1:J:572:LYS:CG	2.28	0.80
1:J:797:PHE:HB2	3:L:149:VAL:CG1	2.12	0.80
2:K:144:VAL:CA	2:K:153:ILE:HD11	2.11	0.80
4:1:223:PHE:HE1	4:1:255:PHE:HB2	1.46	0.80
1:G:218:LEU:HA	1:G:221:GLN:HG2	1.62	0.80
1:G:550:PHE:CA	4:8:46:GLY:CA	2.59	0.80
1:G:769:ALA:HB2	1:G:770:GLY:CA	2.12	0.80
1:A:732:ILE:HG22	1:A:747:LEU:HD12	0.81	0.79
1:A:752:ASP:O	1:A:778:MET:SD	2.39	0.79
3:C:49:ILE:N	3:C:52:ASN:ND2	2.29	0.79
1:D:830:PRO:HB2	2:E:51:PHE:CE2	2.16	0.79
3:F:49:ILE:N	3:F:52:ASN:ND2	2.29	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:374:GLN:HG3	1:G:375:ALA:N	1.96	0.79
1:G:553:MLY:CB	4:8:46:GLY:CA	2.33	0.79
1:J:232:PHE:CZ	1:J:287:ILE:HD13	2.16	0.79
1:J:732:ILE:HG22	1:J:747:LEU:HD12	0.81	0.79
1:J:820:VAL:HG11	2:K:136:MET:HE3	1.64	0.79
1:J:838:ILE:CD1	2:K:54:MET:CE	2.61	0.79
1:D:480:ILE:HG22	1:D:481:ASN:HD22	1.45	0.79
1:J:84:MLY:HE2	1:J:719:ASP:CB	1.63	0.79
1:J:784:ALA:O	1:J:788:THR:N	2.14	0.79
1:A:571:ALA:O	1:A:572:LYS:CG	2.28	0.79
1:D:736:GLN:HA	1:D:743:ALA:HB2	1.51	0.79
2:E:144:VAL:HG12	2:E:153:ILE:CD1	2.10	0.79
1:G:752:ASP:C	1:G:779:ARG:NH1	2.34	0.79
1:J:732:ILE:CG2	1:J:747:LEU:HD13	1.34	0.79
1:J:732:ILE:HG21	1:J:747:LEU:HD13	0.90	0.79
4:6:287:ILE:HB	4:8:204:ALA:N	1.97	0.79
1:A:599:ASN:CA	1:A:649:VAL:CB	2.54	0.79
1:A:732:ILE:HG23	1:A:747:LEU:CB	1.85	0.79
1:D:769:ALA:HA	1:D:771:LEU:N	1.97	0.79
2:E:144:VAL:CA	2:E:153:ILE:HD11	2.11	0.79
1:G:819:ASN:ND2	2:H:92:ASP:HB2	1.96	0.79
2:H:121:LEU:CG	2:H:128:PHE:CA	2.49	0.79
3:I:49:ILE:N	3:I:52:ASN:ND2	2.29	0.79
4:W:223:PHE:HE1	4:W:255:PHE:HB2	1.46	0.79
1:A:174:SER:CB	1:A:667:THR:HG21	2.13	0.79
1:A:557:GLU:N	4:6:48:GLY:HA2	1.90	0.79
1:A:641:LYS:CE	1:A:647:GLN:CG	2.60	0.79
2:H:144:VAL:CA	2:H:153:ILE:HD11	2.11	0.79
4:4:287:ILE:HB	4:6:204:ALA:N	1.97	0.79
2:E:150:TYR:C	2:E:151:LYS:CG	2.48	0.79
1:G:754:ASP:HB2	1:G:776:GLU:CD	2.02	0.79
1:J:530:MET:HE1	4:7:355:MET:SD	2.23	0.79
1:J:817:GLN:OE1	2:K:127:ARG:HD2	1.82	0.79
1:A:218:LEU:CA	1:A:221:GLN:HG2	2.10	0.79
1:A:538:GLU:HG3	4:4:351:THR:C	2.03	0.79
1:D:830:PRO:HD2	2:E:67:MET:CE	2.11	0.79
2:E:141:PRO:CB	2:E:142:PRO:HD2	2.12	0.79
2:H:141:PRO:CB	2:H:142:PRO:HD2	2.12	0.79
1:A:409:GLY:N	1:A:636:LYS:CG	2.44	0.79
1:A:537:GLU:O	4:4:350:SER:N	2.16	0.79
1:A:550:PHE:N	4:6:46:GLY:HA3	1.97	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:141:PRO:HB2	2:B:142:PRO:CD	2.11	0.79
1:D:641:LYS:CE	1:D:647:GLN:HB2	2.13	0.79
1:D:768:MLY:CA	1:D:771:LEU:HD13	2.12	0.79
1:G:537:GLU:O	4:6:350:SER:N	2.16	0.79
1:G:550:PHE:N	4:8:46:GLY:HA3	1.97	0.79
1:G:641:LYS:HD2	4:6:348:SER:HB2	1.54	0.79
1:D:407:GLY:HA2	1:D:412:ALA:HA	1.65	0.79
1:D:409:GLY:N	1:D:636:LYS:CG	2.44	0.79
1:D:537:GLU:O	4:5:350:SER:N	2.16	0.79
1:D:550:PHE:HA	4:7:46:GLY:HA2	1.64	0.79
1:D:793:ARG:HA	3:F:40:ASN:ND2	1.96	0.79
2:E:141:PRO:HB2	2:E:142:PRO:CD	2.12	0.79
3:I:50:LEU:C	3:I:53:PRO:HD2	2.03	0.79
1:J:407:GLY:HA2	1:J:412:ALA:HA	1.65	0.79
3:L:50:LEU:C	3:L:53:PRO:HD2	2.03	0.79
4:W:287:ILE:HB	4:Y:204:ALA:N	1.98	0.79
1:A:641:LYS:HD2	4:4:348:SER:HB2	1.54	0.79
1:A:769:ALA:C	1:A:772:LEU:N	2.33	0.79
1:D:792:ALA:CA	3:F:40:ASN:HB3	2.12	0.79
1:D:834:LEU:HG	2:E:54:MET:CG	2.03	0.79
1:G:174:SER:CB	1:G:667:THR:HG21	2.13	0.79
1:G:218:LEU:CA	1:G:221:GLN:HG2	2.10	0.79
1:G:550:PHE:HA	4:8:46:GLY:HA2	1.64	0.79
1:J:92:ALA:O	1:J:714:ARG:CG	2.31	0.79
2:B:144:VAL:HG12	2:B:153:ILE:CD1	2.09	0.78
1:D:732:ILE:HG23	1:D:747:LEU:CB	1.85	0.78
1:J:642:LYS:CG	4:7:23:GLY:H	1.77	0.78
4:1:287:ILE:HB	4:3:204:ALA:N	1.97	0.78
1:A:817:GLN:HB2	2:B:127:ARG:NH1	1.97	0.78
1:D:291:ILE:HA	1:D:331:LEU:HD11	1.64	0.78
3:F:50:LEU:C	3:F:53:PRO:HD2	2.03	0.78
1:G:407:GLY:HA2	1:G:412:ALA:HA	1.65	0.78
1:A:550:PHE:HA	4:6:46:GLY:HA2	1.65	0.78
1:A:553:MLY:NZ	4:6:45:VAL:HA	1.84	0.78
1:J:409:GLY:N	1:J:636:LYS:CG	2.44	0.78
1:J:538:GLU:HG3	4:7:351:THR:C	2.03	0.78
1:J:550:PHE:HA	4:V:46:GLY:HA2	1.64	0.78
1:J:754:ASP:OD2	1:J:776:GLU:CB	2.32	0.78
4:V:287:ILE:HB	4:X:204:ALA:N	1.97	0.78
1:A:51:THR:O	1:A:62:VAL:HG13	1.84	0.78
3:C:50:LEU:C	3:C:53:PRO:HD2	2.03	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:481:ASN:HD22	1:D:481:ASN:N	1.82	0.78
2:E:162:ASP:HB3	2:K:20:ASP:HB2	1.64	0.78
1:J:291:ILE:HA	1:J:331:LEU:HD11	1.64	0.78
1:J:639:GLY:CA	4:7:345:ILE:N	2.47	0.78
1:J:641:LYS:CE	1:J:647:GLN:HB2	2.13	0.78
1:A:642:LYS:HG2	4:4:22:ALA:HA	1.66	0.78
1:D:550:PHE:N	4:7:46:GLY:HA3	1.97	0.78
1:D:815:CYS:SG	2:E:92:ASP:HB2	2.24	0.78
1:G:642:LYS:HG2	4:6:22:ALA:HA	1.65	0.78
1:G:646:PHE:HE2	1:G:652:LEU:CD2	1.97	0.78
4:5:287:ILE:HB	4:7:204:ALA:N	1.97	0.78
1:G:537:GLU:HG3	4:6:350:SER:O	1.79	0.78
1:J:537:GLU:O	4:7:350:SER:N	2.16	0.78
4:3:287:ILE:HB	4:5:204:ALA:N	1.98	0.78
4:8:287:ILE:HB	4:W:204:ALA:N	1.97	0.78
1:A:556:ASP:HA	4:6:49:GLN:O	1.70	0.78
3:C:49:ILE:N	3:C:52:ASN:HD22	1.82	0.78
1:G:51:THR:O	1:G:62:VAL:HG13	1.84	0.78
1:G:93:MET:SD	1:G:763:THR:HG22	2.24	0.78
1:G:291:ILE:HA	1:G:331:LEU:HD11	1.64	0.78
1:J:174:SER:CB	1:J:667:THR:HG21	2.13	0.78
1:J:646:PHE:HE2	1:J:652:LEU:CD2	1.97	0.78
1:J:797:PHE:HA	3:L:149:VAL:CG1	2.12	0.78
1:A:537:GLU:HG3	4:4:350:SER:O	1.79	0.78
2:B:121:LEU:CG	2:B:128:PHE:HA	2.14	0.78
1:D:800:ARG:CD	3:F:149:VAL:C	2.53	0.78
1:G:93:MET:CA	1:G:764:MLY:NZ	2.35	0.78
1:G:732:ILE:HG21	1:G:747:LEU:HD13	0.91	0.78
1:J:51:THR:O	1:J:62:VAL:HG13	1.84	0.78
1:J:530:MET:CG	4:7:354:GLN:CB	2.30	0.78
1:J:550:PHE:N	4:V:46:GLY:HA3	1.97	0.78
1:J:798:LEU:HD21	3:L:126:LEU:CG	2.14	0.78
4:2:287:ILE:HB	4:4:204:ALA:N	1.98	0.78
4:8:223:PHE:HE1	4:8:255:PHE:HB2	1.46	0.78
1:A:496:PHE:CD2	1:A:514:ASP:HA	2.19	0.78
1:D:831:TRP:HA	2:E:51:PHE:CE1	2.19	0.78
1:D:831:TRP:N	2:E:51:PHE:CZ	2.52	0.78
1:J:95:THR:HA	1:J:713:SER:HA	1.66	0.78
1:A:789:ALA:HB1	3:C:87:PHE:CE2	2.18	0.78
2:B:117:LEU:HB2	2:B:147:ASN:HD21	1.47	0.78
1:D:646:PHE:CE2	1:D:652:LEU:HD21	2.14	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:793:ARG:HE	3:F:147:MET:HA	1.47	0.78
1:D:839:MLY:CH1	2:E:159:HIS:CB	2.61	0.78
1:G:219:GLU:O	1:G:223:ILE:HG13	1.84	0.78
1:G:496:PHE:CD2	1:G:514:ASP:HA	2.19	0.78
1:G:639:GLY:CA	4:6:345:ILE:N	2.47	0.78
1:J:84:MLY:HH11	1:J:715:VAL:HG11	1.66	0.78
1:J:107:MLY:HB3	1:J:686:MET:HE2	1.66	0.78
1:J:496:PHE:CD2	1:J:514:ASP:HA	2.19	0.78
1:A:219:GLU:O	1:A:223:ILE:HG13	1.84	0.77
1:A:795:ARG:CB	3:C:35:ARG:NH2	2.43	0.77
1:D:538:GLU:HG3	4:5:351:THR:C	2.03	0.77
1:D:639:GLY:CA	4:5:345:ILE:N	2.47	0.77
1:G:409:GLY:N	1:G:636:LYS:CG	2.44	0.77
1:G:727:LEU:O	3:I:113:THR:OG1	2.02	0.77
1:J:829:TRP:CZ3	2:K:84:PHE:CE2	2.51	0.77
1:A:530:MET:HE3	4:4:354:GLN:HG2	1.65	0.77
1:D:496:PHE:CD2	1:D:514:ASP:HA	2.19	0.77
1:D:724:TYR:C	1:D:782:MLY:HH11	2.04	0.77
1:D:831:TRP:CH2	2:E:34:ILE:CG2	2.65	0.77
2:K:117:LEU:HB2	2:K:147:ASN:HD21	1.47	0.77
4:5:223:PHE:HD2	4:5:312:ARG:HH21	1.32	0.77
4:V:223:PHE:HD2	4:V:312:ARG:HH21	1.33	0.77
4:Z:223:PHE:HD2	4:Z:312:ARG:HH21	1.33	0.77
1:A:407:GLY:HA2	1:A:412:ALA:HA	1.65	0.77
1:A:502:GLU:CG	1:A:764:MLY:O	2.31	0.77
1:D:530:MET:HE1	4:5:355:MET:SD	2.24	0.77
1:D:831:TRP:CH2	2:E:47:LEU:CA	2.37	0.77
1:J:116:TYR:O	1:J:153:PRO:HB2	1.85	0.77
4:X:223:PHE:HD2	4:X:312:ARG:HH21	1.33	0.77
1:A:291:ILE:HA	1:A:331:LEU:HD11	1.64	0.77
1:D:51:THR:O	1:D:62:VAL:HG13	1.84	0.77
1:D:809:ARG:CZ	2:E:124:GLY:CA	2.61	0.77
1:G:93:MET:CE	1:G:764:MLY:HE3	2.14	0.77
1:G:836:PHE:CZ	2:H:160:GLY:N	2.50	0.77
1:A:793:ARG:HH21	3:C:147:MET:CB	1.97	0.77
1:D:831:TRP:HZ3	2:E:34:ILE:HG23	1.42	0.77
3:I:49:ILE:N	3:I:52:ASN:HD22	1.82	0.77
1:J:725:ARG:HG3	1:J:733:PRO:HA	1.67	0.77
1:A:639:GLY:CA	4:4:345:ILE:N	2.47	0.77
1:D:629:GLU:HA	1:D:643:GLY:C	2.05	0.77
1:G:116:TYR:O	1:G:153:PRO:HB2	1.85	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:218:LEU:HD22	1:G:222:ILE:HG12	1.66	0.77
1:G:641:LYS:CE	1:G:647:GLN:HB2	2.13	0.77
1:G:831:TRP:CZ2	2:H:47:LEU:HD22	2.17	0.77
1:J:93:MET:HG3	1:J:764:MLY:HD3	1.60	0.77
4:7:223:PHE:HD2	4:7:312:ARG:HH21	1.33	0.77
1:A:736:GLN:HA	1:A:743:ALA:HB2	1.51	0.77
1:D:116:TYR:O	1:D:153:PRO:HB2	1.85	0.77
1:D:174:SER:CB	1:D:667:THR:HG21	2.13	0.77
1:G:728:ASN:ND2	3:I:113:THR:OG1	2.18	0.77
1:G:732:ILE:CG2	1:G:747:LEU:HD13	1.34	0.77
1:G:736:GLN:HA	1:G:743:ALA:HB1	1.26	0.77
1:D:94:MET:CE	1:D:101:ALA:HB1	2.15	0.77
1:D:646:PHE:HE2	1:D:652:LEU:CD2	1.97	0.77
3:I:3:SER:O	3:I:4:LYS:HB2	1.84	0.77
1:J:629:GLU:HA	1:J:643:GLY:C	2.05	0.77
2:K:121:LEU:CG	2:K:128:PHE:HA	2.14	0.77
4:0:223:PHE:HD2	4:0:312:ARG:HH21	1.33	0.77
1:A:641:LYS:CE	1:A:647:GLN:HB2	2.13	0.77
1:A:646:PHE:HE2	1:A:652:LEU:CD2	1.97	0.77
1:A:725:ARG:HG3	1:A:733:PRO:HA	1.67	0.77
1:A:757:GLN:HB2	1:A:771:LEU:HD11	1.58	0.77
4:1:223:PHE:HD2	4:1:312:ARG:HH21	1.33	0.77
4:3:223:PHE:HD2	4:3:312:ARG:HH21	1.33	0.77
4:4:223:PHE:HD2	4:4:312:ARG:HH21	1.33	0.77
4:X:287:ILE:HB	4:Z:204:ALA:N	1.97	0.77
1:D:508:ILE:HA	1:D:761:GLY:HA3	1.65	0.77
1:D:642:LYS:HG2	4:5:22:ALA:HA	1.65	0.77
1:D:721:LYS:CA	1:D:736:GLN:OE1	2.33	0.77
1:D:818:TYR:CG	2:E:89:LYS:HB2	2.20	0.77
1:G:725:ARG:HG3	1:G:733:PRO:HA	1.67	0.77
1:G:733:PRO:C	1:G:737:PHE:HD1	1.88	0.77
1:G:769:ALA:O	1:G:773:GLY:CA	2.33	0.77
2:H:141:PRO:HB2	2:H:142:PRO:CD	2.11	0.77
1:J:218:LEU:HD22	1:J:222:ILE:HG12	1.67	0.77
1:J:219:GLU:O	1:J:223:ILE:HG13	1.84	0.77
1:J:646:PHE:CE2	1:J:652:LEU:HD21	2.14	0.77
1:A:502:GLU:CB	1:A:761:GLY:HA3	2.16	0.76
1:A:721:LYS:CA	1:A:736:GLN:OE1	2.33	0.76
1:A:793:ARG:NH2	3:C:147:MET:CE	2.48	0.76
1:D:635:GLY:HA3	4:5:341:ILE:CD1	2.14	0.76
1:D:733:PRO:C	1:D:737:PHE:HD1	1.88	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:49:ILE:N	3:F:52:ASN:HD22	1.82	0.76
1:G:732:ILE:N	1:G:733:PRO:HD2	2.00	0.76
1:J:641:LYS:CE	1:J:647:GLN:CG	2.60	0.76
3:L:3:SER:O	3:L:4:LYS:HB2	1.85	0.76
4:2:223:PHE:HD2	4:2:312:ARG:HH21	1.33	0.76
1:A:732:ILE:N	1:A:733:PRO:HD2	2.00	0.76
1:D:599:ASN:CA	1:D:649:VAL:CB	2.53	0.76
1:G:798:LEU:HD22	3:I:126:LEU:HD11	1.66	0.76
1:J:94:MET:CE	1:J:101:ALA:HB1	2.15	0.76
1:J:635:GLY:HA3	4:7:341:ILE:CD1	2.14	0.76
4:0:287:ILE:HB	4:2:204:ALA:N	1.97	0.76
1:A:94:MET:CE	1:A:101:ALA:HB1	2.15	0.76
1:D:219:GLU:O	1:D:223:ILE:HG13	1.84	0.76
1:D:641:LYS:CE	1:D:647:GLN:CG	2.60	0.76
2:E:121:LEU:CG	2:E:128:PHE:HA	2.14	0.76
1:J:721:LYS:CA	1:J:736:GLN:OE1	2.33	0.76
1:A:623:PHE:CG	1:A:623:PHE:CA	2.68	0.76
1:A:629:GLU:HA	1:A:643:GLY:C	2.05	0.76
1:A:795:ARG:NH1	3:C:43:ASN:N	2.31	0.76
1:D:534:SER:O	4:5:351:THR:N	2.19	0.76
1:G:218:LEU:HB2	1:G:221:GLN:CG	2.09	0.76
1:G:530:MET:CG	4:6:354:GLN:CB	2.30	0.76
1:J:721:LYS:HG2	1:J:736:GLN:CD	1.86	0.76
4:7:287:ILE:HB	4:V:204:ALA:N	1.97	0.76
1:A:218:LEU:HD22	1:A:222:ILE:HG12	1.67	0.76
1:D:732:ILE:N	1:D:733:PRO:HD2	2.00	0.76
1:G:629:GLU:HA	1:G:643:GLY:C	2.05	0.76
1:G:641:LYS:HD2	1:G:647:GLN:OE1	1.81	0.76
2:H:121:LEU:CG	2:H:128:PHE:HA	2.14	0.76
2:H:150:TYR:C	2:H:151:LYS:CG	2.48	0.76
1:J:732:ILE:N	1:J:733:PRO:HD2	2.01	0.76
1:J:733:PRO:C	1:J:737:PHE:HD1	1.88	0.76
1:J:831:TRP:CH2	2:K:47:LEU:CD2	2.68	0.76
4:6:290:ARG:HH22	4:8:202:THR:HG23	1.50	0.76
4:Y:223:PHE:HD2	4:Y:312:ARG:HH21	1.33	0.76
1:A:721:LYS:HG2	1:A:736:GLN:CD	1.86	0.76
1:D:529:PRO:C	4:5:354:GLN:CB	2.49	0.76
1:D:831:TRP:CG	2:E:51:PHE:CZ	2.74	0.76
1:G:530:MET:HE3	4:6:354:GLN:HG2	1.66	0.76
1:G:797:PHE:HD1	3:I:149:VAL:CB	1.97	0.76
1:G:817:GLN:HB3	2:H:127:ARG:HD2	1.53	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:481:ASN:HD22	1:J:481:ASN:N	1.82	0.76
1:J:623:PHE:CG	1:J:623:PHE:CA	2.68	0.76
4:6:223:PHE:HD2	4:6:312:ARG:HH21	1.33	0.76
4:8:223:PHE:HD2	4:8:312:ARG:HH21	1.32	0.76
4:8:290:ARG:NH1	4:W:202:THR:CG2	2.49	0.76
4:8:290:ARG:HH22	4:W:202:THR:HG23	1.50	0.76
4:V:290:ARG:NH1	4:X:202:THR:CG2	2.49	0.76
4:W:223:PHE:HD2	4:W:312:ARG:HH21	1.32	0.76
1:J:550:PHE:HA	4:V:46:GLY:HA3	1.66	0.76
4:0:290:ARG:NH1	4:2:202:THR:CG2	2.49	0.76
4:5:290:ARG:NH1	4:7:202:THR:CG2	2.49	0.76
1:D:553:MLY:NZ	4:7:45:VAL:HA	1.84	0.76
1:D:623:PHE:CG	1:D:623:PHE:CA	2.68	0.76
2:E:117:LEU:HB2	2:E:147:ASN:HD21	1.47	0.76
1:A:116:TYR:O	1:A:153:PRO:HB2	1.85	0.76
1:A:218:LEU:HB2	1:A:221:GLN:CG	2.09	0.76
1:D:550:PHE:HA	4:7:46:GLY:HA3	1.66	0.76
1:D:649:VAL:CG1	1:D:649:VAL:CB	2.64	0.76
1:D:664:LEU:O	1:D:667:THR:HB	1.86	0.76
1:G:649:VAL:CG1	1:G:649:VAL:CB	2.64	0.76
1:G:735:GLY:C	1:G:743:ALA:HB1	1.84	0.76
1:J:820:VAL:HG11	2:K:136:MET:CE	2.16	0.76
4:4:290:ARG:NH1	4:6:202:THR:CG2	2.49	0.76
4:X:290:ARG:NH1	4:Z:202:THR:CG2	2.49	0.76
1:A:218:LEU:HB3	1:A:221:GLN:HG3	1.61	0.76
1:D:538:GLU:OE2	4:5:355:MET:HE3	1.86	0.76
1:G:94:MET:CE	1:G:101:ALA:HB1	2.15	0.76
1:A:768:MLY:HB3	1:A:771:LEU:CB	2.16	0.75
1:G:534:SER:O	4:6:351:THR:N	2.20	0.75
1:G:641:LYS:CE	1:G:647:GLN:CG	2.61	0.75
3:L:49:ILE:N	3:L:52:ASN:HD22	1.82	0.75
1:A:502:GLU:CD	1:A:763:THR:H	1.88	0.75
1:D:831:TRP:CZ2	2:E:47:LEU:HB3	2.19	0.75
1:G:798:LEU:CD1	3:I:126:LEU:CG	2.65	0.75
1:J:818:TYR:CZ	2:K:127:ARG:NH2	2.54	0.75
1:A:793:ARG:HE	3:C:147:MET:HA	1.49	0.75
1:G:481:ASN:HD22	1:G:481:ASN:N	1.82	0.75
1:J:90:ASP:HB3	1:J:764:MLY:HH21	1.69	0.75
1:J:95:THR:HG1	1:J:713:SER:HB3	1.47	0.75
1:J:556:ASP:HA	4:V:49:GLN:O	1.69	0.75
1:A:649:VAL:CG1	1:A:649:VAL:CB	2.64	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:664:LEU:O	1:A:667:THR:HB	1.86	0.75
1:A:831:TRP:HH2	2:B:50:THR:CB	2.00	0.75
1:D:537:GLU:HG3	4:5:350:SER:O	1.79	0.75
1:D:642:LYS:CG	4:5:23:GLY:H	1.77	0.75
1:G:751:GLY:CA	3:I:114:LEU:HD13	2.16	0.75
1:D:166:MET:HE1	1:D:254:PHE:HB2	1.68	0.75
1:J:541:MET:O	4:7:143:TYR:CZ	2.40	0.75
1:G:623:PHE:CG	1:G:623:PHE:CA	2.68	0.75
1:G:721:LYS:CA	1:G:736:GLN:OE1	2.33	0.75
1:J:642:LYS:HG2	4:7:22:ALA:HA	1.65	0.75
1:J:649:VAL:CG1	1:J:649:VAL:CB	2.64	0.75
1:A:502:GLU:CA	1:A:761:GLY:CA	2.65	0.75
4:X:288:ASP:H	4:Z:203:THR:HG22	1.52	0.75
1:A:530:MET:CG	4:4:354:GLN:CB	2.30	0.75
1:A:534:SER:O	4:4:351:THR:N	2.18	0.75
3:C:3:SER:O	3:C:4:LYS:HB2	1.84	0.75
1:D:724:TYR:HA	1:D:782:MLY:CH1	2.16	0.75
1:D:725:ARG:HG3	1:D:733:PRO:HA	1.67	0.75
1:D:818:TYR:HB2	2:E:90:GLY:CA	2.17	0.75
1:D:839:MLY:CH1	2:E:159:HIS:HD2	1.76	0.75
1:G:664:LEU:O	1:G:667:THR:HB	1.86	0.75
1:G:817:GLN:CD	2:H:127:ARG:CD	2.54	0.75
4:O:288:ASP:H	4:2:203:THR:HG22	1.52	0.75
1:A:481:ASN:HD22	1:A:481:ASN:N	1.82	0.75
1:A:636:LYS:O	1:A:637:LYS:HB2	1.86	0.75
1:D:538:GLU:O	4:5:349:LEU:HG	1.86	0.75
1:G:817:GLN:HG3	2:H:128:PHE:CE1	2.22	0.75
1:J:350:ALA:O	1:J:354:LEU:HB2	1.87	0.75
1:J:538:GLU:OE2	4:7:355:MET:HE3	1.87	0.75
1:J:664:LEU:O	1:J:667:THR:HB	1.86	0.75
1:J:823:PHE:CE1	2:K:156:VAL:HG12	2.21	0.75
1:A:350:ALA:O	1:A:354:LEU:HB2	1.87	0.74
1:J:310:TYR:CE2	1:J:320:ILE:HD11	2.22	0.74
1:J:736:GLN:HA	1:J:743:ALA:HB1	1.26	0.74
4:7:290:ARG:NH1	4:V:202:THR:CG2	2.49	0.74
4:W:288:ASP:H	4:Y:203:THR:HG22	1.52	0.74
1:A:793:ARG:NH2	3:C:147:MET:HE3	2.02	0.74
1:A:836:PHE:HZ	2:B:160:GLY:N	1.80	0.74
3:F:3:SER:O	3:F:4:LYS:HB2	1.84	0.74
1:G:783:LEU:O	1:G:787:ILE:CB	2.35	0.74
2:H:117:LEU:HB2	2:H:147:ASN:HD21	1.47	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:90:ASP:OD2	1:J:764:MLY:CH2	2.35	0.74
1:J:93:MET:HG3	1:J:764:MLY:HH12	1.69	0.74
4:5:253:GLU:HA	4:5:256:ARG:HG3	1.69	0.74
4:5:288:ASP:H	4:7:203:THR:HG22	1.52	0.74
4:Y:253:GLU:HA	4:Y:256:ARG:HG3	1.69	0.74
1:A:502:GLU:C	1:A:761:GLY:CA	2.54	0.74
1:D:272:MLY:HH13	1:D:435:GLU:OE1	1.87	0.74
1:D:350:ALA:O	1:D:354:LEU:HB2	1.87	0.74
1:D:732:ILE:N	1:D:733:PRO:CD	2.51	0.74
1:G:541:MET:O	4:6:143:TYR:CZ	2.40	0.74
1:J:636:LYS:O	1:J:637:LYS:HB2	1.86	0.74
4:1:253:GLU:HA	4:1:256:ARG:HG3	1.70	0.74
4:3:288:ASP:H	4:5:203:THR:HG22	1.52	0.74
1:A:215:GLN:NE2	1:A:336:SER:O	2.21	0.74
1:A:541:MET:O	4:4:143:TYR:CZ	2.40	0.74
1:A:732:ILE:N	1:A:733:PRO:CD	2.51	0.74
1:G:350:ALA:O	1:G:354:LEU:HB2	1.87	0.74
1:G:735:GLY:CA	1:G:743:ALA:HA	2.17	0.74
2:H:111:SER:OG	2:H:148:VAL:C	2.15	0.74
4:1:290:ARG:NH1	4:3:202:THR:CG2	2.49	0.74
4:3:290:ARG:HH22	4:5:202:THR:HG23	1.50	0.74
4:7:253:GLU:HA	4:7:256:ARG:HG3	1.69	0.74
4:8:288:ASP:H	4:W:203:THR:HG22	1.52	0.74
1:A:499:GLU:OE1	1:A:766:PHE:CZ	2.40	0.74
1:A:538:GLU:O	4:4:349:LEU:HG	1.86	0.74
1:D:218:LEU:HD22	1:D:222:ILE:HG12	1.67	0.74
1:D:310:TYR:CE2	1:D:320:ILE:HD11	2.22	0.74
1:G:218:LEU:HB3	1:G:221:GLN:HG3	1.60	0.74
1:G:538:GLU:HA	4:6:349:LEU:HD12	0.74	0.74
1:J:538:GLU:HA	4:7:349:LEU:HD12	0.75	0.74
1:J:640:LYS:O	4:7:23:GLY:O	2.06	0.74
1:J:641:LYS:HD2	1:J:647:GLN:OE1	1.81	0.74
4:4:288:ASP:H	4:6:203:THR:HG22	1.52	0.74
4:8:253:GLU:HA	4:8:256:ARG:HG3	1.69	0.74
1:A:436:MLY:HE3	1:A:626:TYR:CE1	2.23	0.74
1:D:215:GLN:NE2	1:D:336:SER:O	2.20	0.74
1:D:541:MET:O	4:5:143:TYR:CZ	2.40	0.74
1:D:636:LYS:O	1:D:637:LYS:HB2	1.86	0.74
1:G:636:LYS:O	1:G:637:LYS:HB2	1.86	0.74
1:G:831:TRP:NE1	2:H:67:MET:SD	2.60	0.74
3:I:4:LYS:N	3:I:5:ALA:O	2.16	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:534:SER:O	4:7:351:THR:N	2.19	0.74
1:J:739:ASP:CB	1:J:742:LYS:HB3	2.12	0.74
4:3:253:GLU:HA	4:3:256:ARG:HG3	1.69	0.74
4:6:288:ASP:H	4:8:203:THR:HG22	1.52	0.74
4:W:253:GLU:HA	4:W:256:ARG:HG3	1.69	0.74
1:A:409:GLY:HA3	4:4:333:PRO:N	2.02	0.74
1:A:640:LYS:O	4:4:23:GLY:O	2.06	0.74
1:J:797:PHE:CA	3:L:149:VAL:CG1	2.65	0.74
1:A:635:GLY:HA3	4:4:341:ILE:CD1	2.14	0.74
1:A:793:ARG:NE	3:C:147:MET:HA	2.03	0.74
1:D:538:GLU:HA	4:5:349:LEU:HD12	0.74	0.74
1:D:769:ALA:CA	1:D:771:LEU:HA	2.17	0.74
1:D:834:LEU:HD13	2:E:51:PHE:HD1	1.53	0.74
1:G:310:TYR:CE2	1:G:320:ILE:HD11	2.22	0.74
1:G:730:SER:CB	3:I:109:HIS:NE2	2.50	0.74
1:J:272:MLY:HH13	1:J:435:GLU:OE1	1.87	0.74
1:J:768:MLY:CD	1:J:772:LEU:HB2	2.18	0.74
4:1:288:ASP:H	4:3:203:THR:HG22	1.52	0.74
4:2:290:ARG:NH1	4:4:202:THR:CG2	2.49	0.74
4:V:253:GLU:HA	4:V:256:ARG:HG3	1.69	0.74
4:V:288:ASP:H	4:X:203:THR:HG22	1.52	0.74
4:V:290:ARG:HH22	4:X:202:THR:HG23	1.50	0.74
1:A:538:GLU:HA	4:4:349:LEU:HD12	0.74	0.74
1:A:538:GLU:CD	4:4:355:MET:HE3	2.08	0.74
1:A:757:GLN:HG3	1:A:771:LEU:HD11	1.70	0.74
1:D:436:MLY:HE3	1:D:626:TYR:CE1	2.23	0.74
1:J:538:GLU:O	4:7:349:LEU:HG	1.86	0.74
1:A:530:MET:CE	4:4:355:MET:SD	2.76	0.74
1:A:733:PRO:C	1:A:737:PHE:HD1	1.88	0.74
1:D:640:LYS:O	4:5:23:GLY:O	2.06	0.74
4:2:288:ASP:H	4:4:203:THR:HG22	1.52	0.74
4:4:290:ARG:HH22	4:6:202:THR:HG23	1.50	0.74
4:W:290:ARG:NH1	4:Y:202:THR:CG2	2.49	0.74
4:X:253:GLU:HA	4:X:256:ARG:HG3	1.69	0.74
1:A:486:MLY:HH13	1:A:527:GLU:OE1	1.88	0.73
1:A:839:MLY:CD	2:B:159:HIS:CB	2.65	0.73
1:D:530:MET:CG	4:5:354:GLN:CB	2.30	0.73
3:I:24:LYS:CA	3:I:63:ILE:O	2.36	0.73
1:J:84:MLY:CH1	1:J:715:VAL:HG12	2.15	0.73
2:K:130:PRO:O	2:K:132:GLU:N	2.21	0.73
1:J:735:GLY:CA	1:J:743:ALA:HA	2.18	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:4:253:GLU:HA	4:4:256:ARG:HG3	1.69	0.73
4:6:253:GLU:HA	4:6:256:ARG:HG3	1.69	0.73
1:A:542:PHE:CD2	4:4:143:TYR:CE1	2.76	0.73
1:D:409:GLY:HA3	4:5:333:PRO:N	2.03	0.73
1:D:487:LEU:O	1:D:490:PHE:HB3	1.89	0.73
1:G:732:ILE:N	1:G:733:PRO:CD	2.51	0.73
1:G:795:ARG:CD	3:I:35:ARG:NH2	2.17	0.73
1:J:166:MET:HE3	1:J:254:PHE:CD2	2.23	0.73
1:J:529:PRO:C	4:7:354:GLN:CB	2.48	0.73
1:J:557:GLU:N	4:V:48:GLY:HA3	1.90	0.73
1:A:709:LYS:O	1:A:710:GLY:CA	2.37	0.73
1:D:534:SER:CA	4:5:351:THR:HA	2.19	0.73
1:G:215:GLN:NE2	1:G:336:SER:O	2.20	0.73
1:J:93:MET:HA	1:J:714:ARG:HG3	1.70	0.73
1:J:441:MET:O	1:J:445:ILE:HG13	1.88	0.73
1:A:310:TYR:CE2	1:A:320:ILE:HD11	2.22	0.73
1:A:529:PRO:C	4:4:354:GLN:CB	2.49	0.73
1:A:735:GLY:C	1:A:743:ALA:HB1	1.84	0.73
1:D:721:LYS:CB	1:D:736:GLN:CD	2.56	0.73
1:D:726:VAL:H	1:D:782:MLY:CH2	2.01	0.73
1:J:486:MLY:HH13	1:J:527:GLU:OE1	1.88	0.73
1:J:487:LEU:O	1:J:490:PHE:HB3	1.88	0.73
1:J:534:SER:CA	4:7:351:THR:HA	2.19	0.73
1:J:818:TYR:CE1	2:K:127:ARG:NH1	2.57	0.73
4:1:290:ARG:HH22	4:3:202:THR:HG23	1.50	0.73
4:6:290:ARG:NH1	4:8:202:THR:CG2	2.49	0.73
1:A:237:THR:HG22	1:A:239:ARG:H	1.53	0.73
1:A:707:CYS:HA	1:A:714:ARG:CZ	2.18	0.73
1:A:831:TRP:CD2	2:B:51:PHE:CE1	2.77	0.73
1:D:542:PHE:CD2	4:5:143:TYR:CE1	2.77	0.73
2:E:130:PRO:O	2:E:132:GLU:N	2.21	0.73
1:G:93:MET:HE2	1:G:764:MLY:HE3	1.69	0.73
1:G:409:GLY:HA3	4:6:333:PRO:N	2.03	0.73
1:G:486:MLY:HH13	1:G:527:GLU:OE1	1.87	0.73
1:G:487:LEU:O	1:G:490:PHE:HB3	1.89	0.73
1:G:536:LEU:HD13	1:G:550:PHE:CZ	2.24	0.73
2:H:130:PRO:O	2:H:132:GLU:N	2.21	0.73
1:A:131:TRP:C	1:A:132:LEU:HD12	2.09	0.73
2:B:130:PRO:O	2:B:132:GLU:N	2.21	0.73
1:D:530:MET:CE	4:5:355:MET:SD	2.77	0.73
1:D:802:GLU:O	1:D:806:MET:HG3	1.89	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:829:TRP:CD1	2:E:67:MET:HG2	2.24	0.73
3:F:24:LYS:CA	3:F:63:ILE:O	2.36	0.73
1:G:410:ASN:OD1	4:6:335:ARG:N	2.21	0.73
1:J:530:MET:CE	4:7:355:MET:SD	2.77	0.73
1:J:640:LYS:O	1:J:645:SER:OG	2.06	0.73
1:J:790:THR:N	3:L:87:PHE:CE2	2.57	0.73
4:0:253:GLU:HA	4:0:256:ARG:HG3	1.69	0.73
4:7:288:ASP:H	4:V:203:THR:HG22	1.52	0.73
1:A:97:LEU:CD2	1:A:712:PRO:HB3	2.19	0.73
1:A:536:LEU:HD13	1:A:550:PHE:CZ	2.24	0.73
1:D:557:GLU:N	4:7:48:GLY:HA3	1.90	0.73
1:G:93:MET:HE2	1:G:764:MLY:CG	2.13	0.73
1:G:190:MLY:HE3	1:G:230:GLU:OE2	1.89	0.73
1:G:635:GLY:HA3	4:6:341:ILE:CD1	2.14	0.73
1:J:436:MLY:HE3	1:J:626:TYR:CE1	2.23	0.73
1:A:410:ASN:OD1	4:4:335:ARG:N	2.22	0.73
1:D:441:MET:O	1:D:445:ILE:HG13	1.88	0.73
1:D:486:MLY:HH13	1:D:527:GLU:OE1	1.88	0.73
1:G:733:PRO:C	1:G:737:PHE:CD1	2.62	0.73
2:H:144:VAL:CB	2:H:153:ILE:HD11	2.19	0.73
4:5:290:ARG:HH22	4:7:202:THR:HG23	1.50	0.73
1:A:735:GLY:CA	1:A:743:ALA:HA	2.18	0.73
1:D:190:MLY:HE3	1:D:230:GLU:OE2	1.89	0.73
1:D:410:ASN:OD1	4:5:335:ARG:N	2.22	0.73
1:D:618:THR:O	1:D:622:LEU:HD13	1.89	0.73
1:D:769:ALA:HB1	1:D:770:GLY:HA3	1.71	0.73
1:G:272:MLY:HH13	1:G:435:GLU:OE1	1.88	0.73
1:G:410:ASN:CG	4:6:334:GLU:CA	2.47	0.73
1:G:640:LYS:O	4:6:23:GLY:O	2.06	0.73
1:G:802:GLU:O	1:G:806:MET:HG3	1.88	0.73
1:J:190:MLY:HE3	1:J:230:GLU:OE2	1.89	0.73
1:J:237:THR:HG22	1:J:239:ARG:H	1.54	0.73
1:J:732:ILE:N	1:J:733:PRO:CD	2.51	0.73
4:Z:253:GLU:HA	4:Z:256:ARG:HG3	1.69	0.73
1:D:36:SER:O	1:D:52:ILE:HG12	1.89	0.72
1:D:214:MET:HA	1:D:340:ILE:HD11	1.71	0.72
1:D:640:LYS:O	1:D:645:SER:OG	2.06	0.72
1:G:436:MLY:HE3	1:G:626:TYR:CE1	2.23	0.72
1:G:538:GLU:O	4:6:349:LEU:HG	1.87	0.72
1:G:817:GLN:CG	2:H:127:ARG:HB2	2.16	0.72
1:J:215:GLN:NE2	1:J:336:SER:O	2.21	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:410:ASN:OD1	4:7:335:ARG:N	2.21	0.72
1:J:553:MLY:NZ	4:V:45:VAL:HA	1.84	0.72
1:A:441:MET:O	1:A:445:ILE:HG13	1.88	0.72
1:A:721:LYS:CB	1:A:736:GLN:CD	2.56	0.72
1:A:802:GLU:O	1:A:806:MET:HG3	1.89	0.72
1:A:834:LEU:HD21	2:B:54:MET:SD	2.29	0.72
1:D:237:THR:HG22	1:D:239:ARG:H	1.54	0.72
1:G:21:GLU:O	1:G:25:ILE:HG13	1.89	0.72
1:J:21:GLU:O	1:J:25:ILE:HG13	1.89	0.72
1:J:36:SER:O	1:J:52:ILE:HG12	1.89	0.72
1:J:557:GLU:N	4:V:48:GLY:HA2	1.90	0.72
1:J:618:THR:O	1:J:622:LEU:HD13	1.89	0.72
1:J:802:GLU:O	1:J:806:MET:HG3	1.88	0.72
3:L:24:LYS:CA	3:L:63:ILE:O	2.37	0.72
4:2:253:GLU:HA	4:2:256:ARG:HG3	1.69	0.72
1:A:272:MLY:HH13	1:A:435:GLU:OE1	1.88	0.72
1:A:534:SER:CA	4:4:351:THR:HA	2.18	0.72
1:A:641:LYS:HD2	1:A:647:GLN:OE1	1.81	0.72
1:D:536:LEU:HD13	1:D:550:PHE:CZ	2.24	0.72
2:E:144:VAL:CB	2:E:153:ILE:HD11	2.19	0.72
1:J:409:GLY:HA3	4:7:333:PRO:N	2.03	0.72
1:J:542:PHE:CD2	4:7:143:TYR:CE1	2.77	0.72
1:J:754:ASP:HB3	1:J:757:GLN:HG2	1.71	0.72
1:D:735:GLY:CA	1:D:743:ALA:HA	2.18	0.72
2:E:117:LEU:CB	2:E:147:ASN:ND2	2.35	0.72
1:G:214:MET:HA	1:G:340:ILE:HD11	1.70	0.72
1:G:618:THR:O	1:G:622:LEU:HD13	1.89	0.72
1:G:640:LYS:O	1:G:645:SER:OG	2.06	0.72
1:J:95:THR:CB	1:J:713:SER:HB3	2.20	0.72
1:J:214:MET:HA	1:J:340:ILE:HD11	1.70	0.72
1:J:295:MLY:HG3	1:J:332:MET:CE	2.19	0.72
1:J:536:LEU:HD13	1:J:550:PHE:CZ	2.24	0.72
3:L:4:LYS:N	3:L:5:ALA:O	2.16	0.72
3:C:24:LYS:CA	3:C:63:ILE:O	2.37	0.72
1:D:295:MLY:HG3	1:D:332:MET:CE	2.20	0.72
1:D:789:ALA:HB2	3:F:81:GLN:HG2	1.72	0.72
1:G:176:LEU:HD12	1:G:176:LEU:N	2.05	0.72
1:G:754:ASP:HB3	1:G:757:GLN:HG2	1.72	0.72
1:G:817:GLN:CB	2:H:127:ARG:HH11	2.02	0.72
1:J:721:LYS:CB	1:J:736:GLN:CD	2.56	0.72
4:0:290:ARG:HH22	4:2:202:THR:HG23	1.50	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:4:3:ASP:HA	4:4:6:THR:CB	2.18	0.72
1:A:21:GLU:O	1:A:25:ILE:HG13	1.88	0.72
1:A:36:SER:O	1:A:52:ILE:HG12	1.89	0.72
1:A:486:MLY:HH22	1:A:527:GLU:OE2	1.90	0.72
1:A:519:LEU:HD12	1:A:519:LEU:N	2.04	0.72
1:G:93:MET:HE1	1:G:763:THR:HG22	1.67	0.72
1:J:769:ALA:HB3	1:J:770:GLY:N	2.04	0.72
2:K:144:VAL:CB	2:K:153:ILE:HD11	2.19	0.72
4:Y:3:ASP:HA	4:Y:6:THR:CB	2.18	0.72
1:A:290:GLN:C	1:A:331:LEU:HD12	2.09	0.72
1:A:707:CYS:CA	1:A:714:ARG:NH1	2.50	0.72
1:D:21:GLU:O	1:D:25:ILE:HG13	1.88	0.72
1:D:817:GLN:OE1	2:E:127:ARG:NE	2.22	0.72
1:G:486:MLY:HH22	1:G:527:GLU:OE2	1.90	0.72
1:G:530:MET:CE	4:6:355:MET:SD	2.78	0.72
1:G:731:ALA:HB2	3:I:109:HIS:ND1	2.04	0.72
2:H:117:LEU:HD12	2:H:147:ASN:CA	2.19	0.72
4:W:3:ASP:HA	4:W:6:THR:CB	2.18	0.72
1:G:237:THR:HG22	1:G:239:ARG:H	1.54	0.72
1:G:290:GLN:C	1:G:331:LEU:HD12	2.09	0.72
1:G:441:MET:O	1:G:445:ILE:HG13	1.88	0.72
1:J:131:TRP:C	1:J:132:LEU:HD12	2.09	0.72
1:J:510:TRP:CZ3	1:J:768:MLY:HH12	2.23	0.72
1:J:795:ARG:HD2	3:L:35:ARG:HH12	1.54	0.72
1:D:217:THR:C	1:D:221:GLN:HE21	1.92	0.72
1:D:290:GLN:C	1:D:331:LEU:HD12	2.09	0.72
1:D:292:MET:HE3	1:D:309:PRO:HA	1.71	0.72
1:D:641:LYS:HD2	1:D:647:GLN:OE1	1.81	0.72
1:D:754:ASP:HB3	1:D:757:GLN:HG2	1.72	0.72
1:G:732:ILE:HG23	1:G:747:LEU:CB	1.84	0.72
2:K:136:MET:O	2:K:140:PHE:HB2	1.90	0.72
4:3:290:ARG:NH1	4:5:202:THR:CG2	2.49	0.72
4:W:290:ARG:HH22	4:Y:202:THR:HG23	1.51	0.72
1:A:14:ALA:HB3	1:A:15:PRO:HD3	1.72	0.72
2:B:144:VAL:CB	2:B:153:ILE:HD11	2.19	0.72
1:D:486:MLY:HH22	1:D:527:GLU:OE2	1.90	0.72
1:G:14:ALA:HB3	1:G:15:PRO:HD3	1.72	0.72
1:G:721:LYS:CB	1:G:736:GLN:CD	2.56	0.72
1:A:217:THR:C	1:A:221:GLN:HE21	1.93	0.71
1:A:754:ASP:HB3	1:A:757:GLN:HG2	1.72	0.71
1:A:795:ARG:HD2	3:C:35:ARG:NH2	2.01	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:834:LEU:HD13	2:E:51:PHE:HA	1.71	0.71
1:J:176:LEU:HD12	1:J:176:LEU:N	2.05	0.71
4:1:3:ASP:HA	4:1:6:THR:CB	2.18	0.71
4:5:3:ASP:HA	4:5:6:THR:CB	2.18	0.71
1:A:217:THR:O	1:A:220:ASP:HB2	1.91	0.71
1:A:487:LEU:O	1:A:490:PHE:HB3	1.88	0.71
1:D:176:LEU:HD12	1:D:176:LEU:N	2.05	0.71
1:D:519:LEU:HD12	1:D:519:LEU:N	2.05	0.71
1:G:131:TRP:C	1:G:132:LEU:HD12	2.09	0.71
1:G:519:LEU:HD12	1:G:519:LEU:N	2.05	0.71
1:G:542:PHE:CD2	4:6:143:TYR:CE1	2.78	0.71
1:G:739:ASP:CB	1:G:742:LYS:HB3	2.12	0.71
1:J:486:MLY:HH22	1:J:527:GLU:OE2	1.90	0.71
1:J:800:ARG:CG	3:L:149:VAL:HG23	2.12	0.71
1:J:816:ILE:HD11	2:K:100:ALA:CB	2.19	0.71
1:A:190:MLY:HE3	1:A:230:GLU:OE2	1.89	0.71
1:A:836:PHE:CE1	2:B:159:HIS:CA	2.71	0.71
1:D:131:TRP:C	1:D:132:LEU:HD12	2.09	0.71
1:D:217:THR:O	1:D:220:ASP:HB2	1.90	0.71
2:E:136:MET:O	2:E:140:PHE:HB2	1.90	0.71
1:G:84:MLY:HH11	1:G:715:VAL:HG11	1.70	0.71
1:G:798:LEU:HD13	3:I:126:LEU:HD21	0.72	0.71
1:J:290:GLN:C	1:J:331:LEU:HD12	2.09	0.71
4:8:3:ASP:HA	4:8:6:THR:CB	2.18	0.71
1:A:793:ARG:HG3	3:C:146:ILE:CG2	2.21	0.71
1:G:534:SER:CA	4:6:351:THR:HA	2.20	0.71
1:G:795:ARG:CB	3:I:35:ARG:HH21	1.91	0.71
1:J:72:VAL:HG13	1:J:76:GLN:CB	2.19	0.71
1:J:510:TRP:CE3	1:J:768:MLY:CH1	2.72	0.71
1:A:214:MET:HA	1:A:340:ILE:HD11	1.71	0.71
1:D:245:ARG:HD3	1:D:271:GLU:OE1	1.90	0.71
1:D:792:ALA:CB	3:F:40:ASN:HB3	2.19	0.71
1:G:36:SER:O	1:G:52:ILE:HG12	1.90	0.71
1:J:217:THR:C	1:J:221:GLN:HE21	1.92	0.71
1:J:823:PHE:CD1	2:K:156:VAL:O	2.44	0.71
1:A:166:MET:HE3	1:A:254:PHE:CD2	2.25	0.71
1:A:618:THR:O	1:A:622:LEU:HD13	1.89	0.71
1:A:640:LYS:O	1:A:645:SER:OG	2.06	0.71
2:B:136:MET:O	2:B:140:PHE:HB2	1.90	0.71
1:D:86:ASP:OD2	1:D:87:MLY:HH13	1.91	0.71
1:D:724:TYR:CA	1:D:782:MLY:NZ	2.53	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:4:LYS:N	3:F:5:ALA:O	2.16	0.71
1:G:217:THR:C	1:G:221:GLN:HE21	1.92	0.71
1:J:295:MLY:HG3	1:J:332:MET:HE1	1.72	0.71
1:J:410:ASN:CG	4:7:334:GLU:CA	2.47	0.71
1:J:519:LEU:HD12	1:J:519:LEU:N	2.04	0.71
4:X:290:ARG:HH22	4:Z:202:THR:HG23	1.50	0.71
4:Z:3:ASP:HA	4:Z:6:THR:CB	2.18	0.71
1:A:206:LYS:HD3	1:A:217:THR:HG23	0.71	0.71
1:A:295:MLY:HG3	1:A:332:MET:CE	2.19	0.71
1:A:798:LEU:HD11	3:C:126:LEU:CG	2.20	0.71
1:A:830:PRO:HG2	2:B:67:MET:CE	2.20	0.71
1:A:831:TRP:CZ3	2:B:50:THR:CG2	2.72	0.71
1:D:56:GLU:CB	1:D:59:MLY:HB3	2.19	0.71
1:G:553:MLY:HG2	4:8:47:MET:N	2.06	0.71
1:J:831:TRP:HH2	2:K:34:ILE:HG21	1.55	0.71
1:A:819:ASN:N	2:B:90:GLY:CA	2.53	0.71
1:D:800:ARG:HB3	3:F:149:VAL:HG23	1.67	0.71
1:D:817:GLN:HG3	2:E:127:ARG:CD	2.19	0.71
1:G:274:ARG:NH2	1:G:282:GLU:OE1	2.24	0.71
1:J:56:GLU:CB	1:J:59:MLY:HB3	2.19	0.71
1:J:84:MLY:CH2	1:J:716:LEU:O	2.38	0.71
1:J:757:GLN:HG3	1:J:776:GLU:HG3	1.64	0.71
4:7:290:ARG:HH22	4:V:202:THR:HG23	1.50	0.71
1:D:14:ALA:HB3	1:D:15:PRO:HD3	1.72	0.71
1:D:831:TRP:CD1	2:E:51:PHE:HZ	2.09	0.71
1:D:834:LEU:HD12	2:E:54:MET:HB2	1.73	0.71
1:G:166:MET:HE1	1:G:254:PHE:HB2	1.72	0.71
1:G:717:TYR:HD1	1:G:744:SER:HG	1.39	0.71
1:G:834:LEU:CD1	2:H:51:PHE:CD1	2.74	0.71
1:J:274:ARG:NH2	1:J:282:GLU:OE1	2.24	0.71
1:J:762:HIS:H	1:J:762:HIS:CD2	2.07	0.71
4:3:3:ASP:HA	4:3:6:THR:CB	2.18	0.71
1:D:831:TRP:CD1	2:E:51:PHE:CZ	2.79	0.71
1:G:86:ASP:OD2	1:G:87:MLY:HH13	1.91	0.71
1:J:14:ALA:HB3	1:J:15:PRO:HD3	1.72	0.71
1:J:245:ARG:HD3	1:J:271:GLU:OE1	1.90	0.71
4:2:290:ARG:HH22	4:4:202:THR:HG23	1.50	0.71
1:A:505:MLY:HB2	1:A:761:GLY:C	2.11	0.70
1:G:245:ARG:HD3	1:G:271:GLU:OE1	1.90	0.70
1:A:72:VAL:HG13	1:A:76:GLN:CB	2.19	0.70
1:A:176:LEU:N	1:A:176:LEU:HD12	2.05	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:530:MET:HE2	4:5:354:GLN:HG3	1.73	0.70
1:D:579:PHE:HD2	1:D:592:ILE:HD11	1.56	0.70
1:G:295:MLY:HG3	1:G:332:MET:CE	2.20	0.70
1:G:550:PHE:HA	4:8:46:GLY:HA3	1.66	0.70
1:G:792:ALA:HA	3:I:35:ARG:NH1	2.04	0.70
1:G:793:ARG:NH1	3:I:40:ASN:HD21	1.90	0.70
1:G:810:ARG:HG2	1:G:810:ARG:HH11	1.56	0.70
1:J:93:MET:SD	1:J:764:MLY:CH2	2.65	0.70
1:J:206:LYS:HD3	1:J:217:THR:HG23	0.71	0.70
1:J:217:THR:O	1:J:220:ASP:HB2	1.91	0.70
4:6:3:ASP:HA	4:6:6:THR:CB	2.18	0.70
3:C:48:LYS:HB3	3:C:52:ASN:HD21	1.57	0.70
1:D:577:ALA:O	1:D:578:HIS:CG	2.45	0.70
1:D:643:GLY:N	4:5:24:ASP:CA	2.46	0.70
1:D:800:ARG:CD	3:F:149:VAL:HG22	2.21	0.70
1:J:86:ASP:OD2	1:J:87:MLY:HH13	1.91	0.70
1:J:754:ASP:CG	1:J:776:GLU:CA	2.59	0.70
1:J:787:ILE:HG22	1:J:788:THR:N	2.07	0.70
1:J:826:VAL:CG2	2:K:88:LEU:HD21	2.12	0.70
1:A:245:ARG:HD3	1:A:271:GLU:OE1	1.90	0.70
1:A:274:ARG:NH2	1:A:282:GLU:OE1	2.24	0.70
1:A:787:ILE:HG22	1:A:788:THR:N	2.07	0.70
1:D:641:LYS:HD2	4:5:348:SER:HA	1.73	0.70
1:D:769:ALA:HB1	1:D:770:GLY:N	2.05	0.70
1:G:579:PHE:HD2	1:G:592:ILE:HD11	1.56	0.70
1:G:721:LYS:HG2	1:G:736:GLN:CD	1.86	0.70
1:J:213:LYS:HA	1:J:220:ASP:OD1	1.92	0.70
1:A:86:ASP:OD2	1:A:87:MLY:HH13	1.91	0.70
1:A:123:CYS:HB2	1:A:158:ILE:HD11	1.73	0.70
1:A:818:TYR:HB2	2:B:90:GLY:CA	2.22	0.70
1:D:72:VAL:HG13	1:D:76:GLN:CB	2.19	0.70
1:D:274:ARG:NH2	1:D:282:GLU:OE1	2.24	0.70
1:D:789:ALA:CB	3:F:81:GLN:O	2.39	0.70
1:D:831:TRP:CG	2:E:51:PHE:HZ	2.10	0.70
1:G:217:THR:O	1:G:220:ASP:HB2	1.91	0.70
2:H:136:MET:O	2:H:140:PHE:HB2	1.90	0.70
1:J:630:ALA:O	4:7:25:ASP:HB2	1.91	0.70
1:D:213:LYS:HA	1:D:220:ASP:OD1	1.92	0.70
1:D:834:LEU:CD1	2:E:51:PHE:HA	2.20	0.70
3:F:25:ILE:O	3:F:63:ILE:HB	1.92	0.70
1:A:579:PHE:HD2	1:A:592:ILE:HD11	1.56	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:839:MLY:CD	2:B:159:HIS:CG	2.70	0.70
3:F:48:LYS:HB3	3:F:52:ASN:HD21	1.57	0.70
1:G:56:GLU:CB	1:G:59:MLY:HB3	2.19	0.70
1:J:123:CYS:HB2	1:J:158:ILE:HD11	1.73	0.70
1:J:641:LYS:HD2	4:7:348:SER:HA	1.73	0.70
1:J:810:ARG:HG2	1:J:810:ARG:HH11	1.57	0.70
1:A:814:PHE:HD1	2:B:127:ARG:NH2	1.70	0.70
1:A:839:MLY:HD2	2:B:159:HIS:CB	2.21	0.70
1:D:789:ALA:HB1	3:F:81:GLN:O	1.92	0.70
1:G:123:CYS:HB2	1:G:158:ILE:HD11	1.73	0.70
1:G:798:LEU:HD23	3:I:122:GLU:CB	2.20	0.70
1:J:577:ALA:O	1:J:578:HIS:CG	2.45	0.70
3:L:25:ILE:O	3:L:63:ILE:HB	1.92	0.70
1:A:546:THR:HG22	1:A:548:THR:N	2.05	0.70
1:A:732:ILE:HG21	1:A:747:LEU:HD11	0.73	0.70
1:G:762:HIS:H	1:G:762:HIS:CD2	2.07	0.70
1:J:800:ARG:HB2	3:L:149:VAL:CG2	2.07	0.70
1:J:818:TYR:CE1	2:K:127:ARG:CZ	2.75	0.70
1:A:813:ILE:HG22	2:B:127:ARG:NH1	2.06	0.70
2:B:111:SER:OG	2:B:148:VAL:HG12	1.92	0.70
1:D:123:CYS:HB2	1:D:158:ILE:HD11	1.73	0.70
1:D:206:LYS:HD3	1:D:217:THR:HG23	0.71	0.70
1:D:630:ALA:O	4:5:25:ASP:HB2	1.92	0.70
1:D:782:MLY:C	1:D:783:LEU:HD12	2.22	0.70
1:D:810:ARG:HG2	1:D:810:ARG:HH11	1.57	0.70
1:G:782:MLY:C	1:G:783:LEU:HD12	2.22	0.70
3:I:25:ILE:O	3:I:63:ILE:HB	1.92	0.70
1:J:215:GLN:CA	1:J:340:ILE:CG2	2.62	0.70
1:A:733:PRO:C	1:A:737:PHE:CD1	2.62	0.69
1:A:769:ALA:N	1:A:771:LEU:HB2	2.07	0.69
1:A:802:GLU:OE1	1:A:802:GLU:HA	1.92	0.69
1:D:726:VAL:H	1:D:782:MLY:HH22	1.55	0.69
1:G:546:THR:HG22	1:G:548:THR:N	2.05	0.69
1:J:838:ILE:HD11	2:K:54:MET:HE1	1.74	0.69
4:8:1:ASP:HA	4:8:4:GLU:HB3	1.74	0.69
4:W:1:ASP:HA	4:W:4:GLU:HB3	1.74	0.69
1:A:800:ARG:CG	3:C:149:VAL:CG2	2.60	0.69
1:G:643:GLY:N	4:6:24:ASP:CA	2.47	0.69
3:L:48:LYS:HB3	3:L:52:ASN:HD21	1.57	0.69
4:0:3:ASP:HA	4:0:6:THR:CB	2.18	0.69
1:A:577:ALA:O	1:A:578:HIS:CG	2.45	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:117:LEU:CB	2:B:147:ASN:OD1	2.39	0.69
2:E:117:LEU:HD12	2:E:147:ASN:CA	2.19	0.69
1:J:530:MET:HE2	4:7:354:GLN:HG3	1.74	0.69
1:J:579:PHE:HD2	1:J:592:ILE:HD11	1.56	0.69
1:J:630:ALA:O	4:7:25:ASP:CB	2.41	0.69
1:J:733:PRO:C	1:J:737:PHE:CD1	2.62	0.69
4:Y:1:ASP:HA	4:Y:4:GLU:HB3	1.74	0.69
1:A:834:LEU:CD2	2:B:54:MET:HG3	2.22	0.69
1:G:72:VAL:HG13	1:G:76:GLN:CB	2.19	0.69
1:G:800:ARG:HD2	3:I:149:VAL:HG23	1.72	0.69
2:H:111:SER:OG	2:H:148:VAL:HG12	1.92	0.69
2:K:111:SER:OG	2:K:148:VAL:HG12	1.92	0.69
4:1:1:ASP:HA	4:1:4:GLU:HB3	1.74	0.69
1:A:641:LYS:HD2	4:4:348:SER:HA	1.73	0.69
1:A:782:MLY:C	1:A:783:LEU:HD12	2.22	0.69
1:A:810:ARG:HG2	1:A:810:ARG:HH11	1.57	0.69
3:C:3:SER:O	3:C:4:LYS:CB	2.41	0.69
1:D:218:LEU:HB2	1:D:221:GLN:CG	2.09	0.69
1:G:93:MET:SD	1:G:716:LEU:HD11	2.32	0.69
1:J:768:MLY:HH23	1:J:772:LEU:CD1	2.21	0.69
1:J:823:PHE:CZ	2:K:156:VAL:HG12	2.27	0.69
1:A:123:CYS:HB2	1:A:158:ILE:CD1	2.23	0.69
1:A:166:MET:HE3	1:A:254:PHE:HD2	1.58	0.69
1:D:553:MLY:HG2	4:7:47:MET:N	2.07	0.69
1:G:787:ILE:HG22	1:G:788:THR:N	2.07	0.69
1:G:817:GLN:CB	2:H:127:ARG:CD	2.53	0.69
4:6:1:ASP:HA	4:6:4:GLU:HB3	1.74	0.69
1:A:553:MLY:HG2	4:6:47:MET:N	2.07	0.69
1:A:818:TYR:CB	2:B:90:GLY:N	2.56	0.69
1:D:541:MET:CG	4:5:345:ILE:O	2.41	0.69
1:G:206:LYS:HD3	1:G:217:THR:HG23	0.70	0.69
1:G:577:ALA:O	1:G:578:HIS:CG	2.45	0.69
1:G:815:CYS:O	1:G:819:ASN:HB2	1.93	0.69
1:J:752:ASP:O	1:J:780:ASP:CG	2.31	0.69
1:J:807:VAL:O	1:J:810:ARG:HB2	1.93	0.69
4:3:1:ASP:HA	4:3:4:GLU:HB3	1.74	0.69
4:7:3:ASP:HA	4:7:6:THR:CB	2.18	0.69
1:A:630:ALA:O	4:4:25:ASP:HB2	1.92	0.69
1:A:793:ARG:CG	3:C:146:ILE:HG22	2.21	0.69
1:A:798:LEU:HD21	3:C:122:GLU:HB3	1.73	0.69
1:D:510:TRP:CH2	1:D:711:PHE:HE2	2.11	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:556:ASP:HA	4:7:49:GLN:O	1.70	0.69
1:D:642:LYS:HB3	4:5:21:PHE:O	1.93	0.69
1:D:769:ALA:CA	1:D:770:GLY:C	2.61	0.69
1:D:800:ARG:HD2	3:F:149:VAL:CG2	2.22	0.69
1:D:807:VAL:O	1:D:810:ARG:HB2	1.93	0.69
1:G:123:CYS:HB2	1:G:158:ILE:CD1	2.23	0.69
1:J:218:LEU:HB2	1:J:221:GLN:CG	2.09	0.69
1:J:530:MET:HE3	4:7:354:GLN:HG2	1.71	0.69
1:J:802:GLU:OE1	1:J:802:GLU:HA	1.93	0.69
3:L:3:SER:O	3:L:4:LYS:CB	2.41	0.69
4:2:3:ASP:HA	4:2:6:THR:CB	2.18	0.69
4:5:1:ASP:HA	4:5:4:GLU:HB3	1.74	0.69
4:V:3:ASP:HA	4:V:6:THR:CB	2.18	0.69
1:A:642:LYS:HB3	4:4:21:PHE:O	1.93	0.69
1:G:641:LYS:HD2	4:6:348:SER:HA	1.73	0.69
1:G:752:ASP:C	1:G:779:ARG:HH12	1.96	0.69
1:G:820:VAL:HG11	2:H:136:MET:HE3	1.73	0.69
1:A:550:PHE:HA	4:6:46:GLY:HA3	1.66	0.69
1:G:93:MET:HE2	1:G:763:THR:HB	1.61	0.69
1:G:832:MET:SD	2:H:84:PHE:HE2	2.17	0.69
1:J:732:ILE:CG2	1:J:747:LEU:HD11	1.26	0.69
1:J:786:ILE:CG1	3:L:86:ASP:HB3	2.23	0.69
4:4:1:ASP:HA	4:4:4:GLU:HB3	1.74	0.69
4:7:1:ASP:HA	4:7:4:GLU:HB3	1.74	0.69
1:D:630:ALA:O	4:5:25:ASP:CB	2.41	0.68
1:D:733:PRO:C	1:D:737:PHE:CD1	2.62	0.68
1:D:797:PHE:CE2	3:F:126:LEU:CD2	2.75	0.68
1:D:817:GLN:CD	2:E:127:ARG:CD	2.61	0.68
2:E:117:LEU:CB	2:E:147:ASN:OD1	2.39	0.68
1:G:652:LEU:O	1:G:655:GLU:N	2.27	0.68
3:I:3:SER:O	3:I:4:LYS:CB	2.41	0.68
1:J:538:GLU:CD	4:7:355:MET:HE1	2.12	0.68
1:J:546:THR:HG22	1:J:548:THR:N	2.05	0.68
1:J:769:ALA:CB	1:J:770:GLY:N	2.57	0.68
1:A:52:ILE:HD13	1:A:52:ILE:N	2.08	0.68
1:A:502:GLU:HG2	1:A:764:MLY:O	1.93	0.68
1:A:815:CYS:O	1:A:819:ASN:HB2	1.93	0.68
2:B:117:LEU:HD12	2:B:147:ASN:CA	2.20	0.68
1:D:732:ILE:HG21	1:D:747:LEU:HD11	0.72	0.68
1:D:815:CYS:O	1:D:819:ASN:HB2	1.93	0.68
1:J:541:MET:CG	4:7:345:ILE:O	2.40	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:5:160:THR:HG21	4:5:274:ILE:HD11	1.76	0.68
4:V:1:ASP:HA	4:V:4:GLU:HB3	1.74	0.68
1:A:213:LYS:HA	1:A:220:ASP:OD1	1.92	0.68
1:D:62:VAL:HG12	1:D:63:MLY:O	1.93	0.68
2:E:111:SER:OG	2:E:148:VAL:HG12	1.92	0.68
3:F:48:LYS:C	3:F:52:ASN:HD21	1.96	0.68
1:G:213:LYS:HA	1:G:220:ASP:OD1	1.92	0.68
1:G:533:PHE:O	1:G:537:GLU:HG2	1.93	0.68
1:G:807:VAL:O	1:G:810:ARG:HB2	1.93	0.68
1:J:90:ASP:OD1	1:J:764:MLY:HH11	1.92	0.68
1:J:538:GLU:CD	4:7:355:MET:CE	2.62	0.68
4:1:160:THR:HG21	4:1:274:ILE:HD11	1.76	0.68
4:3:160:THR:HG21	4:3:274:ILE:HD11	1.76	0.68
1:A:166:MET:HE1	1:A:254:PHE:HB2	1.75	0.68
1:A:652:LEU:O	1:A:655:GLU:N	2.27	0.68
2:E:117:LEU:HD11	2:E:147:ASN:HB3	1.75	0.68
3:F:3:SER:O	3:F:4:LYS:CB	2.41	0.68
1:G:52:ILE:HD13	1:G:52:ILE:N	2.09	0.68
2:H:117:LEU:CB	2:H:147:ASN:OD1	2.39	0.68
1:J:90:ASP:HB2	1:J:764:MLY:HH21	1.74	0.68
1:J:553:MLY:HG2	4:V:47:MET:N	2.07	0.68
4:2:1:ASP:HA	4:2:4:GLU:HB3	1.74	0.68
4:7:160:THR:HG21	4:7:274:ILE:HD11	1.76	0.68
4:Z:1:ASP:HA	4:Z:4:GLU:HB3	1.74	0.68
1:A:732:ILE:CG2	1:A:747:LEU:HD11	1.26	0.68
1:D:533:PHE:O	1:D:537:GLU:HG2	1.93	0.68
1:D:762:HIS:H	1:D:762:HIS:CD2	2.08	0.68
1:D:787:ILE:HG22	1:D:788:THR:N	2.07	0.68
2:H:114:LYS:HA	2:H:146:GLY:C	2.02	0.68
3:I:48:LYS:C	3:I:52:ASN:HD21	1.96	0.68
1:J:533:PHE:O	1:J:537:GLU:HG2	1.93	0.68
2:K:117:LEU:HD12	2:K:147:ASN:CA	2.19	0.68
4:V:160:THR:HG21	4:V:274:ILE:HD11	1.75	0.68
4:X:1:ASP:HA	4:X:4:GLU:HB3	1.74	0.68
4:X:3:ASP:HA	4:X:6:THR:CB	2.18	0.68
4:Y:160:THR:HG21	4:Y:274:ILE:HD11	1.76	0.68
1:A:807:VAL:O	1:A:810:ARG:HB2	1.93	0.68
3:C:25:ILE:O	3:C:63:ILE:HB	1.92	0.68
1:J:166:MET:HE3	1:J:254:PHE:HD2	1.56	0.68
1:J:798:LEU:HD21	3:L:126:LEU:CD1	2.21	0.68
2:K:117:LEU:CB	2:K:147:ASN:ND2	2.35	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:0:1:ASP:HA	4:0:4:GLU:HB3	1.74	0.68
4:Z:153:LEU:HD11	4:Z:274:ILE:HG13	1.76	0.68
1:A:408:VAL:HG12	4:4:332:PRO:HB3	1.76	0.68
3:C:4:LYS:N	3:C:5:ALA:O	2.16	0.68
1:D:123:CYS:HB2	1:D:158:ILE:CD1	2.23	0.68
1:D:550:PHE:HE2	1:D:592:ILE:HG23	1.59	0.68
1:G:408:VAL:HG12	4:6:332:PRO:HB3	1.76	0.68
3:I:48:LYS:HB3	3:I:52:ASN:HD21	1.57	0.68
1:J:707:CYS:CA	1:J:714:ARG:HH22	2.07	0.68
1:J:800:ARG:NH1	3:L:149:VAL:CG2	2.35	0.68
1:J:817:GLN:HG3	2:K:128:PHE:CE1	2.29	0.68
4:2:153:LEU:HD11	4:2:274:ILE:HG13	1.76	0.68
1:A:630:ALA:O	4:4:25:ASP:CB	2.41	0.68
2:B:117:LEU:CB	2:B:147:ASN:ND2	2.35	0.68
1:D:507:GLY:O	1:D:762:HIS:N	2.27	0.68
1:D:538:GLU:CD	4:5:355:MET:CE	2.62	0.68
1:D:789:ALA:C	3:F:87:PHE:CE2	2.67	0.68
1:D:802:GLU:OE1	1:D:802:GLU:HA	1.93	0.68
3:F:102:VAL:HG23	3:F:139:TYR:HD1	1.59	0.68
1:G:166:MET:HE3	1:G:254:PHE:CD2	2.29	0.68
1:G:541:MET:CG	4:6:345:ILE:O	2.41	0.68
1:G:550:PHE:HE2	1:G:592:ILE:HG23	1.59	0.68
1:G:819:ASN:OD1	2:H:90:GLY:O	2.12	0.68
1:J:537:GLU:HG3	4:7:350:SER:O	1.78	0.68
1:J:782:MLY:C	1:J:783:LEU:HD12	2.22	0.68
1:A:793:ARG:HE	3:C:147:MET:CA	2.06	0.68
1:D:530:MET:HE3	4:5:354:GLN:HG2	1.73	0.68
1:D:817:GLN:CG	2:E:127:ARG:HD3	2.22	0.68
1:D:830:PRO:CB	2:E:51:PHE:CZ	2.68	0.68
1:D:831:TRP:CH2	2:E:47:LEU:HD23	2.26	0.68
2:E:117:LEU:CG	2:E:147:ASN:HB3	2.24	0.68
1:G:642:LYS:HB3	4:6:21:PHE:O	1.92	0.68
1:J:62:VAL:HG12	1:J:63:MLY:O	1.93	0.68
1:J:815:CYS:O	1:J:819:ASN:HB2	1.93	0.68
2:K:117:LEU:CB	2:K:147:ASN:OD1	2.39	0.68
4:0:153:LEU:HD11	4:0:274:ILE:HG13	1.76	0.68
1:A:56:GLU:CB	1:A:59:MLY:HB3	2.20	0.67
1:A:58:GLY:HA2	1:A:74:GLU:OE1	1.94	0.67
1:A:541:MET:CG	4:4:345:ILE:O	2.40	0.67
1:D:215:GLN:HA	1:D:340:ILE:CB	2.23	0.67
1:D:652:LEU:O	1:D:655:GLU:N	2.27	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:735:GLY:C	1:D:743:ALA:HB1	1.84	0.67
1:G:768:MLY:CD	1:G:772:LEU:CD2	2.68	0.67
1:G:792:ALA:HB3	3:I:40:ASN:HB3	1.76	0.67
2:H:117:LEU:CG	2:H:147:ASN:HB3	2.24	0.67
1:J:612:GLN:NE2	1:J:627:GLY:N	2.43	0.67
4:V:153:LEU:HD11	4:V:274:ILE:HG13	1.76	0.67
4:W:160:THR:HG21	4:W:274:ILE:HD11	1.76	0.67
4:X:153:LEU:HD11	4:X:274:ILE:HG13	1.76	0.67
4:X:160:THR:HG21	4:X:274:ILE:HD11	1.76	0.67
1:A:762:HIS:H	1:A:762:HIS:CD2	2.08	0.67
1:A:800:ARG:CZ	3:C:149:VAL:C	2.62	0.67
1:A:836:PHE:CE1	2:B:159:HIS:HA	2.26	0.67
1:D:52:ILE:HD13	1:D:52:ILE:N	2.09	0.67
1:D:788:THR:HG23	3:F:42:THR:CG2	2.20	0.67
1:J:123:CYS:HB2	1:J:158:ILE:CD1	2.23	0.67
1:J:546:THR:H	1:J:549:SER:HB3	1.59	0.67
1:A:797:PHE:CD2	3:C:126:LEU:HD22	2.29	0.67
2:B:141:PRO:O	2:B:145:ALA:CB	2.43	0.67
1:D:723:ARG:NH2	1:D:783:LEU:HD11	2.08	0.67
1:D:795:ARG:CZ	3:F:43:ASN:CG	2.62	0.67
1:G:538:GLU:CD	4:6:355:MET:CE	2.62	0.67
3:I:24:LYS:HA	3:I:63:ILE:O	1.95	0.67
1:J:750:GLY:HA2	3:L:114:LEU:CD2	2.25	0.67
1:J:795:ARG:HB3	3:L:35:ARG:NH2	2.09	0.67
2:K:114:LYS:HA	2:K:146:GLY:C	2.03	0.67
4:8:160:THR:HG21	4:8:274:ILE:HD11	1.76	0.67
1:A:546:THR:H	1:A:549:SER:HB3	1.60	0.67
1:D:538:GLU:CD	4:5:355:MET:HE1	2.13	0.67
2:E:162:ASP:O	2:K:21:GLU:CB	2.41	0.67
1:J:374:GLN:HG3	1:J:375:ALA:H	1.59	0.67
1:J:642:LYS:HB3	4:7:21:PHE:O	1.92	0.67
1:J:821:ARG:HH22	2:K:127:ARG:NE	1.91	0.67
1:J:838:ILE:HD11	2:K:54:MET:SD	2.34	0.67
1:D:546:THR:H	1:D:549:SER:HB3	1.59	0.67
1:G:58:GLY:HA2	1:G:74:GLU:OE1	1.95	0.67
1:J:769:ALA:HB3	1:J:770:GLY:HA3	1.68	0.67
1:J:798:LEU:HD23	3:L:122:GLU:HB3	1.75	0.67
2:K:117:LEU:CG	2:K:147:ASN:HB3	2.25	0.67
3:L:102:VAL:HG23	3:L:139:TYR:HD1	1.59	0.67
4:4:153:LEU:HD11	4:4:274:ILE:HG13	1.76	0.67
4:6:153:LEU:HD11	4:6:274:ILE:HG13	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:831:TRP:CZ3	2:E:50:THR:HB	2.29	0.67
1:G:84:MLY:HH12	1:G:715:VAL:HG12	1.67	0.67
1:G:217:THR:O	1:G:221:GLN:HG2	1.95	0.67
1:G:784:ALA:O	1:G:788:THR:HB	1.94	0.67
1:J:480:ILE:HG22	1:J:481:ASN:ND2	2.09	0.67
1:J:643:GLY:N	4:7:24:ASP:CA	2.46	0.67
1:J:795:ARG:CD	3:L:35:ARG:NH1	2.53	0.67
4:7:153:LEU:HD11	4:7:274:ILE:HG13	1.76	0.67
1:A:217:THR:O	1:A:221:GLN:HG2	1.95	0.67
3:C:102:VAL:HG23	3:C:139:TYR:HD1	1.60	0.67
1:D:480:ILE:HG22	1:D:481:ASN:ND2	2.09	0.67
1:D:732:ILE:HG22	1:D:747:LEU:CD1	1.55	0.67
1:D:769:ALA:CA	1:D:771:LEU:N	2.57	0.67
1:J:652:LEU:O	1:J:655:GLU:N	2.27	0.67
3:L:24:LYS:HA	3:L:63:ILE:O	1.95	0.67
4:Z:160:THR:HG21	4:Z:274:ILE:HD11	1.76	0.67
3:C:24:LYS:HA	3:C:63:ILE:O	1.95	0.67
1:D:131:TRP:O	1:D:132:LEU:HD12	1.95	0.67
1:D:546:THR:HG22	1:D:548:THR:N	2.05	0.67
1:G:62:VAL:HG12	1:G:63:MLY:O	1.94	0.67
1:G:202:SER:HA	1:G:207:LYS:HE3	1.72	0.67
1:G:292:MET:HE3	1:G:309:PRO:HA	1.77	0.67
1:J:58:GLY:HA2	1:J:74:GLU:OE1	1.95	0.67
1:J:290:GLN:O	1:J:331:LEU:HD12	1.95	0.67
1:A:61:THR:HG23	1:A:71:THR:OG1	1.94	0.67
1:A:62:VAL:HG12	1:A:63:MLY:O	1.93	0.67
1:A:533:PHE:O	1:A:537:GLU:HG2	1.93	0.67
2:B:144:VAL:CG1	2:B:153:ILE:HD13	2.20	0.67
1:D:612:GLN:NE2	1:D:627:GLY:N	2.43	0.67
1:D:642:LYS:CD	4:5:24:ASP:O	2.42	0.67
1:D:739:ASP:CB	1:D:742:LYS:HB3	2.12	0.67
1:G:290:GLN:O	1:G:331:LEU:HD12	1.95	0.67
1:G:802:GLU:OE1	1:G:802:GLU:HA	1.93	0.67
2:K:141:PRO:O	2:K:145:ALA:CB	2.43	0.67
4:6:160:THR:HG21	4:6:274:ILE:HD11	1.76	0.67
1:A:504:MLY:C	1:A:762:HIS:NE2	2.57	0.67
1:A:550:PHE:HE2	1:A:592:ILE:HG23	1.59	0.67
1:A:818:TYR:CB	2:B:89:LYS:C	2.63	0.67
1:D:58:GLY:HA2	1:D:74:GLU:OE1	1.95	0.67
1:G:78:PHE:HB3	1:G:98:HIS:CD2	2.30	0.67
1:G:537:GLU:C	4:6:351:THR:H	1.99	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:546:THR:H	1:G:549:SER:HB3	1.59	0.67
1:J:131:TRP:O	1:J:132:LEU:HD12	1.95	0.67
1:J:749:GLY:C	3:L:114:LEU:HD21	2.15	0.67
4:0:160:THR:HG21	4:0:274:ILE:HD11	1.76	0.67
4:2:160:THR:HG21	4:2:274:ILE:HD11	1.76	0.67
4:4:160:THR:HG21	4:4:274:ILE:HD11	1.76	0.67
1:A:78:PHE:HB3	1:A:98:HIS:CD2	2.30	0.66
1:D:374:GLN:HG3	1:D:375:ALA:H	1.60	0.66
1:D:648:THR:CB	4:5:350:SER:OG	2.43	0.66
2:E:141:PRO:O	2:E:145:ALA:CB	2.43	0.66
2:H:141:PRO:O	2:H:145:ALA:CB	2.43	0.66
1:J:408:VAL:HG12	4:7:332:PRO:HB3	1.76	0.66
1:J:541:MET:O	4:7:143:TYR:OH	2.14	0.66
1:J:635:GLY:O	4:7:341:ILE:HG21	1.95	0.66
1:J:831:TRP:CE3	2:K:34:ILE:CD1	2.77	0.66
1:A:290:GLN:O	1:A:331:LEU:HD12	1.95	0.66
1:A:795:ARG:CD	3:C:35:ARG:NH1	2.43	0.66
1:D:418:THR:HG22	1:D:419:VAL:N	2.11	0.66
1:D:724:TYR:HE1	1:D:778:MET:CG	2.08	0.66
1:G:174:SER:O	1:G:670:HIS:HB2	1.96	0.66
1:G:599:ASN:OD1	1:G:649:VAL:N	2.29	0.66
2:K:117:LEU:HD11	2:K:147:ASN:HB3	1.76	0.66
4:5:153:LEU:HD11	4:5:274:ILE:HG13	1.76	0.66
1:A:174:SER:O	1:A:670:HIS:HB2	1.96	0.66
1:A:648:THR:CB	4:4:350:SER:OG	2.43	0.66
1:G:93:MET:HE1	1:G:763:THR:O	1.94	0.66
1:G:131:TRP:O	1:G:132:LEU:HD12	1.95	0.66
1:G:783:LEU:O	1:G:787:ILE:CA	2.43	0.66
1:J:52:ILE:HD13	1:J:52:ILE:N	2.09	0.66
1:J:322:VAL:HB	1:J:325:ILE:CD1	2.26	0.66
1:J:550:PHE:HE2	1:J:592:ILE:HG23	1.59	0.66
4:8:153:LEU:HD11	4:8:274:ILE:HG13	1.76	0.66
1:A:418:THR:HG22	1:A:419:VAL:N	2.11	0.66
1:A:817:GLN:HE21	2:B:127:ARG:HG2	1.59	0.66
2:B:117:LEU:CG	2:B:147:ASN:HB3	2.24	0.66
2:E:141:PRO:O	2:E:145:ALA:HB2	1.96	0.66
1:G:61:THR:HG23	1:G:71:THR:OG1	1.94	0.66
1:J:339:ASP:OD1	1:J:348:MLY:HH13	1.95	0.66
4:1:153:LEU:HD11	4:1:274:ILE:HG13	1.76	0.66
1:A:502:GLU:HA	1:A:761:GLY:C	2.15	0.66
1:A:537:GLU:C	4:4:351:THR:H	1.99	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:834:LEU:HD21	2:B:54:MET:HG3	1.76	0.66
1:D:226:ASN:HB2	1:D:227:PRO:HD3	1.78	0.66
1:D:290:GLN:O	1:D:331:LEU:HD12	1.95	0.66
1:D:339:ASP:OD1	1:D:348:MLY:HH13	1.95	0.66
1:D:408:VAL:HG12	4:5:332:PRO:HB3	1.76	0.66
1:D:599:ASN:OD1	1:D:649:VAL:N	2.28	0.66
1:G:648:THR:CB	4:6:350:SER:OG	2.44	0.66
1:J:707:CYS:CB	1:J:714:ARG:HH22	2.08	0.66
1:J:754:ASP:CB	1:J:776:GLU:CB	2.56	0.66
1:A:480:ILE:HG22	1:A:481:ASN:ND2	2.10	0.66
1:A:541:MET:HG2	4:4:345:ILE:C	2.16	0.66
1:A:642:LYS:CD	4:4:24:ASP:O	2.42	0.66
1:D:174:SER:O	1:D:670:HIS:HB2	1.96	0.66
1:D:507:GLY:HA3	1:D:762:HIS:CB	2.24	0.66
1:D:537:GLU:C	4:5:351:THR:H	1.98	0.66
1:G:612:GLN:NE2	1:G:627:GLY:N	2.42	0.66
1:G:800:ARG:NH1	3:I:149:VAL:C	2.49	0.66
3:I:102:VAL:HG23	3:I:139:TYR:HD1	1.59	0.66
1:J:166:MET:HE1	1:J:254:PHE:HB2	1.78	0.66
1:J:174:SER:O	1:J:670:HIS:HB2	1.96	0.66
1:J:648:THR:CB	4:7:350:SER:OG	2.43	0.66
1:J:754:ASP:HB2	1:J:776:GLU:CB	2.14	0.66
1:J:831:TRP:CH2	2:K:47:LEU:HD23	2.31	0.66
2:K:146:GLY:O	2:K:147:ASN:HB2	1.96	0.66
4:3:153:LEU:HD11	4:3:274:ILE:HG13	1.76	0.66
1:A:91:MET:HE3	1:A:119:SER:HB2	1.78	0.66
1:A:131:TRP:O	1:A:132:LEU:HD12	1.95	0.66
2:B:141:PRO:O	2:B:145:ALA:HB2	1.96	0.66
1:D:322:VAL:HB	1:D:325:ILE:CD1	2.26	0.66
3:F:48:LYS:O	3:F:52:ASN:CG	2.34	0.66
1:G:374:GLN:HG3	1:G:375:ALA:H	1.60	0.66
1:G:553:MLY:CE	4:8:45:VAL:CA	2.49	0.66
1:G:797:PHE:CD1	3:I:149:VAL:HG12	2.25	0.66
1:J:78:PHE:HB3	1:J:98:HIS:CD2	2.30	0.66
1:J:790:THR:CA	3:L:87:PHE:CE2	2.79	0.66
1:J:795:ARG:NE	3:L:118:MET:HE1	2.01	0.66
2:K:141:PRO:O	2:K:145:ALA:HB2	1.96	0.66
1:A:538:GLU:HA	4:4:349:LEU:HB3	1.78	0.66
1:A:612:GLN:NE2	1:A:627:GLY:N	2.43	0.66
1:A:717:TYR:HD1	1:A:744:SER:HG	1.44	0.66
1:A:818:TYR:HB3	2:B:89:LYS:C	2.16	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:541:MET:O	4:5:143:TYR:OH	2.14	0.66
2:E:146:GLY:O	2:E:147:ASN:HB2	1.96	0.66
1:G:757:GLN:CD	1:G:772:LEU:HG	2.15	0.66
1:G:831:TRP:NE1	2:H:67:MET:CB	2.55	0.66
2:H:117:LEU:CB	2:H:147:ASN:ND2	2.35	0.66
2:H:146:GLY:O	2:H:147:ASN:HB2	1.96	0.66
1:J:226:ASN:HB2	1:J:227:PRO:HD3	1.78	0.66
1:J:541:MET:HG2	4:7:345:ILE:C	2.16	0.66
4:W:153:LEU:HD11	4:W:274:ILE:HG13	1.76	0.66
1:A:530:MET:CG	4:4:354:GLN:CG	2.71	0.66
1:G:226:ASN:HB2	1:G:227:PRO:HD3	1.78	0.66
1:G:635:GLY:O	4:6:341:ILE:HG21	1.95	0.66
1:J:537:GLU:C	4:7:351:THR:H	1.98	0.66
1:J:599:ASN:OD1	1:J:649:VAL:N	2.28	0.66
2:K:150:TYR:C	2:K:151:LYS:CG	2.49	0.66
1:A:144:ARG:NH1	1:A:160:ASP:OD1	2.29	0.66
1:A:161:ASN:O	1:A:165:PHE:HB2	1.96	0.66
1:A:339:ASP:OD1	1:A:348:MLY:HH13	1.95	0.66
1:A:530:MET:CA	4:4:354:GLN:CB	2.74	0.66
3:C:45:GLU:O	3:C:49:ILE:HG13	1.96	0.66
1:G:541:MET:HG2	4:6:345:ILE:C	2.17	0.66
2:H:117:LEU:HD11	2:H:147:ASN:HB3	1.75	0.66
1:J:144:ARG:NH1	1:J:160:ASP:OD1	2.29	0.66
1:A:296:MLY:HH11	1:A:348:MLY:HH21	1.78	0.65
1:A:643:GLY:N	4:4:24:ASP:CA	2.46	0.65
1:D:466:GLY:HA2	1:D:484:ASN:HD21	1.61	0.65
1:D:635:GLY:O	4:5:341:ILE:HG21	1.95	0.65
1:D:769:ALA:CA	1:D:771:LEU:CA	2.63	0.65
1:G:144:ARG:NH1	1:G:160:ASP:OD1	2.29	0.65
1:G:480:ILE:HG22	1:G:481:ASN:ND2	2.10	0.65
1:G:480:ILE:HG22	1:G:481:ASN:N	2.11	0.65
1:G:530:MET:HE2	4:6:354:GLN:HG3	1.76	0.65
1:G:557:GLU:N	4:8:48:GLY:HA3	1.90	0.65
3:I:48:LYS:O	3:I:52:ASN:CG	2.34	0.65
1:J:90:ASP:OD2	1:J:764:MLY:HH13	1.96	0.65
1:J:418:THR:HG22	1:J:419:VAL:N	2.11	0.65
3:L:45:GLU:O	3:L:49:ILE:HG13	1.96	0.65
3:L:48:LYS:C	3:L:52:ASN:HD21	1.96	0.65
1:A:538:GLU:CD	4:4:355:MET:CE	2.62	0.65
1:D:217:THR:O	1:D:221:GLN:HG2	1.94	0.65
1:D:691:VAL:O	1:D:695:LEU:HD13	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:818:TYR:CB	2:E:89:LYS:C	2.65	0.65
1:G:161:ASN:O	1:G:165:PHE:HB2	1.96	0.65
1:G:541:MET:O	4:6:143:TYR:OH	2.13	0.65
1:G:769:ALA:O	1:G:773:GLY:HA3	1.95	0.65
1:J:61:THR:HG23	1:J:71:THR:OG1	1.95	0.65
1:J:217:THR:O	1:J:221:GLN:HG2	1.95	0.65
1:J:642:LYS:HA	4:7:21:PHE:O	1.96	0.65
1:J:691:VAL:O	1:J:695:LEU:HD13	1.96	0.65
1:A:502:GLU:HA	1:A:761:GLY:CA	2.26	0.65
1:A:822:SER:HG	2:B:88:LEU:HA	1.60	0.65
1:A:831:TRP:CH2	2:B:34:ILE:HG23	2.31	0.65
1:D:61:THR:HG23	1:D:71:THR:OG1	1.95	0.65
1:D:78:PHE:HB3	1:D:98:HIS:CD2	2.30	0.65
1:D:709:LYS:O	1:D:710:GLY:HA2	1.96	0.65
1:G:296:MLY:HH11	1:G:348:MLY:HH21	1.78	0.65
1:G:339:ASP:OD1	1:G:348:MLY:HH13	1.95	0.65
1:G:466:GLY:HA2	1:G:484:ASN:HD21	1.61	0.65
1:G:538:GLU:CD	4:6:355:MET:HE3	2.17	0.65
2:H:141:PRO:O	2:H:145:ALA:HB2	1.96	0.65
4:Y:153:LEU:HD11	4:Y:274:ILE:HG13	1.76	0.65
1:D:530:MET:CA	4:5:354:GLN:CB	2.74	0.65
2:E:114:LYS:HA	2:E:146:GLY:C	2.03	0.65
3:F:24:LYS:HA	3:F:63:ILE:O	1.95	0.65
3:I:45:GLU:O	3:I:49:ILE:HG13	1.97	0.65
1:A:635:GLY:O	4:4:341:ILE:HG21	1.95	0.65
1:A:691:VAL:O	1:A:695:LEU:HD13	1.97	0.65
1:A:739:ASP:CB	1:A:742:LYS:HB3	2.12	0.65
1:D:530:MET:CG	4:5:354:GLN:CG	2.71	0.65
1:D:541:MET:HG2	4:5:345:ILE:C	2.16	0.65
1:G:691:VAL:O	1:G:695:LEU:HD13	1.97	0.65
1:G:769:ALA:CB	1:G:770:GLY:N	2.59	0.65
1:G:820:VAL:HG11	2:H:136:MET:CE	2.26	0.65
1:G:822:SER:O	1:G:825:ASN:HB2	1.97	0.65
1:J:84:MLY:NZ	1:J:719:ASP:O	2.13	0.65
1:J:161:ASN:O	1:J:165:PHE:HB2	1.96	0.65
1:J:818:TYR:HB3	2:K:90:GLY:HA2	1.75	0.65
3:L:3:SER:HG	3:L:5:ALA:N	1.95	0.65
1:A:107:MLY:HB3	1:A:686:MET:CE	2.27	0.65
1:A:480:ILE:HG22	1:A:481:ASN:N	2.11	0.65
1:A:501:GLU:O	1:A:762:HIS:CG	2.48	0.65
1:A:599:ASN:OD1	1:A:649:VAL:N	2.29	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:793:ARG:CZ	3:C:147:MET:HG2	2.27	0.65
1:D:612:GLN:HE22	1:D:627:GLY:N	1.94	0.65
1:D:822:SER:O	1:D:825:ASN:HB2	1.97	0.65
1:G:769:ALA:HB2	1:G:770:GLY:N	2.09	0.65
1:A:226:ASN:HB2	1:A:227:PRO:HD3	1.77	0.65
1:A:322:VAL:HB	1:A:325:ILE:CD1	2.26	0.65
3:F:45:GLU:O	3:F:49:ILE:HG13	1.97	0.65
1:G:466:GLY:HA2	1:G:484:ASN:ND2	2.12	0.65
1:G:530:MET:CG	4:6:354:GLN:CG	2.72	0.65
1:G:725:ARG:NE	1:G:737:PHE:HE1	1.95	0.65
3:I:48:LYS:C	3:I:52:ASN:HD22	1.97	0.65
1:J:95:THR:CA	1:J:713:SER:HB3	2.27	0.65
1:J:530:MET:CA	4:7:354:GLN:CB	2.74	0.65
1:J:725:ARG:NE	1:J:737:PHE:HE1	1.95	0.65
1:A:217:THR:HB	1:A:220:ASP:OD2	1.97	0.65
1:A:818:TYR:HB3	2:B:90:GLY:N	2.12	0.65
1:D:94:MET:HE1	1:D:101:ALA:HB1	1.79	0.65
1:D:725:ARG:NE	1:D:737:PHE:HE1	1.95	0.65
1:G:418:THR:HG22	1:G:419:VAL:N	2.11	0.65
1:G:798:LEU:HD11	3:I:126:LEU:HG	1.78	0.65
1:J:792:ALA:HB1	3:L:40:ASN:HB3	0.73	0.65
1:A:374:GLN:HG3	1:A:375:ALA:H	1.60	0.65
1:A:636:LYS:HG3	4:4:334:GLU:CD	2.17	0.65
1:A:822:SER:O	1:A:825:ASN:HB2	1.97	0.65
3:C:49:ILE:HA	3:C:52:ASN:ND2	2.05	0.65
1:D:642:LYS:CD	4:5:340:TRP:CZ3	2.79	0.65
1:J:822:SER:O	1:J:825:ASN:HB2	1.97	0.65
1:A:94:MET:HE1	1:A:101:ALA:HB1	1.79	0.65
1:A:642:LYS:HA	4:4:21:PHE:O	1.96	0.65
1:D:144:ARG:NH1	1:D:160:ASP:OD1	2.29	0.65
1:D:202:SER:CA	1:D:207:LYS:HE3	2.27	0.65
1:G:90:ASP:O	1:G:764:MLY:CH2	2.44	0.65
1:G:93:MET:HE3	1:G:763:THR:CG2	2.08	0.65
1:G:818:TYR:CD1	2:H:127:ARG:NH1	2.65	0.65
1:J:636:LYS:HG3	4:7:334:GLU:CD	2.17	0.65
2:K:144:VAL:CG1	2:K:153:ILE:HD13	2.20	0.65
1:A:292:MET:HE3	1:A:309:PRO:HA	1.78	0.64
1:A:466:GLY:HA2	1:A:484:ASN:ND2	2.12	0.64
1:A:642:LYS:CD	4:4:340:TRP:CZ3	2.79	0.64
1:D:479:CYS:HB3	1:D:653:PHE:CE2	2.32	0.64
1:D:636:LYS:O	1:D:637:LYS:CB	2.45	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:642:LYS:HA	4:5:21:PHE:O	1.96	0.64
1:D:831:TRP:NE1	2:E:47:LEU:CD2	2.36	0.64
1:G:107:MLY:HB3	1:G:686:MET:CE	2.26	0.64
1:J:823:PHE:CE2	2:K:140:PHE:CZ	2.86	0.64
3:L:48:LYS:O	3:L:52:ASN:CG	2.34	0.64
1:A:93:MET:O	1:A:713:SER:HB3	1.97	0.64
1:A:505:MLY:HG3	1:A:741:LYS:HZ2	1.63	0.64
1:A:814:PHE:HA	2:B:127:ARG:HH22	1.54	0.64
1:D:161:ASN:O	1:D:165:PHE:HB2	1.96	0.64
1:D:480:ILE:HG22	1:D:481:ASN:N	2.11	0.64
1:D:636:LYS:HG3	4:5:334:GLU:CD	2.17	0.64
1:D:834:LEU:HD21	2:E:54:MET:CE	2.27	0.64
1:G:322:VAL:HB	1:G:325:ILE:CD1	2.26	0.64
1:G:538:GLU:HA	4:6:349:LEU:HB3	1.79	0.64
1:A:466:GLY:HA2	1:A:484:ASN:HD21	1.61	0.64
1:D:806:MET:O	1:D:809:ARG:HB2	1.98	0.64
3:F:3:SER:HG	3:F:5:ALA:N	1.95	0.64
1:G:642:LYS:CD	4:6:24:ASP:O	2.43	0.64
1:G:642:LYS:HA	4:6:21:PHE:O	1.97	0.64
1:J:107:MLY:HB3	1:J:686:MET:CE	2.27	0.64
1:J:133:PRO:O	1:J:136:ASN:HB2	1.98	0.64
1:J:466:GLY:HA2	1:J:484:ASN:ND2	2.12	0.64
1:J:612:GLN:HE22	1:J:627:GLY:N	1.94	0.64
1:J:783:LEU:HD12	1:J:783:LEU:N	2.13	0.64
1:J:793:ARG:HG3	3:L:146:ILE:HG22	1.79	0.64
1:J:795:ARG:HH11	3:L:35:ARG:CZ	2.09	0.64
1:A:133:PRO:O	1:A:136:ASN:HB2	1.97	0.64
1:A:218:LEU:CD2	1:A:222:ILE:HG12	2.28	0.64
1:A:557:GLU:N	4:6:48:GLY:HA3	1.90	0.64
1:A:612:GLN:HE22	1:A:627:GLY:N	1.94	0.64
2:B:140:PHE:HB3	2:B:144:VAL:CG1	2.28	0.64
1:D:466:GLY:HA2	1:D:484:ASN:ND2	2.12	0.64
1:G:84:MLY:HH11	1:G:720:PHE:N	2.13	0.64
1:G:210:GLN:O	1:G:211:SER:OG	2.15	0.64
1:J:217:THR:HB	1:J:220:ASP:OD2	1.97	0.64
1:J:479:CYS:HB3	1:J:653:PHE:CE2	2.33	0.64
2:K:117:LEU:CG	2:K:147:ASN:CB	2.76	0.64
1:A:202:SER:CA	1:A:207:LYS:HE3	2.27	0.64
1:D:107:MLY:HB3	1:D:686:MET:CE	2.26	0.64
1:D:217:THR:HB	1:D:220:ASP:OD2	1.97	0.64
1:D:296:MLY:HH11	1:D:348:MLY:HH21	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:133:PRO:O	1:G:136:ASN:HB2	1.98	0.64
1:G:217:THR:HB	1:G:220:ASP:OD2	1.97	0.64
1:J:90:ASP:CG	1:J:764:MLY:HH21	2.18	0.64
1:J:466:GLY:HA2	1:J:484:ASN:HD21	1.61	0.64
1:J:806:MET:O	1:J:809:ARG:HB2	1.98	0.64
1:J:819:ASN:N	2:K:90:GLY:O	2.29	0.64
1:J:831:TRP:HH2	2:K:47:LEU:HD23	1.61	0.64
1:A:553:MLY:CE	4:6:45:VAL:CA	2.49	0.64
1:A:642:LYS:CA	4:4:21:PHE:O	2.46	0.64
3:C:48:LYS:O	3:C:52:ASN:CG	2.34	0.64
2:E:140:PHE:O	2:E:141:PRO:C	2.33	0.64
1:G:218:LEU:CD2	1:G:222:ILE:HG12	2.28	0.64
1:G:406:VAL:HG12	1:G:407:GLY:N	2.13	0.64
1:G:530:MET:CA	4:6:354:GLN:CB	2.75	0.64
1:G:612:GLN:HE22	1:G:627:GLY:N	1.94	0.64
1:G:636:LYS:HG3	4:6:334:GLU:CD	2.18	0.64
1:G:730:SER:CB	3:I:109:HIS:CD2	2.80	0.64
2:H:140:PHE:HB3	2:H:144:VAL:CG1	2.28	0.64
1:J:296:MLY:HH11	1:J:348:MLY:HH21	1.78	0.64
1:J:538:GLU:HA	4:7:349:LEU:HB3	1.78	0.64
1:J:642:LYS:CA	4:7:21:PHE:O	2.45	0.64
2:K:140:PHE:HB3	2:K:144:VAL:CG1	2.28	0.64
1:A:534:SER:C	4:4:351:THR:CA	2.47	0.64
1:A:725:ARG:NE	1:A:737:PHE:HE1	1.95	0.64
2:E:140:PHE:HB3	2:E:144:VAL:CG1	2.27	0.64
2:E:149:ASP:OD2	2:E:150:TYR:C	2.36	0.64
1:G:541:MET:HG2	4:6:345:ILE:O	1.98	0.64
1:J:510:TRP:CZ3	1:J:772:LEU:CD2	2.80	0.64
1:J:537:GLU:C	4:7:351:THR:N	2.51	0.64
1:J:636:LYS:O	1:J:637:LYS:CB	2.45	0.64
1:J:795:ARG:CD	3:L:35:ARG:HH12	2.11	0.64
2:K:144:VAL:HA	2:K:153:ILE:HD11	1.80	0.64
1:A:479:CYS:HB3	1:A:653:PHE:CE2	2.32	0.64
1:A:636:LYS:O	1:A:637:LYS:CB	2.45	0.64
1:D:795:ARG:NH2	3:F:116:GLU:OE1	2.29	0.64
1:D:830:PRO:CB	2:E:67:MET:HE3	2.23	0.64
2:E:117:LEU:CG	2:E:147:ASN:CB	2.76	0.64
1:G:166:MET:HE3	1:G:254:PHE:HD2	1.61	0.64
1:G:642:LYS:CA	4:6:21:PHE:O	2.46	0.64
1:J:127:ASN:HD22	1:J:128:PRO:CD	2.11	0.64
4:4:190:MET:SD	4:4:209:VAL:HG11	2.38	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:541:MET:O	4:4:143:TYR:OH	2.14	0.64
1:D:127:ASN:HD22	1:D:128:PRO:CD	2.11	0.64
1:D:537:GLU:HB3	1:D:648:THR:HB	1.80	0.64
1:D:818:TYR:HB2	2:E:89:LYS:C	2.18	0.64
1:G:479:CYS:HB3	1:G:653:PHE:CE2	2.32	0.64
1:G:751:GLY:N	3:I:114:LEU:CD1	2.61	0.64
1:J:292:MET:HE3	1:J:309:PRO:HA	1.78	0.64
1:J:636:LYS:N	4:7:334:GLU:OE1	2.31	0.64
1:J:642:LYS:CD	4:7:340:TRP:CZ3	2.79	0.64
1:J:838:ILE:CD1	2:K:54:MET:HE3	2.27	0.64
4:V:190:MET:SD	4:V:209:VAL:HG11	2.38	0.64
4:X:190:MET:SD	4:X:209:VAL:HG11	2.38	0.64
1:A:530:MET:HE3	4:4:354:GLN:CG	2.23	0.64
1:A:806:MET:O	1:A:809:ARG:HB2	1.98	0.64
1:A:831:TRP:NE1	2:B:51:PHE:CE2	2.63	0.64
1:G:529:PRO:C	4:6:354:GLN:CB	2.50	0.64
1:G:724:TYR:HB3	1:G:727:LEU:HD12	1.80	0.64
1:G:784:ALA:O	1:G:788:THR:CB	2.45	0.64
3:I:49:ILE:HA	3:I:52:ASN:ND2	2.05	0.64
1:J:406:VAL:HG12	1:J:407:GLY:N	2.13	0.64
4:2:190:MET:SD	4:2:209:VAL:HG11	2.38	0.64
1:A:538:GLU:HA	4:4:349:LEU:CG	2.27	0.63
1:D:830:PRO:CB	2:E:67:MET:CE	2.74	0.63
1:J:480:ILE:HG22	1:J:481:ASN:N	2.11	0.63
1:J:577:ALA:O	1:J:578:HIS:CD2	2.51	0.63
4:5:190:MET:SD	4:5:209:VAL:HG11	2.38	0.63
1:A:636:LYS:N	4:4:334:GLU:OE1	2.31	0.63
1:A:724:TYR:HB3	1:A:727:LEU:HD12	1.80	0.63
2:B:132:GLU:O	2:B:136:MET:HG2	1.99	0.63
2:B:146:GLY:O	2:B:147:ASN:HB2	1.96	0.63
1:G:91:MET:HE3	1:G:119:SER:HB2	1.80	0.63
1:G:215:GLN:CA	1:G:340:ILE:CG2	2.63	0.63
1:G:577:ALA:O	1:G:578:HIS:CD2	2.52	0.63
1:G:724:TYR:HD1	1:G:727:LEU:HD11	1.64	0.63
1:G:829:TRP:CZ2	2:H:87:LYS:HE2	2.34	0.63
1:J:725:ARG:NE	1:J:737:PHE:CE1	2.66	0.63
1:A:502:GLU:OE2	1:A:764:MLY:N	2.31	0.63
1:A:795:ARG:CB	3:C:35:ARG:CZ	2.75	0.63
1:A:822:SER:CB	2:B:88:LEU:CD2	2.67	0.63
1:D:218:LEU:CD2	1:D:222:ILE:HG12	2.28	0.63
1:D:577:ALA:O	1:D:578:HIS:CD2	2.51	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:537:GLU:HB3	1:G:648:THR:HB	1.80	0.63
1:G:754:ASP:CG	1:G:776:GLU:OE2	2.36	0.63
1:G:783:LEU:HD12	1:G:783:LEU:N	2.13	0.63
1:J:642:LYS:CG	4:7:22:ALA:C	2.67	0.63
1:A:406:VAL:HG12	1:A:407:GLY:N	2.13	0.63
1:A:530:MET:HA	4:4:354:GLN:CB	2.29	0.63
1:A:725:ARG:NE	1:A:737:PHE:CE1	2.67	0.63
1:D:133:PRO:O	1:D:136:ASN:HB2	1.98	0.63
1:D:783:LEU:HD12	1:D:783:LEU:N	2.13	0.63
1:D:817:GLN:CD	2:E:127:ARG:HE	1.90	0.63
1:G:642:LYS:CG	4:6:22:ALA:C	2.67	0.63
1:G:643:GLY:H	4:6:23:GLY:C	2.02	0.63
1:J:534:SER:C	4:7:351:THR:CA	2.47	0.63
4:0:190:MET:SD	4:0:209:VAL:HG11	2.38	0.63
4:7:190:MET:SD	4:7:209:VAL:HG11	2.38	0.63
1:A:577:ALA:O	1:A:578:HIS:CD2	2.52	0.63
2:B:117:LEU:CG	2:B:147:ASN:CB	2.76	0.63
1:D:538:GLU:HA	4:5:349:LEU:HB3	1.78	0.63
1:G:827:MLY:HH21	2:H:139:ALA:HB3	1.81	0.63
1:G:829:TRP:CH2	2:H:87:LYS:NZ	2.66	0.63
1:J:541:MET:CA	4:7:143:TYR:OH	2.46	0.63
1:J:724:TYR:HB3	1:J:727:LEU:HD12	1.80	0.63
2:K:146:GLY:O	2:K:147:ASN:CB	2.46	0.63
4:0:257:CYS:HB3	4:0:258:PRO:HD3	1.81	0.63
4:7:257:CYS:HB3	4:7:258:PRO:HD3	1.81	0.63
4:V:257:CYS:HB3	4:V:258:PRO:HD3	1.81	0.63
1:A:537:GLU:C	4:4:351:THR:N	2.52	0.63
1:A:542:PHE:CZ	1:A:553:MLY:HH11	2.34	0.63
1:A:724:TYR:HD1	1:A:727:LEU:HD11	1.64	0.63
1:A:800:ARG:HD2	3:C:149:VAL:CB	2.27	0.63
2:B:144:VAL:HA	2:B:153:ILE:HD11	1.80	0.63
1:D:793:ARG:HE	3:F:147:MET:CA	2.11	0.63
1:D:829:TRP:NE1	2:E:67:MET:CG	2.39	0.63
2:E:132:GLU:O	2:E:136:MET:HG2	1.99	0.63
1:G:636:LYS:O	1:G:637:LYS:CB	2.45	0.63
1:G:771:LEU:O	1:G:774:LEU:N	2.32	0.63
2:H:117:LEU:CG	2:H:147:ASN:CB	2.76	0.63
1:J:141:LEU:H	1:J:141:LEU:HD12	1.64	0.63
1:J:278:GLN:CG	1:J:317:GLU:HB2	2.27	0.63
3:L:49:ILE:HA	3:L:52:ASN:ND2	2.06	0.63
4:3:257:CYS:HB3	4:3:258:PRO:HD3	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:X:257:CYS:HB3	4:X:258:PRO:HD3	1.81	0.63
4:Z:257:CYS:HB3	4:Z:258:PRO:HD3	1.81	0.63
1:A:541:MET:HG2	4:4:345:ILE:O	1.98	0.63
1:D:818:TYR:HD2	2:E:89:LYS:O	1.81	0.63
2:E:146:GLY:O	2:E:147:ASN:CB	2.46	0.63
3:F:24:LYS:HB3	3:F:63:ILE:H	1.64	0.63
1:G:806:MET:O	1:G:809:ARG:HB2	1.98	0.63
1:J:218:LEU:CD2	1:J:222:ILE:HG12	2.28	0.63
1:J:537:GLU:HB3	1:J:648:THR:HB	1.80	0.63
1:J:541:MET:HG2	4:7:345:ILE:O	1.98	0.63
1:J:768:MLY:HH21	1:J:772:LEU:HD22	1.66	0.63
1:A:127:ASN:HD22	1:A:128:PRO:CD	2.11	0.63
1:A:831:TRP:HZ3	2:B:50:THR:CG2	2.11	0.63
2:B:121:LEU:HA	2:B:128:PHE:CG	2.34	0.63
2:B:146:GLY:O	2:B:147:ASN:CB	2.46	0.63
1:D:538:GLU:HA	4:5:349:LEU:CG	2.28	0.63
1:D:725:ARG:NE	1:D:737:PHE:CE1	2.66	0.63
1:G:141:LEU:H	1:G:141:LEU:HD12	1.64	0.63
1:G:541:MET:CA	4:6:143:TYR:OH	2.47	0.63
1:J:84:MLY:HH11	1:J:715:VAL:HG12	1.76	0.63
1:J:641:LYS:CE	1:J:647:GLN:CB	2.75	0.63
2:K:132:GLU:O	2:K:136:MET:HG2	1.99	0.63
1:A:93:MET:HE1	1:A:716:LEU:H	1.64	0.63
1:A:707:CYS:CA	1:A:714:ARG:CZ	2.77	0.63
3:C:24:LYS:HB3	3:C:63:ILE:H	1.64	0.63
1:D:166:MET:HE3	1:D:254:PHE:CD2	2.34	0.63
1:D:278:GLN:CG	1:D:317:GLU:HB2	2.27	0.63
1:D:411:GLU:N	4:5:333:PRO:HB2	2.11	0.63
1:D:541:MET:HG2	4:5:345:ILE:O	1.98	0.63
1:D:642:LYS:CG	4:5:22:ALA:C	2.67	0.63
1:D:726:VAL:HB	1:D:782:MLY:HH13	0.82	0.63
1:D:771:LEU:O	1:D:774:LEU:N	2.32	0.63
1:G:251:ARG:HB2	1:G:264:ASP:CB	2.29	0.63
1:G:537:GLU:C	4:6:351:THR:N	2.51	0.63
1:G:831:TRP:NE1	2:H:67:MET:HB3	2.14	0.63
1:J:553:MLY:O	4:V:48:GLY:HA2	1.99	0.63
4:1:190:MET:SD	4:1:209:VAL:HG11	2.38	0.63
4:2:257:CYS:HB3	4:2:258:PRO:HD3	1.81	0.63
4:5:257:CYS:HB3	4:5:258:PRO:HD3	1.81	0.63
4:W:190:MET:SD	4:W:209:VAL:HG11	2.38	0.63
1:A:541:MET:CA	4:4:143:TYR:OH	2.47	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:578:HIS:CB	1:A:592:ILE:HD12	2.29	0.62
1:A:817:GLN:HE21	2:B:127:ARG:CG	2.12	0.62
1:D:210:GLN:O	1:D:211:SER:OG	2.15	0.62
1:D:551:MLY:C	4:7:46:GLY:O	2.47	0.62
1:D:793:ARG:NE	3:F:147:MET:HA	2.14	0.62
1:G:636:LYS:N	4:6:334:GLU:OE1	2.31	0.62
1:G:725:ARG:NE	1:G:737:PHE:CE1	2.67	0.62
1:G:728:ASN:HD22	3:I:113:THR:HG1	1.46	0.62
1:G:791:GLN:CD	3:I:116:GLU:HB2	2.20	0.62
2:H:149:ASP:OD2	2:H:150:TYR:C	2.36	0.62
3:I:3:SER:HG	3:I:5:ALA:N	1.96	0.62
1:J:541:MET:HE1	4:7:346:LEU:HD12	1.81	0.62
4:3:190:MET:SD	4:3:209:VAL:HG11	2.38	0.62
4:8:190:MET:SD	4:8:209:VAL:HG11	2.38	0.62
4:Z:190:MET:SD	4:Z:209:VAL:HG11	2.38	0.62
1:A:274:ARG:HB2	1:A:285:TYR:CE2	2.34	0.62
1:A:502:GLU:CD	1:A:764:MLY:O	2.37	0.62
1:A:542:PHE:N	4:4:143:TYR:OH	2.33	0.62
1:A:643:GLY:H	4:4:23:GLY:C	2.02	0.62
1:A:783:LEU:HD12	1:A:783:LEU:N	2.13	0.62
1:D:724:TYR:HB3	1:D:727:LEU:HD12	1.80	0.62
1:D:724:TYR:HD1	1:D:727:LEU:HD11	1.64	0.62
1:D:767:PHE:HB3	1:D:771:LEU:HD11	1.80	0.62
1:D:800:ARG:HB2	3:F:149:VAL:HG22	1.80	0.62
2:E:121:LEU:HA	2:E:128:PHE:CG	2.34	0.62
1:G:544:LYS:HB2	4:6:147:ARG:HA	1.80	0.62
2:H:111:SER:OG	2:H:148:VAL:CG1	2.47	0.62
2:H:121:LEU:HA	2:H:128:PHE:CG	2.34	0.62
1:J:94:MET:HE1	1:J:101:ALA:HB1	1.80	0.62
1:J:817:GLN:HG2	2:K:127:ARG:HB2	1.81	0.62
1:A:251:ARG:HB2	1:A:264:ASP:CB	2.29	0.62
1:A:501:GLU:CG	1:A:762:HIS:ND1	2.45	0.62
1:A:537:GLU:HB3	1:A:648:THR:HB	1.80	0.62
1:A:551:MLY:C	4:6:46:GLY:O	2.47	0.62
1:D:251:ARG:HB2	1:D:264:ASP:CB	2.29	0.62
1:D:507:GLY:HA2	1:D:762:HIS:ND1	2.15	0.62
1:D:642:LYS:CA	4:5:21:PHE:O	2.46	0.62
1:D:795:ARG:C	3:F:35:ARG:HD3	2.20	0.62
1:G:202:SER:CA	1:G:207:LYS:HE3	2.28	0.62
1:G:508:ILE:HG21	1:G:711:PHE:HZ	1.64	0.62
1:J:278:GLN:HG3	1:J:318:GLY:N	2.15	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:771:LEU:O	1:J:774:LEU:N	2.32	0.62
4:1:257:CYS:HB3	4:1:258:PRO:HD3	1.81	0.62
4:4:257:CYS:HB3	4:4:258:PRO:HD3	1.81	0.62
4:6:190:MET:SD	4:6:209:VAL:HG11	2.38	0.62
1:A:302:MET:HG2	1:A:303:LEU:CD1	2.30	0.62
1:A:797:PHE:CE2	3:C:126:LEU:HD22	2.33	0.62
2:B:149:ASP:OD2	2:B:150:TYR:C	2.37	0.62
1:D:541:MET:HE2	4:5:346:LEU:HD12	1.82	0.62
1:D:542:PHE:CZ	1:D:553:MLY:HH11	2.34	0.62
1:D:580:SER:HA	1:D:588:VAL:O	2.00	0.62
1:D:636:LYS:N	4:5:334:GLU:OE1	2.31	0.62
2:H:146:GLY:O	2:H:147:ASN:CB	2.46	0.62
3:I:24:LYS:HB3	3:I:63:ILE:H	1.64	0.62
1:J:544:LYS:HB2	4:7:147:ARG:HA	1.80	0.62
1:J:551:MLY:C	4:V:46:GLY:O	2.47	0.62
1:J:724:TYR:HD1	1:J:727:LEU:HD11	1.64	0.62
3:L:24:LYS:HB3	3:L:63:ILE:H	1.64	0.62
4:6:361:GLU:HB3	4:6:369:ILE:HG12	1.82	0.62
1:A:506:GLU:N	1:A:761:GLY:HA2	2.13	0.62
1:A:543:PRO:HG2	4:4:143:TYR:O	1.98	0.62
1:A:544:LYS:HB2	4:4:147:ARG:HA	1.80	0.62
1:G:542:PHE:N	4:6:143:TYR:OH	2.33	0.62
1:J:251:ARG:HB2	1:J:264:ASP:CB	2.29	0.62
1:J:580:SER:HA	1:J:588:VAL:O	2.00	0.62
2:K:149:ASP:OD2	2:K:150:TYR:C	2.36	0.62
4:0:361:GLU:HB3	4:0:369:ILE:HG12	1.82	0.62
4:4:361:GLU:HB3	4:4:369:ILE:HG12	1.82	0.62
2:B:114:LYS:HA	2:B:146:GLY:C	2.03	0.62
1:D:730:SER:C	1:D:733:PRO:HD2	2.20	0.62
1:J:161:ASN:HA	1:J:164:GLN:HE21	1.63	0.62
2:K:111:SER:OG	2:K:148:VAL:CG1	2.47	0.62
4:2:361:GLU:HB3	4:2:369:ILE:HG12	1.82	0.62
4:5:361:GLU:HB3	4:5:369:ILE:HG12	1.82	0.62
4:6:257:CYS:HB3	4:6:258:PRO:HD3	1.81	0.62
4:7:361:GLU:HB3	4:7:369:ILE:HG12	1.82	0.62
4:8:361:GLU:HB3	4:8:369:ILE:HG12	1.82	0.62
1:A:161:ASN:HA	1:A:164:GLN:HE21	1.63	0.62
1:A:520:ALA:O	1:A:524:GLU:HG2	2.00	0.62
1:A:541:MET:HE2	4:4:346:LEU:HD12	1.82	0.62
1:D:91:MET:HE3	1:D:119:SER:HB2	1.82	0.62
1:D:537:GLU:C	4:5:351:THR:N	2.51	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:578:HIS:CB	1:D:592:ILE:HD12	2.30	0.62
2:E:111:SER:OG	2:E:148:VAL:CG1	2.48	0.62
1:G:127:ASN:HD22	1:G:128:PRO:CD	2.11	0.62
1:G:154:HIS:CE1	1:G:156:PHE:CD2	2.88	0.62
1:G:543:PRO:HG2	4:6:143:TYR:O	1.98	0.62
1:G:553:MLY:O	4:8:48:GLY:HA2	1.99	0.62
1:G:580:SER:HA	1:G:588:VAL:O	2.00	0.62
1:G:798:LEU:HD21	3:I:122:GLU:O	2.00	0.62
1:J:530:MET:CG	4:7:354:GLN:CG	2.72	0.62
1:J:538:GLU:HA	4:7:349:LEU:CG	2.28	0.62
1:J:542:PHE:CZ	1:J:553:MLY:HH11	2.34	0.62
1:J:732:ILE:HG21	1:J:747:LEU:HD11	0.73	0.62
1:J:754:ASP:CG	1:J:776:GLU:HA	2.20	0.62
2:K:121:LEU:HA	2:K:128:PHE:CG	2.34	0.62
4:W:361:GLU:HB3	4:W:369:ILE:HG12	1.82	0.62
4:Y:190:MET:SD	4:Y:209:VAL:HG11	2.38	0.62
1:D:295:MLY:HG3	1:D:332:MET:HE1	1.80	0.62
1:D:542:PHE:CB	4:5:143:TYR:HE1	2.13	0.62
1:D:831:TRP:N	2:E:51:PHE:CE1	2.68	0.62
1:G:98:HIS:HB3	1:G:100:PRO:CD	2.25	0.62
1:G:278:GLN:HG3	1:G:318:GLY:N	2.14	0.62
1:G:510:TRP:CE3	1:G:768:MLY:CH1	2.83	0.62
1:G:541:MET:C	4:6:143:TYR:CZ	2.73	0.62
1:G:578:HIS:CB	1:G:592:ILE:HD12	2.30	0.62
1:J:541:MET:C	4:7:143:TYR:CZ	2.72	0.62
1:J:707:CYS:HB3	1:J:714:ARG:NH2	2.14	0.62
4:1:361:GLU:HB3	4:1:369:ILE:HG12	1.82	0.62
4:V:361:GLU:HB3	4:V:369:ILE:HG12	1.82	0.62
4:X:361:GLU:HB3	4:X:369:ILE:HG12	1.82	0.62
4:Y:257:CYS:HB3	4:Y:258:PRO:HD3	1.81	0.62
4:Y:361:GLU:HB3	4:Y:369:ILE:HG12	1.82	0.62
4:Z:361:GLU:HB3	4:Z:369:ILE:HG12	1.82	0.62
1:A:98:HIS:HB3	1:A:100:PRO:CD	2.25	0.62
1:A:643:GLY:O	1:A:644:SER:CB	2.48	0.62
1:D:161:ASN:HA	1:D:164:GLN:HE21	1.64	0.62
1:D:302:MET:HG2	1:D:303:LEU:CD1	2.30	0.62
1:D:406:VAL:HG12	1:D:407:GLY:N	2.13	0.62
1:D:520:ALA:O	1:D:524:GLU:HG2	2.00	0.62
1:D:541:MET:CA	4:5:143:TYR:OH	2.47	0.62
1:D:830:PRO:CG	2:E:67:MET:HE2	2.15	0.62
1:G:302:MET:HG2	1:G:303:LEU:CD1	2.30	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:542:PHE:CZ	1:G:553:MLY:HH11	2.34	0.62
1:G:730:SER:C	1:G:733:PRO:HD2	2.20	0.62
1:G:768:MLY:CH2	1:G:772:LEU:HD22	2.27	0.62
1:G:791:GLN:OE1	3:I:116:GLU:CG	2.48	0.62
1:A:553:MLY:O	4:6:48:GLY:HA2	1.99	0.62
1:A:580:SER:HA	1:A:588:VAL:O	2.00	0.62
1:A:730:SER:C	1:A:733:PRO:HD2	2.20	0.62
1:A:771:LEU:O	1:A:774:LEU:N	2.32	0.62
3:C:50:LEU:O	3:C:53:PRO:HD2	2.00	0.62
1:D:202:SER:HA	1:D:207:LYS:HE3	1.72	0.62
1:J:557:GLU:HG3	1:J:557:GLU:O	2.00	0.62
1:J:730:SER:C	1:J:733:PRO:HD2	2.20	0.62
1:J:817:GLN:CG	2:K:127:ARG:CD	2.75	0.62
4:3:361:GLU:HB3	4:3:369:ILE:HG12	1.82	0.62
1:A:81:ASN:OD1	1:A:96:HIS:HB2	2.00	0.61
1:A:141:LEU:H	1:A:141:LEU:HD12	1.64	0.61
1:A:278:GLN:HG3	1:A:318:GLY:N	2.15	0.61
1:A:579:PHE:CE1	1:A:581:LEU:HD13	2.35	0.61
1:A:732:ILE:HG22	1:A:747:LEU:CD1	1.55	0.61
1:A:818:TYR:HB2	2:B:90:GLY:N	2.15	0.61
1:D:278:GLN:HG3	1:D:318:GLY:N	2.15	0.61
1:D:507:GLY:HA2	1:D:762:HIS:CG	2.34	0.61
1:D:543:PRO:HG2	4:5:143:TYR:O	1.98	0.61
1:G:551:MLY:C	4:8:46:GLY:O	2.48	0.61
4:8:257:CYS:HB3	4:8:258:PRO:HD3	1.81	0.61
4:W:257:CYS:HB3	4:W:258:PRO:HD3	1.81	0.61
1:A:154:HIS:CE1	1:A:156:PHE:CD2	2.88	0.61
1:A:278:GLN:CG	1:A:317:GLU:HB2	2.27	0.61
1:D:544:LYS:HB2	4:5:147:ARG:HA	1.80	0.61
3:F:50:LEU:O	3:F:53:PRO:HD2	2.00	0.61
1:G:278:GLN:CG	1:G:317:GLU:HB2	2.26	0.61
2:H:132:GLU:O	2:H:136:MET:HG2	1.99	0.61
3:I:50:LEU:O	3:I:53:PRO:HD2	2.00	0.61
1:J:542:PHE:CB	4:7:143:TYR:HE1	2.13	0.61
1:J:732:ILE:HG22	1:J:747:LEU:CD1	1.55	0.61
1:A:642:LYS:CG	4:4:22:ALA:C	2.67	0.61
1:A:686:MET:HG3	1:A:691:VAL:HG21	1.83	0.61
1:A:797:PHE:CD2	3:C:126:LEU:HD21	2.35	0.61
3:C:3:SER:HG	3:C:5:ALA:N	1.97	0.61
3:C:48:LYS:C	3:C:52:ASN:HD21	1.97	0.61
1:D:141:LEU:H	1:D:141:LEU:HD12	1.64	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:553:MLY:O	4:7:48:GLY:HA2	1.99	0.61
1:D:831:TRP:CZ2	2:E:47:LEU:C	2.70	0.61
1:G:728:ASN:HD21	3:I:110:VAL:CA	2.13	0.61
1:G:797:PHE:CB	3:I:149:VAL:HG11	2.29	0.61
1:J:411:GLU:N	4:7:333:PRO:HB2	2.11	0.61
1:A:99:GLU:OE2	1:A:696:ARG:NH2	2.30	0.61
1:D:274:ARG:HB2	1:D:285:TYR:CE2	2.34	0.61
1:D:634:GLY:N	4:5:25:ASP:O	2.31	0.61
2:E:114:LYS:HG3	2:E:146:GLY:HA2	1.82	0.61
1:G:81:ASN:OD1	1:G:96:HIS:HB2	2.00	0.61
1:G:161:ASN:HA	1:G:164:GLN:HE21	1.63	0.61
1:G:579:PHE:CE1	1:G:581:LEU:HD13	2.35	0.61
1:G:639:GLY:N	4:6:344:SER:C	2.54	0.61
1:G:732:ILE:HG22	1:G:747:LEU:CD1	1.55	0.61
2:H:144:VAL:HA	2:H:153:ILE:HD11	1.80	0.61
1:J:578:HIS:CB	1:J:592:ILE:HD12	2.30	0.61
1:J:642:LYS:CD	4:7:24:ASP:O	2.43	0.61
2:K:114:LYS:HG3	2:K:146:GLY:HA2	1.82	0.61
3:L:52:ASN:N	3:L:53:PRO:HD2	2.16	0.61
1:A:800:ARG:CD	3:C:149:VAL:CG2	2.41	0.61
2:B:117:LEU:HD11	2:B:147:ASN:HB3	1.76	0.61
1:D:831:TRP:CA	2:E:51:PHE:CE1	2.83	0.61
2:E:144:VAL:HA	2:E:153:ILE:HD11	1.80	0.61
1:G:541:MET:HE2	4:6:346:LEU:HD12	1.82	0.61
1:J:274:ARG:HB2	1:J:285:TYR:CE2	2.34	0.61
1:J:579:PHE:CE1	1:J:581:LEU:HD13	2.35	0.61
1:J:643:GLY:H	4:7:23:GLY:C	2.01	0.61
1:A:798:LEU:HD23	3:C:122:GLU:HB3	1.83	0.61
1:D:507:GLY:CA	1:D:762:HIS:CD2	2.84	0.61
1:D:541:MET:C	4:5:143:TYR:CZ	2.73	0.61
1:D:557:GLU:HG3	1:D:557:GLU:O	2.00	0.61
1:D:724:TYR:C	1:D:782:MLY:CH2	2.66	0.61
1:G:274:ARG:HB2	1:G:285:TYR:CE2	2.34	0.61
1:G:643:GLY:O	1:G:644:SER:CB	2.48	0.61
1:J:95:THR:HA	1:J:713:SER:HB3	1.82	0.61
1:J:99:GLU:OE2	1:J:696:ARG:NH2	2.30	0.61
1:J:623:PHE:CG	1:J:623:PHE:HA	2.35	0.61
1:J:813:ILE:O	1:J:817:GLN:N	2.30	0.61
1:A:530:MET:HE2	4:4:354:GLN:HG3	1.80	0.61
1:A:542:PHE:CB	4:4:143:TYR:HE1	2.12	0.61
2:B:111:SER:OG	2:B:148:VAL:CG1	2.47	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:541:MET:SD	4:5:346:LEU:O	2.48	0.61
1:D:686:MET:HG3	1:D:691:VAL:HG21	1.83	0.61
3:F:52:ASN:HB2	3:F:53:PRO:CD	2.28	0.61
1:G:524:GLU:O	1:G:528:MLY:HB3	2.01	0.61
1:G:821:ARG:HH22	2:H:127:ARG:HG2	0.78	0.61
1:J:302:MET:HG2	1:J:303:LEU:CD1	2.30	0.61
1:J:639:GLY:N	4:7:344:SER:C	2.54	0.61
1:J:643:GLY:O	1:J:644:SER:CB	2.49	0.61
2:B:34:ILE:O	2:B:46:ASP:HB3	2.01	0.61
1:D:217:THR:C	1:D:221:GLN:HG2	2.21	0.61
1:G:792:ALA:HA	3:I:35:ARG:CZ	2.31	0.61
2:H:144:VAL:CG1	2:H:153:ILE:HD13	2.19	0.61
1:J:93:MET:SD	1:J:764:MLY:HH23	2.33	0.61
2:B:114:LYS:HG3	2:B:146:GLY:HA2	1.82	0.61
3:C:63:ILE:HG22	3:C:64:THR:O	2.01	0.61
1:D:154:HIS:CE1	1:D:156:PHE:CD2	2.88	0.61
1:D:576:GLU:CG	1:D:577:ALA:N	2.44	0.61
1:D:579:PHE:CE1	1:D:581:LEU:HD13	2.35	0.61
3:F:49:ILE:HA	3:F:52:ASN:ND2	2.05	0.61
1:G:557:GLU:HG3	1:G:557:GLU:O	2.01	0.61
1:G:730:SER:OG	3:I:109:HIS:CE1	2.53	0.61
1:J:154:HIS:CE1	1:J:156:PHE:CD2	2.88	0.61
1:J:202:SER:HA	1:J:207:LYS:HE3	1.72	0.61
1:J:769:ALA:CB	1:J:770:GLY:HA3	2.28	0.61
4:5:223:PHE:HD2	4:5:312:ARG:NH2	1.99	0.61
1:A:411:GLU:N	4:4:333:PRO:HB2	2.11	0.61
1:D:643:GLY:O	1:D:644:SER:CB	2.48	0.61
1:D:643:GLY:H	4:5:23:GLY:C	2.02	0.61
3:F:52:ASN:N	3:F:53:PRO:HD2	2.15	0.61
1:G:94:MET:HE1	1:G:101:ALA:HB1	1.80	0.61
1:G:530:MET:HE3	4:6:354:GLN:CG	2.25	0.61
1:G:686:MET:HG3	1:G:691:VAL:HG21	1.83	0.61
1:G:732:ILE:HG21	1:G:747:LEU:HD11	0.72	0.61
1:G:769:ALA:O	1:G:773:GLY:HA2	2.01	0.61
1:G:838:ILE:CG1	2:H:54:MET:HE1	2.30	0.61
1:J:798:LEU:CD2	3:L:126:LEU:HG	2.18	0.61
3:L:50:LEU:O	3:L:53:PRO:HD2	2.00	0.61
4:4:223:PHE:HD2	4:4:312:ARG:NH2	1.99	0.61
1:A:40:VAL:HG22	1:A:41:VAL:N	2.16	0.60
1:A:156:PHE:CD1	1:A:195:TYR:CD1	2.89	0.60
1:D:530:MET:CG	4:5:354:GLN:HG3	2.30	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:578:HIS:CD2	1:D:591:ASN:HA	2.32	0.60
1:D:623:PHE:CG	1:D:623:PHE:HA	2.36	0.60
1:G:520:ALA:O	1:G:524:GLU:HG2	2.00	0.60
1:G:755:HIS:HA	1:G:758:TYR:HE1	1.64	0.60
2:H:114:LYS:HG3	2:H:146:GLY:HA2	1.82	0.60
1:J:524:GLU:O	1:J:528:MLY:HB3	2.01	0.60
1:J:795:ARG:CD	3:L:35:ARG:CZ	2.53	0.60
4:Z:223:PHE:HD2	4:Z:312:ARG:NH2	1.99	0.60
1:A:217:THR:C	1:A:221:GLN:HG2	2.21	0.60
1:A:524:GLU:O	1:A:528:MLY:HB3	2.01	0.60
1:A:813:ILE:CG2	2:B:127:ARG:CZ	2.68	0.60
3:C:52:ASN:N	3:C:53:PRO:HD2	2.16	0.60
1:D:38:VAL:HB	1:D:52:ILE:HD11	1.84	0.60
1:D:81:ASN:OD1	1:D:96:HIS:HB2	2.00	0.60
1:G:40:VAL:HG22	1:G:41:VAL:N	2.16	0.60
1:G:124:VAL:CG1	1:G:675:ILE:HD13	2.31	0.60
1:G:553:MLY:NZ	4:8:45:VAL:HG13	2.16	0.60
1:J:81:ASN:OD1	1:J:96:HIS:HB2	2.00	0.60
1:J:95:THR:HG23	1:J:96:HIS:ND1	2.17	0.60
1:J:520:ALA:O	1:J:524:GLU:HG2	2.00	0.60
1:J:543:PRO:HG2	4:7:143:TYR:O	1.98	0.60
1:J:665:ARG:C	1:J:667:THR:H	2.05	0.60
1:J:686:MET:HG3	1:J:691:VAL:HG21	1.83	0.60
2:K:34:ILE:O	2:K:46:ASP:HB3	2.01	0.60
4:2:223:PHE:HD2	4:2:312:ARG:NH2	1.99	0.60
1:A:557:GLU:HG3	1:A:557:GLU:O	2.00	0.60
1:A:665:ARG:C	1:A:667:THR:H	2.05	0.60
1:D:166:MET:HE3	1:D:254:PHE:HD2	1.66	0.60
1:D:410:ASN:CG	4:5:334:GLU:CA	2.47	0.60
1:D:721:LYS:HG2	1:D:736:GLN:CD	1.86	0.60
1:D:837:MLY:O	1:D:840:PRO:HD2	2.02	0.60
1:J:217:THR:C	1:J:221:GLN:HG2	2.21	0.60
1:A:553:MLY:NZ	4:6:45:VAL:HG13	2.16	0.60
1:J:530:MET:CG	4:7:354:GLN:HG3	2.30	0.60
1:A:40:VAL:HG22	1:A:41:VAL:H	1.67	0.60
1:A:124:VAL:CG1	1:A:675:ILE:HD13	2.31	0.60
1:A:546:THR:HG22	1:A:547:ASP:N	2.17	0.60
1:D:40:VAL:HG22	1:D:41:VAL:N	2.16	0.60
1:D:124:VAL:CG1	1:D:675:ILE:HD13	2.31	0.60
1:D:612:GLN:HE22	1:D:627:GLY:HA2	1.66	0.60
1:D:817:GLN:CG	2:E:127:ARG:CD	2.78	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:38:VAL:HB	1:G:52:ILE:HD11	1.83	0.60
1:G:623:PHE:CG	1:G:623:PHE:HA	2.36	0.60
1:G:730:SER:HB2	3:I:109:HIS:NE2	2.17	0.60
1:J:38:VAL:HB	1:J:52:ILE:HD11	1.83	0.60
1:J:546:THR:HG22	1:J:547:ASP:N	2.17	0.60
1:J:823:PHE:CD1	2:K:157:ILE:HA	2.36	0.60
1:J:837:MLY:O	1:J:840:PRO:HD2	2.02	0.60
2:K:130:PRO:HA	2:K:133:ILE:HD12	1.83	0.60
3:L:63:ILE:HG22	3:L:64:THR:O	2.01	0.60
4:6:223:PHE:HD2	4:6:312:ARG:NH2	1.99	0.60
4:Y:287:ILE:H	4:Y:287:ILE:HD12	1.67	0.60
1:A:38:VAL:HB	1:A:52:ILE:HD11	1.84	0.60
1:A:787:ILE:O	1:A:790:THR:N	2.35	0.60
1:D:530:MET:HA	4:5:354:GLN:CB	2.29	0.60
1:D:542:PHE:N	4:5:143:TYR:OH	2.32	0.60
2:E:34:ILE:O	2:E:46:ASP:HB3	2.01	0.60
1:G:542:PHE:CB	4:6:143:TYR:HE1	2.13	0.60
1:G:837:MLY:O	1:G:840:PRO:HD2	2.02	0.60
1:J:60:VAL:O	1:J:71:THR:HA	2.02	0.60
1:J:124:VAL:HG13	1:J:675:ILE:HD13	1.84	0.60
1:J:202:SER:CA	1:J:207:LYS:HE3	2.27	0.60
1:J:542:PHE:N	4:7:143:TYR:OH	2.33	0.60
4:2:287:ILE:H	4:2:287:ILE:HD12	1.67	0.60
4:3:223:PHE:HD2	4:3:312:ARG:NH2	1.99	0.60
4:5:287:ILE:H	4:5:287:ILE:HD12	1.67	0.60
4:V:287:ILE:H	4:V:287:ILE:HD12	1.67	0.60
4:X:223:PHE:HD2	4:X:312:ARG:NH2	1.99	0.60
1:A:504:MLY:HB2	1:A:762:HIS:CE1	2.37	0.60
1:A:550:PHE:CE2	1:A:592:ILE:HG23	2.37	0.60
1:A:837:MLY:O	1:A:840:PRO:HD2	2.02	0.60
1:D:524:GLU:O	1:D:528:MLY:HB3	2.01	0.60
1:D:639:GLY:N	4:5:344:SER:C	2.54	0.60
1:D:796:GLY:HA2	3:F:35:ARG:HB3	1.83	0.60
2:E:130:PRO:HA	2:E:133:ILE:HD12	1.84	0.60
2:E:144:VAL:CG1	2:E:153:ILE:HD13	2.19	0.60
1:G:60:VAL:O	1:G:71:THR:HA	2.02	0.60
1:G:84:MLY:CH1	1:G:716:LEU:O	2.50	0.60
1:G:156:PHE:CD1	1:G:195:TYR:CD1	2.90	0.60
1:J:40:VAL:HG22	1:J:41:VAL:N	2.16	0.60
1:J:124:VAL:CG1	1:J:675:ILE:HD13	2.31	0.60
1:J:578:HIS:CD2	1:J:591:ASN:HA	2.31	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:787:ILE:O	1:J:790:THR:N	2.35	0.60
4:3:287:ILE:H	4:3:287:ILE:HD12	1.67	0.60
4:X:287:ILE:H	4:X:287:ILE:HD12	1.67	0.60
4:Y:223:PHE:HD2	4:Y:312:ARG:NH2	1.99	0.60
1:A:60:VAL:O	1:A:71:THR:HA	2.02	0.60
1:A:634:GLY:N	4:4:25:ASP:O	2.31	0.60
1:J:827:MLY:HH21	2:K:139:ALA:HB3	1.83	0.60
4:7:287:ILE:HD12	4:7:287:ILE:H	1.67	0.60
1:A:506:GLU:OE2	1:A:760:PHE:CD2	2.49	0.60
1:A:542:PHE:CD1	4:4:143:TYR:CE1	2.90	0.60
3:C:46:ILE:O	3:C:50:LEU:CG	2.47	0.60
3:C:52:ASN:N	3:C:53:PRO:CD	2.65	0.60
1:D:49:MLY:HH13	1:D:108:GLU:OE2	2.02	0.60
1:D:124:VAL:HG13	1:D:675:ILE:HD13	1.84	0.60
1:D:553:MLY:NZ	4:7:45:VAL:HG13	2.16	0.60
1:D:665:ARG:C	1:D:667:THR:H	2.05	0.60
1:D:769:ALA:HA	1:D:771:LEU:HB2	1.81	0.60
1:D:789:ALA:O	3:F:87:PHE:CZ	2.55	0.60
1:J:786:ILE:HG12	3:L:86:ASP:CB	2.30	0.60
3:L:52:ASN:N	3:L:53:PRO:CD	2.65	0.60
4:0:223:PHE:HD2	4:0:312:ARG:NH2	1.99	0.60
4:0:287:ILE:H	4:0:287:ILE:HD12	1.67	0.60
4:Z:287:ILE:HD12	4:Z:287:ILE:H	1.67	0.60
1:A:95:THR:HG23	1:A:96:HIS:ND1	2.16	0.60
1:G:217:THR:C	1:G:221:GLN:HG2	2.21	0.60
1:G:578:HIS:CD2	1:G:591:ASN:HA	2.31	0.60
1:A:505:MLY:HH23	1:A:762:HIS:O	2.02	0.59
1:A:541:MET:SD	4:4:346:LEU:O	2.48	0.59
3:C:49:ILE:CA	3:C:52:ASN:ND2	2.53	0.59
1:D:536:LEU:HD13	1:D:550:PHE:CE1	2.37	0.59
1:D:755:HIS:HA	1:D:758:TYR:HE1	1.64	0.59
3:F:63:ILE:HG22	3:F:64:THR:O	2.01	0.59
1:G:665:ARG:C	1:G:667:THR:H	2.05	0.59
2:H:34:ILE:O	2:H:46:ASP:HB3	2.01	0.59
3:I:63:ILE:HG22	3:I:64:THR:O	2.01	0.59
1:J:768:MLY:CH2	1:J:772:LEU:HD13	2.32	0.59
1:J:820:VAL:CG1	2:K:136:MET:CE	2.80	0.59
4:4:287:ILE:H	4:4:287:ILE:HD12	1.67	0.59
1:D:60:VAL:O	1:D:71:THR:HA	2.02	0.59
1:D:95:THR:HG23	1:D:96:HIS:ND1	2.17	0.59
1:G:536:LEU:HD13	1:G:550:PHE:CE1	2.37	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:52:ASN:HB2	3:I:53:PRO:CD	2.28	0.59
3:I:52:ASN:N	3:I:53:PRO:CD	2.65	0.59
3:L:49:ILE:CA	3:L:52:ASN:ND2	2.54	0.59
4:1:287:ILE:H	4:1:287:ILE:HD12	1.67	0.59
4:W:287:ILE:H	4:W:287:ILE:HD12	1.67	0.59
1:A:530:MET:CG	4:4:354:GLN:HG3	2.30	0.59
1:A:536:LEU:HD13	1:A:550:PHE:CE1	2.37	0.59
1:D:549:SER:OG	1:D:550:PHE:N	2.36	0.59
1:G:541:MET:SD	4:6:346:LEU:O	2.48	0.59
1:G:546:THR:HG22	1:G:547:ASP:N	2.17	0.59
1:J:549:SER:OG	1:J:550:PHE:N	2.35	0.59
1:A:116:TYR:HB2	1:A:153:PRO:O	2.03	0.59
1:A:135:TYR:N	1:A:135:TYR:CD1	2.70	0.59
1:A:195:TYR:O	1:A:199:ILE:HG23	2.03	0.59
1:D:7:MET:HE3	1:D:14:ALA:HB1	1.84	0.59
1:D:599:ASN:CB	1:D:649:VAL:HB	2.32	0.59
1:D:776:GLU:O	1:D:779:ARG:HB3	2.03	0.59
1:D:783:LEU:O	1:D:787:ILE:N	2.28	0.59
1:D:787:ILE:O	1:D:790:THR:N	2.35	0.59
1:G:7:MET:HE3	1:G:14:ALA:HB1	1.83	0.59
1:G:550:PHE:CE2	1:G:592:ILE:HG23	2.37	0.59
1:G:787:ILE:O	1:G:790:THR:N	2.35	0.59
1:G:792:ALA:CB	3:I:40:ASN:HB3	2.32	0.59
1:J:156:PHE:CD1	1:J:195:TYR:CD1	2.90	0.59
1:J:530:MET:HA	4:7:354:GLN:CB	2.28	0.59
4:8:223:PHE:HD2	4:8:312:ARG:NH2	1.99	0.59
1:A:578:HIS:CD2	1:A:591:ASN:HA	2.31	0.59
1:A:623:PHE:CG	1:A:623:PHE:HA	2.36	0.59
1:A:776:GLU:O	1:A:779:ARG:HB3	2.03	0.59
1:G:530:MET:CG	4:6:354:GLN:HG3	2.30	0.59
1:G:538:GLU:HA	4:6:349:LEU:CG	2.28	0.59
1:G:728:ASN:HA	3:I:113:THR:OG1	2.03	0.59
1:G:817:GLN:OE1	2:H:127:ARG:CD	2.47	0.59
1:G:818:TYR:CG	2:H:127:ARG:NH1	2.70	0.59
3:I:52:ASN:N	3:I:53:PRO:HD2	2.16	0.59
1:J:542:PHE:CD1	4:7:143:TYR:CE1	2.91	0.59
4:W:223:PHE:HD2	4:W:312:ARG:NH2	1.99	0.59
1:A:295:MLY:HG3	1:A:332:MET:HE1	1.85	0.59
1:A:529:PRO:HG3	4:4:353:GLN:OE1	2.03	0.59
1:D:156:PHE:CD1	1:D:195:TYR:CD1	2.90	0.59
1:D:464:ILE:HG22	1:D:465:ALA:N	2.18	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:534:SER:C	4:5:351:THR:CA	2.47	0.59
1:G:599:ASN:CB	1:G:649:VAL:HB	2.32	0.59
1:J:49:MLY:HH13	1:J:108:GLU:OE2	2.02	0.59
1:J:230:GLU:O	1:J:234:ASN:HB2	2.03	0.59
1:A:735:GLY:O	1:A:743:ALA:HA	1.94	0.59
1:D:40:VAL:HG22	1:D:41:VAL:H	1.67	0.59
1:D:542:PHE:CD1	4:5:143:TYR:CE1	2.90	0.59
1:D:831:TRP:CH2	2:E:50:THR:HB	2.37	0.59
3:F:52:ASN:N	3:F:53:PRO:CD	2.65	0.59
1:G:40:VAL:HG22	1:G:41:VAL:H	1.67	0.59
1:G:93:MET:CB	1:G:716:LEU:HD12	2.33	0.59
1:G:195:TYR:O	1:G:199:ILE:HG23	2.03	0.59
1:G:549:SER:OG	1:G:550:PHE:N	2.36	0.59
1:G:646:PHE:CD2	1:G:652:LEU:CD1	2.85	0.59
1:G:715:VAL:HG11	1:G:720:PHE:HD1	1.68	0.59
1:G:836:PHE:CE1	2:H:159:HIS:CA	2.63	0.59
1:J:265:ILE:HG22	1:J:266:GLU:N	2.18	0.59
1:J:550:PHE:CE2	1:J:592:ILE:HG23	2.37	0.59
1:J:817:GLN:HG2	2:K:127:ARG:CB	2.32	0.59
4:1:223:PHE:HD2	4:1:312:ARG:NH2	1.99	0.59
1:A:48:VAL:HG22	1:A:49:MLY:N	2.18	0.59
1:A:265:ILE:HG22	1:A:266:GLU:N	2.18	0.59
1:D:601:ASP:N	1:D:602:PRO:HD3	2.18	0.59
1:D:724:TYR:CE1	1:D:778:MET:CG	2.86	0.59
1:G:542:PHE:CD1	4:6:143:TYR:CE1	2.91	0.59
1:J:599:ASN:CB	1:J:649:VAL:HB	2.32	0.59
1:A:230:GLU:O	1:A:234:ASN:HB2	2.03	0.59
1:D:792:ALA:CB	3:F:40:ASN:CB	2.75	0.59
1:G:116:TYR:HB2	1:G:153:PRO:O	2.03	0.59
1:J:776:GLU:O	1:J:779:ARG:HB3	2.02	0.59
1:J:784:ALA:O	1:J:788:THR:HB	2.02	0.59
4:V:223:PHE:HD2	4:V:312:ARG:NH2	1.99	0.59
1:A:599:ASN:CB	1:A:649:VAL:HB	2.32	0.59
1:A:601:ASP:N	1:A:602:PRO:HD3	2.18	0.59
1:A:755:HIS:HA	1:A:758:TYR:HE1	1.64	0.59
1:D:135:TYR:N	1:D:135:TYR:CD1	2.69	0.59
1:D:141:LEU:O	1:D:144:ARG:HB3	2.03	0.59
1:D:649:VAL:HA	1:D:649:VAL:HG22	1.80	0.59
1:D:817:GLN:NE2	2:E:127:ARG:CD	2.66	0.59
1:D:831:TRP:N	2:E:51:PHE:HZ	1.98	0.59
1:J:195:TYR:O	1:J:199:ILE:HG23	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:536:LEU:HD13	1:J:550:PHE:CE1	2.37	0.59
1:J:715:VAL:HG11	1:J:720:PHE:HD1	1.68	0.59
1:D:722:GLN:O	1:D:782:MLY:HH23	2.02	0.58
1:D:769:ALA:CB	1:D:771:LEU:N	2.66	0.58
1:G:95:THR:HG23	1:G:96:HIS:ND1	2.17	0.58
1:G:124:VAL:HG13	1:G:675:ILE:HD13	1.84	0.58
1:G:135:TYR:N	1:G:135:TYR:CD1	2.69	0.58
1:G:230:GLU:O	1:G:234:ASN:HB2	2.03	0.58
1:J:7:MET:HE3	1:J:14:ALA:HB1	1.85	0.58
1:J:210:GLN:O	1:J:211:SER:OG	2.15	0.58
1:J:601:ASP:N	1:J:602:PRO:HD3	2.18	0.58
1:J:643:GLY:HA2	4:7:24:ASP:OD1	2.04	0.58
4:6:287:ILE:H	4:6:287:ILE:HD12	1.67	0.58
1:A:538:GLU:O	1:A:541:MET:HB2	2.04	0.58
1:A:794:CYS:O	1:A:798:LEU:N	2.37	0.58
1:A:831:TRP:CH2	2:B:50:THR:CB	2.81	0.58
1:D:124:VAL:HG13	1:D:675:ILE:CD1	2.33	0.58
1:D:550:PHE:CE2	1:D:592:ILE:HG23	2.37	0.58
1:D:629:GLU:HB3	1:D:645:SER:N	2.18	0.58
1:J:553:MLY:NZ	4:V:45:VAL:HG13	2.17	0.58
1:J:754:ASP:OD2	1:J:776:GLU:HB3	2.01	0.58
1:A:410:ASN:CG	4:4:334:GLU:CA	2.48	0.58
1:A:549:SER:OG	1:A:550:PHE:N	2.36	0.58
1:D:529:PRO:HG3	4:5:353:GLN:OE1	2.03	0.58
1:D:794:CYS:O	1:D:798:LEU:N	2.36	0.58
1:G:265:ILE:HG22	1:G:266:GLU:N	2.18	0.58
1:G:464:ILE:HG22	1:G:465:ALA:N	2.18	0.58
2:H:130:PRO:HA	2:H:133:ILE:HD12	1.84	0.58
1:J:116:TYR:HB2	1:J:153:PRO:O	2.03	0.58
1:J:646:PHE:CD2	1:J:652:LEU:CD1	2.85	0.58
1:J:820:VAL:CG1	2:K:136:MET:HE1	2.33	0.58
1:A:7:MET:HE3	1:A:14:ALA:HB1	1.84	0.58
1:A:715:VAL:HG11	1:A:720:PHE:HD1	1.68	0.58
1:A:831:TRP:CZ3	2:B:34:ILE:HG12	2.39	0.58
2:B:140:PHE:O	2:B:141:PRO:C	2.33	0.58
1:D:218:LEU:N	1:D:221:GLN:HE21	2.01	0.58
1:D:643:GLY:HA2	4:5:24:ASP:OD1	2.04	0.58
1:D:813:ILE:O	1:D:817:GLN:N	2.30	0.58
1:G:601:ASP:N	1:G:602:PRO:HD3	2.18	0.58
1:G:642:LYS:CG	4:6:22:ALA:CA	2.80	0.58
1:J:40:VAL:HG22	1:J:41:VAL:H	1.67	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:629:GLU:HB3	1:J:645:SER:N	2.18	0.58
1:J:649:VAL:HA	1:J:649:VAL:HG22	1.80	0.58
3:L:52:ASN:HB2	3:L:53:PRO:CD	2.28	0.58
1:A:124:VAL:HG13	1:A:675:ILE:HD13	1.84	0.58
1:D:48:VAL:HG22	1:D:49:MLY:N	2.18	0.58
1:D:220:ASP:O	1:D:224:SER:N	2.27	0.58
1:D:546:THR:HG22	1:D:547:ASP:N	2.17	0.58
1:D:715:VAL:HG11	1:D:720:PHE:HD1	1.68	0.58
1:G:629:GLU:HB3	1:G:645:SER:N	2.18	0.58
1:G:751:GLY:HA2	3:I:114:LEU:CD1	2.24	0.58
1:G:836:PHE:CE2	2:H:160:GLY:CA	2.86	0.58
1:J:48:VAL:HG22	1:J:49:MLY:N	2.18	0.58
1:J:135:TYR:N	1:J:135:TYR:CD1	2.69	0.58
1:J:529:PRO:HG3	4:7:353:GLN:OE1	2.04	0.58
4:8:287:ILE:H	4:8:287:ILE:HD12	1.67	0.58
1:A:839:MLY:CD	2:B:159:HIS:HB3	2.33	0.58
1:D:127:ASN:ND2	1:D:128:PRO:HD2	2.16	0.58
1:D:230:GLU:O	1:D:234:ASN:HB2	2.03	0.58
1:D:538:GLU:O	1:D:541:MET:HB2	2.04	0.58
1:G:124:VAL:HG13	1:G:675:ILE:CD1	2.33	0.58
1:G:508:ILE:CD1	1:G:759:ALA:CB	2.49	0.58
1:G:538:GLU:O	1:G:541:MET:HB2	2.04	0.58
1:G:776:GLU:O	1:G:779:ARG:HB3	2.03	0.58
1:J:218:LEU:N	1:J:221:GLN:HE21	2.01	0.58
1:J:510:TRP:CE2	1:J:768:MLY:CH1	2.86	0.58
1:A:64:THR:HG22	1:A:65:GLU:N	2.19	0.58
1:A:124:VAL:HG13	1:A:675:ILE:CD1	2.33	0.58
1:D:175:ILE:HA	1:D:670:HIS:O	2.03	0.58
1:G:64:THR:HG22	1:G:65:GLU:N	2.19	0.58
1:G:254:PHE:CE2	1:G:459:ILE:HD12	2.39	0.58
1:G:831:TRP:CE2	2:H:67:MET:CG	2.86	0.58
1:G:831:TRP:CE2	2:H:67:MET:HB3	2.38	0.58
1:J:127:ASN:ND2	1:J:128:PRO:HD2	2.16	0.58
1:J:175:ILE:HA	1:J:670:HIS:O	2.03	0.58
1:J:755:HIS:HA	1:J:758:TYR:HE1	1.64	0.58
3:L:102:VAL:HG11	3:L:107:LEU:HB2	1.84	0.58
2:B:130:PRO:HA	2:B:133:ILE:HD12	1.84	0.58
1:D:818:TYR:HB2	2:E:90:GLY:HA3	1.86	0.58
1:J:279:LEU:HB3	1:J:280:PRO:HD2	1.86	0.58
1:J:464:ILE:HG22	1:J:465:ALA:N	2.18	0.58
1:J:481:ASN:N	1:J:481:ASN:ND2	2.51	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:49:MLY:HH13	1:A:108:GLU:OE2	2.03	0.58
1:A:141:LEU:O	1:A:144:ARG:HB3	2.03	0.58
1:A:175:ILE:HA	1:A:670:HIS:O	2.04	0.58
1:A:409:GLY:HA3	4:4:333:PRO:CD	2.34	0.58
1:A:541:MET:C	4:4:143:TYR:CZ	2.73	0.58
1:A:642:LYS:CG	4:4:22:ALA:CA	2.81	0.58
1:D:279:LEU:HB3	1:D:280:PRO:HD2	1.86	0.58
1:D:724:TYR:CA	1:D:782:MLY:CH2	2.81	0.58
1:D:735:GLY:O	1:D:743:ALA:HA	1.94	0.58
1:G:529:PRO:HG3	4:6:353:GLN:OE1	2.04	0.58
1:G:568:PRO:HG3	1:G:578:HIS:H	1.69	0.58
1:D:254:PHE:CE2	1:D:459:ILE:HD12	2.39	0.58
1:D:506:GLU:OE2	1:D:764:MLY:HH22	2.04	0.58
1:G:48:VAL:HG22	1:G:49:MLY:N	2.18	0.58
1:J:538:GLU:O	1:J:541:MET:HB2	2.03	0.58
1:A:813:ILE:O	1:A:817:GLN:N	2.30	0.57
1:A:814:PHE:CA	2:B:127:ARG:HH22	2.17	0.57
3:C:102:VAL:HG11	3:C:107:LEU:HB2	1.85	0.57
1:D:817:GLN:OE1	2:E:127:ARG:NH2	2.37	0.57
2:E:112:ILE:C	2:E:147:ASN:O	2.42	0.57
1:G:49:MLY:HH13	1:G:108:GLU:OE2	2.03	0.57
1:G:84:MLY:CH1	1:G:719:ASP:C	2.50	0.57
1:G:141:LEU:O	1:G:144:ARG:HB3	2.03	0.57
1:J:95:THR:HA	1:J:713:SER:CA	2.32	0.57
1:J:124:VAL:HG13	1:J:675:ILE:CD1	2.33	0.57
1:J:541:MET:SD	4:7:346:LEU:O	2.48	0.57
1:A:464:ILE:HG22	1:A:465:ALA:N	2.18	0.57
1:A:629:GLU:HB3	1:A:645:SER:N	2.18	0.57
1:A:676:ILE:HG23	1:A:676:ILE:O	2.03	0.57
1:A:831:TRP:CZ2	2:B:51:PHE:CZ	2.88	0.57
1:D:265:ILE:HG22	1:D:266:GLU:N	2.18	0.57
1:D:322:VAL:HG11	1:D:325:ILE:HD11	1.86	0.57
1:D:676:ILE:HG23	1:D:676:ILE:O	2.03	0.57
1:D:717:TYR:HD1	1:D:744:SER:HG	1.52	0.57
1:G:99:GLU:OE2	1:G:696:ARG:NH2	2.30	0.57
1:G:279:LEU:HB3	1:G:280:PRO:HD2	1.86	0.57
1:G:411:GLU:N	4:6:333:PRO:HB2	2.10	0.57
1:A:254:PHE:CE2	1:A:459:ILE:HD12	2.39	0.57
1:A:783:LEU:O	1:A:787:ILE:N	2.28	0.57
1:D:541:MET:HG2	4:5:345:ILE:CG2	2.35	0.57
1:D:831:TRP:CD2	2:E:51:PHE:CZ	2.92	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:102:VAL:HG11	3:F:107:LEU:HB2	1.84	0.57
1:G:295:MLY:HG3	1:G:332:MET:HE1	1.87	0.57
1:J:322:VAL:HG11	1:J:325:ILE:HD11	1.86	0.57
1:J:717:TYR:HD1	1:J:744:SER:HG	1.52	0.57
1:A:279:LEU:HB3	1:A:280:PRO:HD2	1.86	0.57
1:A:418:THR:HG22	1:A:419:VAL:H	1.69	0.57
1:A:831:TRP:CD2	2:B:51:PHE:CZ	2.88	0.57
1:D:418:THR:HG22	1:D:419:VAL:H	1.69	0.57
1:G:409:GLY:HA3	4:6:333:PRO:CD	2.35	0.57
1:G:813:ILE:O	1:G:816:ILE:N	2.37	0.57
3:I:102:VAL:HG11	3:I:107:LEU:HB2	1.85	0.57
1:J:64:THR:HG22	1:J:65:GLU:N	2.19	0.57
1:J:254:PHE:CE2	1:J:459:ILE:HD12	2.39	0.57
1:J:676:ILE:HG23	1:J:676:ILE:O	2.03	0.57
1:J:784:ALA:O	1:J:788:THR:CB	2.52	0.57
1:A:220:ASP:O	1:A:224:SER:N	2.27	0.57
1:A:635:GLY:HA3	4:4:334:GLU:CG	2.30	0.57
1:A:768:MLY:C	1:A:771:LEU:HB3	2.35	0.57
2:B:112:ILE:C	2:B:147:ASN:O	2.42	0.57
1:D:64:THR:HG22	1:D:65:GLU:N	2.19	0.57
1:D:195:TYR:O	1:D:199:ILE:HG23	2.03	0.57
1:D:831:TRP:CA	2:E:51:PHE:HE1	2.17	0.57
1:G:218:LEU:N	1:G:221:GLN:HE21	2.01	0.57
1:G:508:ILE:HD11	1:G:759:ALA:HB2	0.75	0.57
1:J:91:MET:HE3	1:J:119:SER:HB2	1.85	0.57
1:J:409:GLY:HA3	4:7:333:PRO:CD	2.35	0.57
1:J:794:CYS:O	1:J:798:LEU:N	2.36	0.57
1:A:173:GLN:C	1:A:667:THR:HG23	2.25	0.57
1:A:541:MET:HG2	4:4:345:ILE:CG2	2.35	0.57
1:A:818:TYR:HB2	2:B:90:GLY:HA3	1.86	0.57
3:C:102:VAL:HG23	3:C:139:TYR:CD1	2.39	0.57
1:D:22:LYS:O	1:D:26:GLU:N	2.29	0.57
1:D:173:GLN:C	1:D:667:THR:HG23	2.25	0.57
1:D:579:PHE:CD2	1:D:592:ILE:HD11	2.39	0.57
1:D:822:SER:HG	2:E:87:LYS:C	2.07	0.57
3:F:102:VAL:HG23	3:F:139:TYR:CD1	2.39	0.57
1:G:599:ASN:CG	1:G:649:VAL:HB	2.25	0.57
1:G:813:ILE:O	1:G:817:GLN:N	2.30	0.57
1:J:82:PRO:HD2	1:J:85:TYR:CD2	2.40	0.57
1:J:141:LEU:O	1:J:144:ARG:HB3	2.04	0.57
1:J:541:MET:HG2	4:7:345:ILE:CG2	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:789:ALA:HB2	3:L:81:GLN:HG2	1.86	0.57
1:A:218:LEU:N	1:A:221:GLN:HE21	2.02	0.57
1:D:409:GLY:HA3	4:5:333:PRO:CD	2.35	0.57
1:D:834:LEU:HD21	2:E:54:MET:HE2	1.86	0.57
1:G:175:ILE:HA	1:G:670:HIS:O	2.04	0.57
1:J:173:GLN:C	1:J:667:THR:HG23	2.25	0.57
1:J:752:ASP:O	1:J:780:ASP:OD2	2.23	0.57
1:A:322:VAL:HG11	1:A:325:ILE:HD11	1.86	0.57
1:A:502:GLU:CG	1:A:761:GLY:C	2.69	0.57
1:A:639:GLY:N	4:4:344:SER:C	2.54	0.57
1:D:82:PRO:HD2	1:D:85:TYR:CD2	2.40	0.57
1:D:116:TYR:HB2	1:D:153:PRO:O	2.03	0.57
1:D:813:ILE:O	1:D:816:ILE:N	2.38	0.57
1:D:830:PRO:C	2:E:51:PHE:CE1	2.78	0.57
1:G:173:GLN:C	1:G:667:THR:HG23	2.25	0.57
1:G:642:LYS:CD	4:6:340:TRP:CZ3	2.80	0.57
1:A:109:ARG:O	1:A:114:MET:N	2.37	0.57
1:A:643:GLY:HA2	4:4:24:ASP:OD1	2.04	0.57
1:A:813:ILE:O	1:A:816:ILE:N	2.37	0.57
1:D:481:ASN:N	1:D:481:ASN:ND2	2.51	0.57
1:D:530:MET:CA	4:5:354:GLN:HB3	2.35	0.57
1:J:530:MET:CA	4:7:354:GLN:HB3	2.35	0.57
1:J:579:PHE:CD2	1:J:592:ILE:HD11	2.40	0.57
1:J:783:LEU:O	1:J:787:ILE:CB	2.52	0.57
1:A:529:PRO:CG	4:4:353:GLN:OE1	2.53	0.57
1:A:768:MLY:HB3	1:A:771:LEU:CG	2.35	0.57
1:A:795:ARG:NH2	3:C:116:GLU:CG	2.68	0.57
1:D:646:PHE:CD2	1:D:652:LEU:CD1	2.85	0.57
1:D:724:TYR:OH	1:D:778:MET:SD	2.63	0.57
1:G:82:PRO:HD2	1:G:85:TYR:CD2	2.40	0.57
1:G:612:GLN:HE22	1:G:627:GLY:HA2	1.66	0.57
1:G:820:VAL:CG1	2:H:136:MET:HE1	2.34	0.57
1:J:747:LEU:O	1:J:747:LEU:HD23	2.05	0.57
1:A:82:PRO:HD2	1:A:85:TYR:CD2	2.40	0.56
1:A:599:ASN:CG	1:A:649:VAL:HB	2.25	0.56
1:A:795:ARG:CG	3:C:118:MET:CE	2.82	0.56
1:A:830:PRO:HG2	2:B:67:MET:HE1	1.87	0.56
1:D:599:ASN:CG	1:D:649:VAL:HB	2.25	0.56
1:D:831:TRP:HE1	2:E:47:LEU:HD22	1.58	0.56
1:G:541:MET:HG2	4:6:345:ILE:CG2	2.35	0.56
1:G:747:LEU:HD23	1:G:747:LEU:O	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:797:PHE:HE2	3:I:126:LEU:HD23	1.69	0.56
1:G:831:TRP:CZ2	2:H:67:MET:HB3	2.40	0.56
1:J:677:PRO:HB2	1:J:678:ASN:ND2	2.20	0.56
1:J:768:MLY:NZ	1:J:772:LEU:CD2	2.40	0.56
1:A:481:ASN:N	1:A:481:ASN:ND2	2.51	0.56
1:A:753:VAL:HG12	1:A:775:LEU:HG	1.86	0.56
1:A:834:LEU:HD21	2:B:54:MET:CG	2.35	0.56
1:D:411:GLU:H	4:5:333:PRO:HG2	1.70	0.56
1:D:568:PRO:HG3	1:D:578:HIS:H	1.69	0.56
1:D:724:TYR:CZ	1:D:778:MET:HB3	2.37	0.56
1:D:733:PRO:CB	1:D:737:PHE:HE1	2.19	0.56
1:J:821:ARG:NH2	2:K:127:ARG:HD3	2.18	0.56
3:L:46:ILE:O	3:L:50:LEU:CG	2.47	0.56
3:L:102:VAL:HG23	3:L:139:TYR:CD1	2.39	0.56
1:A:135:TYR:N	1:A:135:TYR:HD1	2.04	0.56
1:A:302:MET:HG2	1:A:303:LEU:HD13	1.87	0.56
1:A:411:GLU:H	4:4:333:PRO:HG2	1.71	0.56
1:A:568:PRO:HG3	1:A:578:HIS:H	1.69	0.56
1:A:640:LYS:C	4:4:23:GLY:CA	2.64	0.56
1:A:733:PRO:CA	1:A:737:PHE:HE1	2.19	0.56
1:A:831:TRP:CH2	2:B:50:THR:CG2	2.88	0.56
1:D:22:LYS:HA	1:D:25:ILE:HB	1.87	0.56
1:D:733:PRO:CA	1:D:737:PHE:HE1	2.18	0.56
1:D:831:TRP:NE1	2:E:67:MET:SD	2.77	0.56
2:E:163:ALA:C	2:K:22:THR:CB	2.74	0.56
1:G:302:MET:HG2	1:G:303:LEU:HD13	1.88	0.56
1:G:322:VAL:HG11	1:G:325:ILE:HD11	1.86	0.56
1:G:338:ILE:HG21	1:G:348:MLY:HB3	1.87	0.56
1:G:642:LYS:CA	4:6:22:ALA:C	2.70	0.56
1:G:643:GLY:N	4:6:23:GLY:C	2.55	0.56
1:G:676:ILE:HG23	1:G:676:ILE:O	2.03	0.56
1:G:677:PRO:HB2	1:G:678:ASN:ND2	2.20	0.56
1:G:757:GLN:NE2	1:G:772:LEU:HG	2.20	0.56
2:H:112:ILE:C	2:H:147:ASN:O	2.42	0.56
3:I:102:VAL:HG23	3:I:139:TYR:CD1	2.39	0.56
1:J:568:PRO:HG3	1:J:578:HIS:H	1.69	0.56
1:J:735:GLY:O	1:J:743:ALA:HA	1.94	0.56
1:J:813:ILE:O	1:J:816:ILE:N	2.37	0.56
4:7:223:PHE:HD2	4:7:312:ARG:NH2	1.99	0.56
1:A:210:GLN:O	1:A:211:SER:OG	2.15	0.56
1:A:630:ALA:CA	4:4:25:ASP:OD2	2.53	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:768:MLY:HG2	1:A:771:LEU:HD13	1.87	0.56
1:A:800:ARG:HD2	3:C:149:VAL:CA	2.35	0.56
1:A:830:PRO:HG2	2:B:67:MET:HE2	1.87	0.56
1:A:839:MLY:HD2	2:B:159:HIS:CD2	2.38	0.56
1:D:135:TYR:N	1:D:135:TYR:HD1	2.04	0.56
1:D:677:PRO:HB2	1:D:678:ASN:ND2	2.20	0.56
1:D:786:ILE:HG12	3:F:86:ASP:HB3	1.87	0.56
1:D:815:CYS:HA	2:E:90:GLY:HA2	1.87	0.56
1:J:418:THR:HG22	1:J:419:VAL:H	1.69	0.56
1:J:638:GLY:CA	4:7:345:ILE:H	2.18	0.56
1:A:649:VAL:HA	1:A:649:VAL:HG23	1.83	0.56
1:A:677:PRO:HB2	1:A:678:ASN:ND2	2.20	0.56
1:A:753:VAL:CG1	1:A:775:LEU:HG	2.36	0.56
1:A:834:LEU:HD21	2:B:54:MET:CE	2.36	0.56
3:C:48:LYS:C	3:C:52:ASN:HD22	1.97	0.56
1:D:116:TYR:CE2	1:D:154:HIS:CD2	2.94	0.56
1:D:406:VAL:HG12	1:D:407:GLY:H	1.71	0.56
1:G:733:PRO:CA	1:G:737:PHE:HE1	2.19	0.56
1:G:817:GLN:HG2	2:H:127:ARG:CD	2.34	0.56
1:J:116:TYR:CE2	1:J:154:HIS:CD2	2.94	0.56
1:J:338:ILE:HG21	1:J:348:MLY:HB3	1.87	0.56
1:A:338:ILE:HG21	1:A:348:MLY:HB3	1.87	0.56
1:A:546:THR:HG21	1:A:548:THR:HB	1.88	0.56
1:A:646:PHE:CD2	1:A:652:LEU:CD1	2.85	0.56
1:A:649:VAL:HG22	1:A:649:VAL:HA	1.80	0.56
1:A:733:PRO:CB	1:A:737:PHE:HE1	2.19	0.56
2:B:150:TYR:C	2:B:151:LYS:CG	2.49	0.56
1:G:135:TYR:N	1:G:135:TYR:HD1	2.04	0.56
1:J:599:ASN:CG	1:J:649:VAL:HB	2.25	0.56
1:A:116:TYR:CE2	1:A:154:HIS:CD2	2.94	0.56
1:A:747:LEU:HD23	1:A:747:LEU:O	2.05	0.56
1:A:768:MLY:CG	1:A:771:LEU:HD13	2.35	0.56
1:A:797:PHE:HD2	3:C:126:LEU:CD2	2.18	0.56
1:D:215:GLN:CA	1:D:340:ILE:CG2	2.63	0.56
1:D:834:LEU:HD22	2:E:50:THR:HG22	1.87	0.56
1:G:84:MLY:HH11	1:G:720:PHE:CA	2.35	0.56
1:G:638:GLY:CA	4:6:345:ILE:H	2.18	0.56
1:G:643:GLY:HA2	4:6:24:ASP:OD1	2.04	0.56
1:J:95:THR:HA	1:J:713:SER:CB	2.36	0.56
1:J:135:TYR:N	1:J:135:TYR:HD1	2.04	0.56
1:J:503:TYR:OH	1:J:711:PHE:CD2	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:630:ALA:CA	4:7:25:ASP:OD2	2.53	0.56
1:J:754:ASP:OD1	1:J:779:ARG:HD2	2.06	0.56
1:A:206:LYS:HB3	1:A:217:THR:OG1	2.06	0.56
1:A:502:GLU:HA	1:A:762:HIS:H	1.71	0.56
1:A:530:MET:CA	4:4:354:GLN:HB3	2.34	0.56
1:A:795:ARG:HG2	3:C:118:MET:CE	2.35	0.56
1:D:435:GLU:O	1:D:438:PHE:HB3	2.06	0.56
1:D:747:LEU:HD23	1:D:747:LEU:O	2.05	0.56
1:D:834:LEU:CD2	2:E:54:MET:CG	2.61	0.56
1:G:109:ARG:O	1:G:114:MET:N	2.37	0.56
1:G:538:GLU:CG	4:6:351:THR:C	2.73	0.56
1:A:217:THR:HG22	1:A:218:LEU:O	2.05	0.56
1:D:99:GLU:OE2	1:D:696:ARG:NH2	2.31	0.56
1:D:529:PRO:CB	4:5:354:GLN:HA	2.36	0.56
1:D:529:PRO:CG	4:5:353:GLN:OE1	2.53	0.56
1:G:410:ASN:CG	4:6:334:GLU:C	2.64	0.56
1:G:529:PRO:CG	4:6:353:GLN:OE1	2.54	0.56
1:G:649:VAL:CG1	1:G:649:VAL:HA	2.35	0.56
1:G:733:PRO:CB	1:G:737:PHE:HE1	2.19	0.56
1:J:503:TYR:HH	1:J:711:PHE:HD2	0.72	0.56
1:J:530:MET:CB	4:7:354:GLN:HG3	2.36	0.56
1:A:22:LYS:O	1:A:26:GLU:HG3	2.06	0.56
1:A:546:THR:HB	1:A:549:SER:H	1.71	0.56
1:D:290:GLN:HG2	1:D:331:LEU:HA	1.87	0.56
1:D:630:ALA:CA	4:5:25:ASP:OD2	2.53	0.56
1:D:640:LYS:C	1:D:645:SER:OG	2.44	0.56
1:G:22:LYS:O	1:G:26:GLU:HG3	2.06	0.56
1:G:217:THR:HG22	1:G:218:LEU:O	2.06	0.56
1:G:418:THR:HG22	1:G:419:VAL:H	1.69	0.56
1:G:435:GLU:O	1:G:438:PHE:HB3	2.06	0.56
1:G:537:GLU:HB3	1:G:648:THR:CB	2.36	0.56
1:G:794:CYS:O	1:G:798:LEU:N	2.37	0.56
3:I:46:ILE:O	3:I:50:LEU:CG	2.47	0.56
1:J:530:MET:HE3	4:7:354:GLN:CG	2.30	0.56
1:J:629:GLU:O	1:J:643:GLY:HA3	2.06	0.56
1:J:733:PRO:CA	1:J:737:PHE:HE1	2.19	0.56
1:A:97:LEU:HD22	1:A:712:PRO:CB	2.32	0.55
1:A:290:GLN:HG2	1:A:331:LEU:HA	1.87	0.55
1:A:530:MET:HE3	4:4:354:GLN:CB	2.37	0.55
1:A:797:PHE:HD2	3:C:126:LEU:HD21	1.71	0.55
1:A:798:LEU:CD1	3:C:126:LEU:CG	2.79	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:32:PHE:CG	1:D:83:PRO:HD3	2.41	0.55
1:D:789:ALA:C	3:F:87:PHE:CZ	2.79	0.55
1:G:206:LYS:HB3	1:G:217:THR:OG1	2.06	0.55
1:G:411:GLU:H	4:6:333:PRO:HG2	1.70	0.55
1:G:530:MET:CA	4:6:354:GLN:HB3	2.35	0.55
1:G:649:VAL:HA	1:G:649:VAL:HG22	1.80	0.55
1:G:820:VAL:CG1	2:H:136:MET:CE	2.84	0.55
1:J:90:ASP:OD2	1:J:764:MLY:HH22	2.05	0.55
4:7:365:ALA:HB3	4:7:369:ILE:HB	1.88	0.55
1:A:529:PRO:CB	4:4:354:GLN:HA	2.36	0.55
1:A:538:GLU:CG	4:4:351:THR:C	2.74	0.55
1:A:640:LYS:C	1:A:645:SER:OG	2.44	0.55
1:D:638:GLY:CA	4:5:345:ILE:H	2.19	0.55
1:D:725:ARG:H	1:D:782:MLY:HH21	1.65	0.55
1:G:84:MLY:HH12	1:G:716:LEU:O	2.05	0.55
1:G:116:TYR:CE2	1:G:154:HIS:CD2	2.94	0.55
1:J:217:THR:HG22	1:J:218:LEU:O	2.05	0.55
1:J:750:GLY:HA2	3:L:114:LEU:HD23	1.87	0.55
4:V:365:ALA:HB3	4:V:369:ILE:HB	1.88	0.55
1:A:32:PHE:CG	1:A:83:PRO:HD3	2.42	0.55
1:D:530:MET:HE3	4:5:355:MET:SD	2.46	0.55
1:D:537:GLU:HB3	1:D:648:THR:CB	2.36	0.55
1:D:546:THR:HG21	1:D:548:THR:HB	1.88	0.55
2:E:162:ASP:O	2:K:21:GLU:HB2	2.07	0.55
1:J:206:LYS:HB3	1:J:217:THR:OG1	2.06	0.55
1:J:579:PHE:HE1	1:J:581:LEU:HD13	1.72	0.55
1:J:634:GLY:N	4:7:25:ASP:O	2.31	0.55
1:J:733:PRO:CB	1:J:737:PHE:HE1	2.19	0.55
3:L:123:VAL:O	3:L:127:MET:HG2	2.06	0.55
1:A:290:GLN:NE2	1:A:334:THR:OG1	2.40	0.55
1:A:345:ALA:O	1:A:349:THR:N	2.40	0.55
1:A:537:GLU:HB3	1:A:648:THR:CB	2.36	0.55
1:A:629:GLU:O	1:A:643:GLY:HA3	2.06	0.55
1:A:765:VAL:HG12	1:A:766:PHE:N	2.22	0.55
1:A:793:ARG:NH2	3:C:147:MET:HE2	2.22	0.55
1:D:217:THR:HG22	1:D:218:LEU:O	2.06	0.55
1:D:629:GLU:O	1:D:643:GLY:HA3	2.06	0.55
1:D:789:ALA:HB2	3:F:81:GLN:O	2.06	0.55
1:G:127:ASN:ND2	1:G:128:PRO:HD2	2.17	0.55
1:G:732:ILE:CG2	1:G:747:LEU:HD11	1.26	0.55
1:J:643:GLY:N	4:7:23:GLY:C	2.55	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:646:PHE:CE2	1:J:652:LEU:CG	2.90	0.55
4:5:365:ALA:HB3	4:5:369:ILE:HB	1.88	0.55
1:A:7:MET:HE3	1:A:14:ALA:CB	2.36	0.55
1:A:406:VAL:HG12	1:A:407:GLY:H	1.71	0.55
1:A:604:ASN:OD1	1:A:607:VAL:HG23	2.06	0.55
1:D:604:ASN:OD1	1:D:607:VAL:HG23	2.06	0.55
1:D:646:PHE:CE2	1:D:652:LEU:CG	2.90	0.55
1:G:22:LYS:HA	1:G:25:ILE:HB	1.87	0.55
1:G:93:MET:HB2	1:G:764:MLY:NZ	2.18	0.55
1:G:629:GLU:O	1:G:643:GLY:HA3	2.06	0.55
1:G:646:PHE:CE2	1:G:652:LEU:CG	2.90	0.55
1:J:7:MET:HE3	1:J:14:ALA:CB	2.36	0.55
1:J:302:MET:HG2	1:J:303:LEU:HD13	1.87	0.55
1:J:406:VAL:HG12	1:J:407:GLY:H	1.71	0.55
1:J:640:LYS:C	1:J:645:SER:OG	2.44	0.55
1:J:768:MLY:CH2	1:J:772:LEU:CD1	2.83	0.55
3:L:35:ARG:HA	3:L:39:GLN:O	2.07	0.55
4:1:365:ALA:HB3	4:1:369:ILE:HB	1.88	0.55
1:A:612:GLN:HE22	1:A:627:GLY:HA2	1.66	0.55
2:E:156:VAL:HA	2:E:159:HIS:O	2.07	0.55
1:G:579:PHE:HE1	1:G:581:LEU:HD13	1.72	0.55
1:G:604:ASN:OD1	1:G:607:VAL:HG23	2.06	0.55
1:G:795:ARG:HE	3:I:118:MET:HE1	1.72	0.55
1:J:32:PHE:CG	1:J:83:PRO:HD3	2.41	0.55
1:J:410:ASN:CG	4:7:334:GLU:C	2.65	0.55
1:J:435:GLU:O	1:J:438:PHE:HB3	2.06	0.55
4:X:365:ALA:HB3	4:X:369:ILE:HB	1.88	0.55
1:A:530:MET:CB	4:4:354:GLN:HG3	2.36	0.55
1:A:642:LYS:CA	4:4:22:ALA:C	2.71	0.55
1:A:725:ARG:HG3	1:A:733:PRO:CA	2.36	0.55
1:A:757:GLN:OE1	1:A:771:LEU:HD12	2.06	0.55
1:D:338:ILE:HG21	1:D:348:MLY:HB3	1.87	0.55
1:D:530:MET:CB	4:5:354:GLN:HG3	2.36	0.55
1:G:7:MET:HE3	1:G:14:ALA:CB	2.37	0.55
1:G:290:GLN:NE2	1:G:334:THR:OG1	2.40	0.55
1:G:546:THR:HB	1:G:549:SER:H	1.71	0.55
3:I:35:ARG:HA	3:I:39:GLN:O	2.07	0.55
1:J:22:LYS:HA	1:J:25:ILE:HB	1.87	0.55
1:J:82:PRO:HD2	1:J:85:TYR:HD2	1.72	0.55
1:J:345:ALA:O	1:J:349:THR:N	2.40	0.55
1:J:529:PRO:CB	4:7:354:GLN:HA	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:725:ARG:HG3	1:J:733:PRO:CA	2.36	0.55
4:3:365:ALA:HB3	4:3:369:ILE:HB	1.88	0.55
1:D:302:MET:HG2	1:D:303:LEU:HD13	1.87	0.55
1:D:723:ARG:HH21	1:D:783:LEU:HD11	1.71	0.55
1:G:640:LYS:C	1:G:645:SER:OG	2.44	0.55
2:H:156:VAL:HA	2:H:159:HIS:O	2.07	0.55
1:J:411:GLU:H	4:7:333:PRO:HG2	1.71	0.55
1:J:635:GLY:HA3	4:7:334:GLU:CG	2.30	0.55
2:K:156:VAL:HA	2:K:159:HIS:O	2.07	0.55
1:A:292:MET:HE1	1:A:309:PRO:CD	2.37	0.55
1:A:646:PHE:CE2	1:A:652:LEU:CG	2.90	0.55
1:A:817:GLN:NE2	2:B:127:ARG:CG	2.70	0.55
3:C:35:ARG:HA	3:C:39:GLN:O	2.07	0.55
1:D:7:MET:HE3	1:D:14:ALA:CB	2.36	0.55
1:D:135:TYR:HD2	1:D:191:ARG:HG2	1.72	0.55
1:D:206:LYS:HB3	1:D:217:THR:OG1	2.07	0.55
2:E:121:LEU:CA	2:E:128:PHE:CG	2.89	0.55
3:F:46:ILE:O	3:F:50:LEU:CG	2.47	0.55
1:G:290:GLN:HG2	1:G:331:LEU:HA	1.87	0.55
1:G:730:SER:HG	3:I:109:HIS:CG	2.20	0.55
1:G:751:GLY:N	3:I:114:LEU:HD11	2.21	0.55
2:H:121:LEU:CA	2:H:128:PHE:CG	2.89	0.55
2:H:140:PHE:O	2:H:141:PRO:C	2.33	0.55
1:J:290:GLN:HG2	1:J:331:LEU:HA	1.88	0.55
1:J:529:PRO:CG	4:7:353:GLN:OE1	2.54	0.55
1:J:723:ARG:HH11	1:J:723:ARG:CG	2.20	0.55
4:Y:365:ALA:HB3	4:Y:369:ILE:HB	1.88	0.55
1:A:127:ASN:ND2	1:A:128:PRO:HD2	2.16	0.55
1:A:643:GLY:N	4:4:23:GLY:C	2.55	0.55
1:A:723:ARG:CG	1:A:723:ARG:HH11	2.20	0.55
1:G:553:MLY:HG3	4:8:44:MET:O	2.07	0.55
1:G:638:GLY:HA2	4:6:345:ILE:H	1.71	0.55
1:G:723:ARG:HH11	1:G:723:ARG:CG	2.20	0.55
1:J:84:MLY:CH1	1:J:719:ASP:C	2.63	0.55
4:W:365:ALA:HB3	4:W:369:ILE:HB	1.88	0.55
1:A:10:PHE:O	1:A:12:GLU:N	2.41	0.54
1:A:22:LYS:HA	1:A:25:ILE:HB	1.88	0.54
1:A:435:GLU:O	1:A:438:PHE:HB3	2.06	0.54
1:A:630:ALA:HA	4:4:25:ASP:OD2	2.07	0.54
1:A:638:GLY:CA	4:4:345:ILE:H	2.19	0.54
1:A:638:GLY:HA2	4:4:345:ILE:H	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:795:ARG:CG	3:C:118:MET:HE3	2.37	0.54
1:D:305:ILE:HG22	1:D:312:TYR:CE2	2.42	0.54
1:D:635:GLY:HA3	4:5:334:GLU:CG	2.30	0.54
1:D:638:GLY:HA2	4:5:345:ILE:H	1.72	0.54
1:D:788:THR:HG22	3:F:81:GLN:NE2	2.22	0.54
1:D:819:ASN:H	2:E:90:GLY:HA3	1.72	0.54
1:G:508:ILE:HG21	1:G:711:PHE:CZ	2.42	0.54
1:G:649:VAL:HA	1:G:649:VAL:HG23	1.83	0.54
1:J:290:GLN:NE2	1:J:334:THR:OG1	2.40	0.54
1:J:292:MET:HE1	1:J:309:PRO:CD	2.37	0.54
1:J:604:ASN:OD1	1:J:607:VAL:HG23	2.06	0.54
1:J:649:VAL:CG1	1:J:649:VAL:HA	2.35	0.54
4:Z:365:ALA:HB3	4:Z:369:ILE:HB	1.88	0.54
1:A:82:PRO:HD2	1:A:85:TYR:HD2	1.72	0.54
1:A:305:ILE:HG22	1:A:312:TYR:CE2	2.43	0.54
1:A:797:PHE:CG	3:C:149:VAL:HG11	2.35	0.54
3:C:123:VAL:O	3:C:127:MET:HG2	2.06	0.54
1:D:470:PHE:O	1:D:473:ASN:ND2	2.40	0.54
1:D:553:MLY:HG3	4:7:44:MET:O	2.07	0.54
1:D:649:VAL:CG1	1:D:649:VAL:HA	2.35	0.54
1:D:793:ARG:HE	3:F:147:MET:HG2	1.71	0.54
1:D:839:MLY:HH11	2:E:159:HIS:CG	2.30	0.54
3:F:123:VAL:O	3:F:127:MET:HG2	2.07	0.54
1:G:32:PHE:CG	1:G:83:PRO:HD3	2.41	0.54
1:G:78:PHE:HB3	1:G:98:HIS:NE2	2.23	0.54
1:G:126:VAL:HG13	1:G:675:ILE:HG22	1.89	0.54
1:G:735:GLY:O	1:G:743:ALA:HA	1.94	0.54
1:G:751:GLY:CA	3:I:114:LEU:CD1	2.84	0.54
1:G:765:VAL:HG12	1:G:766:PHE:N	2.22	0.54
1:J:470:PHE:O	1:J:473:ASN:ND2	2.40	0.54
1:J:546:THR:HG21	1:J:548:THR:HB	1.88	0.54
1:J:556:ASP:CA	4:V:49:GLN:O	2.51	0.54
1:J:797:PHE:CD2	3:L:126:LEU:CD2	2.91	0.54
4:8:365:ALA:HB3	4:8:369:ILE:HB	1.88	0.54
1:A:78:PHE:HB3	1:A:98:HIS:NE2	2.22	0.54
1:A:126:VAL:HG13	1:A:675:ILE:HG22	1.90	0.54
1:D:22:LYS:O	1:D:26:GLU:HG3	2.07	0.54
1:D:724:TYR:OH	1:D:778:MET:HB2	2.07	0.54
1:G:82:PRO:HD2	1:G:85:TYR:HD2	1.72	0.54
1:G:220:ASP:O	1:G:224:SER:N	2.27	0.54
1:G:530:MET:CB	4:6:354:GLN:HG3	2.37	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:546:THR:HG21	1:G:548:THR:HB	1.88	0.54
3:I:123:VAL:O	3:I:127:MET:HG2	2.07	0.54
1:J:756:THR:HB	1:J:776:GLU:CD	2.28	0.54
4:0:365:ALA:HB3	4:0:369:ILE:HB	1.88	0.54
4:2:365:ALA:HB3	4:2:369:ILE:HB	1.88	0.54
1:A:579:PHE:HE1	1:A:581:LEU:HD13	1.71	0.54
1:D:10:PHE:O	1:D:12:GLU:N	2.41	0.54
1:D:82:PRO:HD2	1:D:85:TYR:HD2	1.72	0.54
1:D:126:VAL:HG13	1:D:675:ILE:HG22	1.90	0.54
1:D:290:GLN:NE2	1:D:334:THR:OG1	2.40	0.54
1:G:38:VAL:CB	1:G:52:ILE:HD11	2.38	0.54
1:G:305:ILE:HG22	1:G:312:TYR:CZ	2.42	0.54
1:G:345:ALA:O	1:G:349:THR:N	2.40	0.54
1:G:783:LEU:HA	1:G:786:ILE:HB	1.87	0.54
1:J:305:ILE:HG22	1:J:312:TYR:CE2	2.43	0.54
2:K:146:GLY:O	2:K:147:ASN:ND2	2.41	0.54
4:4:288:ASP:CA	4:6:204:ALA:HB2	2.31	0.54
2:B:156:VAL:HA	2:B:159:HIS:O	2.07	0.54
1:D:571:ALA:O	1:D:572:LYS:CB	2.56	0.54
1:D:739:ASP:CB	1:D:742:LYS:CB	2.81	0.54
1:G:305:ILE:HG22	1:G:312:TYR:CE2	2.42	0.54
1:G:406:VAL:HG12	1:G:407:GLY:H	1.71	0.54
1:G:529:PRO:CB	4:6:354:GLN:HA	2.37	0.54
1:J:126:VAL:HG13	1:J:675:ILE:HG22	1.90	0.54
1:J:305:ILE:HG22	1:J:312:TYR:CZ	2.42	0.54
1:J:537:GLU:HB3	1:J:648:THR:CB	2.36	0.54
1:J:757:GLN:OE1	1:J:773:GLY:N	2.40	0.54
4:4:365:ALA:HB3	4:4:369:ILE:HB	1.88	0.54
4:6:365:ALA:HB3	4:6:369:ILE:HB	1.88	0.54
1:A:95:THR:OG1	1:A:769:ALA:CA	2.53	0.54
1:A:571:ALA:O	1:A:572:LYS:CB	2.56	0.54
1:A:629:GLU:CB	1:A:643:GLY:C	2.75	0.54
1:A:800:ARG:HH11	3:C:149:VAL:CB	2.20	0.54
1:D:78:PHE:HB3	1:D:98:HIS:NE2	2.22	0.54
1:D:292:MET:HE1	1:D:309:PRO:CD	2.37	0.54
1:D:345:ALA:O	1:D:349:THR:N	2.40	0.54
1:D:630:ALA:HA	4:5:25:ASP:OD2	2.07	0.54
1:D:649:VAL:HA	1:D:649:VAL:HG23	1.82	0.54
1:G:836:PHE:CD2	2:H:160:GLY:N	2.75	0.54
2:H:117:LEU:CG	2:H:147:ASN:OD1	2.52	0.54
1:J:10:PHE:O	1:J:12:GLU:N	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:78:PHE:HB3	1:J:98:HIS:NE2	2.22	0.54
1:J:538:GLU:CG	4:7:351:THR:C	2.73	0.54
1:J:546:THR:HB	1:J:549:SER:H	1.71	0.54
1:J:831:TRP:CZ3	2:K:34:ILE:HG21	2.42	0.54
1:A:642:LYS:HG2	4:4:22:ALA:C	2.28	0.54
1:A:721:LYS:C	1:A:736:GLN:OE1	2.46	0.54
1:D:38:VAL:CB	1:D:52:ILE:HD11	2.38	0.54
1:D:640:LYS:C	4:5:23:GLY:CA	2.64	0.54
1:D:792:ALA:O	3:F:40:ASN:HB3	2.06	0.54
1:G:530:MET:HE3	4:6:354:GLN:CB	2.38	0.54
1:G:725:ARG:HG3	1:G:733:PRO:CA	2.36	0.54
1:G:791:GLN:O	1:G:794:CYS:HB2	2.08	0.54
1:J:22:LYS:O	1:J:26:GLU:HG3	2.07	0.54
1:J:135:TYR:HD2	1:J:191:ARG:HG2	1.72	0.54
1:J:503:TYR:CE1	1:J:711:PHE:CE2	2.94	0.54
1:J:791:GLN:O	1:J:794:CYS:HB2	2.08	0.54
1:A:135:TYR:HD2	1:A:191:ARG:HG2	1.72	0.54
1:A:410:ASN:CG	4:4:334:GLU:C	2.65	0.54
1:A:649:VAL:CG1	1:A:649:VAL:HA	2.35	0.54
1:D:218:LEU:HA	1:D:221:GLN:HG3	1.71	0.54
1:D:218:LEU:CD2	1:D:222:ILE:CG1	2.86	0.54
1:D:721:LYS:C	1:D:736:GLN:OE1	2.46	0.54
1:D:732:ILE:CG2	1:D:747:LEU:HD11	1.26	0.54
1:G:10:PHE:O	1:G:12:GLU:N	2.41	0.54
1:G:292:MET:HE1	1:G:309:PRO:CD	2.37	0.54
1:J:493:HIS:ND1	1:J:514:ASP:OD2	2.41	0.54
1:J:629:GLU:CB	1:J:643:GLY:C	2.76	0.54
1:J:638:GLY:HA2	4:7:345:ILE:H	1.72	0.54
3:L:92:ARG:HA	3:L:139:TYR:OH	2.08	0.54
1:A:305:ILE:HG22	1:A:312:TYR:CZ	2.43	0.54
1:A:470:PHE:O	1:A:473:ASN:ND2	2.40	0.54
1:D:305:ILE:HG22	1:D:312:TYR:CZ	2.43	0.54
1:D:724:TYR:OH	1:D:778:MET:CB	2.56	0.54
2:E:146:GLY:O	2:E:147:ASN:ND2	2.41	0.54
1:G:404:PRO:CG	1:G:417:GLU:HG3	2.38	0.54
1:G:470:PHE:O	1:G:473:ASN:ND2	2.40	0.54
1:G:493:HIS:ND1	1:G:514:ASP:OD2	2.41	0.54
1:G:629:GLU:CB	1:G:643:GLY:C	2.76	0.54
1:A:38:VAL:CB	1:A:52:ILE:HD11	2.38	0.54
1:A:538:GLU:HG3	4:4:352:PHE:CA	2.38	0.54
2:B:146:GLY:O	2:B:147:ASN:ND2	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:507:GLY:CA	1:D:762:HIS:ND1	2.71	0.54
1:D:546:THR:HB	1:D:549:SER:H	1.71	0.54
1:D:765:VAL:HG12	1:D:766:PHE:N	2.22	0.54
1:D:792:ALA:C	3:F:40:ASN:CB	2.69	0.54
1:G:571:ALA:O	1:G:572:LYS:CB	2.56	0.54
1:G:576:GLU:CG	1:G:577:ALA:N	2.43	0.54
1:D:98:HIS:HB3	1:D:100:PRO:CD	2.25	0.53
1:D:793:ARG:HE	3:F:147:MET:CB	2.21	0.53
1:G:539:GLU:OE2	4:8:45:VAL:C	2.47	0.53
1:G:769:ALA:C	1:G:773:GLY:HA3	2.29	0.53
3:I:92:ARG:HA	3:I:139:TYR:OH	2.08	0.53
1:J:38:VAL:CB	1:J:52:ILE:HD11	2.38	0.53
1:J:553:MLY:O	4:V:48:GLY:CA	2.56	0.53
1:J:630:ALA:HA	4:7:25:ASP:OD2	2.07	0.53
1:J:640:LYS:C	4:7:23:GLY:CA	2.64	0.53
1:J:642:LYS:HG2	4:7:22:ALA:C	2.27	0.53
1:J:800:ARG:HB3	3:L:149:VAL:HG23	1.85	0.53
1:A:218:LEU:N	1:A:221:GLN:HG2	2.24	0.53
1:A:404:PRO:CG	1:A:417:GLU:HG3	2.38	0.53
1:A:553:MLY:O	4:6:48:GLY:CA	2.56	0.53
1:A:584:TYR:CD1	1:A:585:ALA:N	2.77	0.53
1:A:836:PHE:CE2	2:B:160:GLY:C	2.82	0.53
1:D:529:PRO:HB2	4:5:354:GLN:HA	1.91	0.53
1:D:629:GLU:CB	1:D:643:GLY:C	2.76	0.53
1:D:815:CYS:O	2:E:90:GLY:HA3	2.08	0.53
1:G:135:TYR:HD2	1:G:191:ARG:HD3	1.73	0.53
1:G:135:TYR:HD2	1:G:191:ARG:HG2	1.73	0.53
1:G:538:GLU:HG3	4:6:352:PHE:CA	2.38	0.53
1:G:640:LYS:C	4:6:23:GLY:CA	2.64	0.53
1:G:795:ARG:HH22	3:I:43:ASN:HB2	1.73	0.53
2:H:146:GLY:O	2:H:147:ASN:ND2	2.41	0.53
1:J:135:TYR:HD2	1:J:191:ARG:HD3	1.73	0.53
1:J:530:MET:HE3	4:7:355:MET:SD	2.48	0.53
1:J:538:GLU:HG3	4:7:352:PHE:CA	2.38	0.53
1:J:707:CYS:C	1:J:714:ARG:HH22	2.11	0.53
4:X:185:LEU:HD23	4:X:306:TYR:OH	2.09	0.53
1:D:508:ILE:HG23	1:D:766:PHE:CD1	2.44	0.53
1:D:723:ARG:CG	1:D:723:ARG:HH11	2.20	0.53
1:G:661:MET:O	1:G:665:ARG:HG3	2.08	0.53
1:J:553:MLY:HG3	4:V:44:MET:O	2.07	0.53
1:J:793:ARG:HG2	3:L:147:MET:HG2	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:135:TYR:HD2	1:A:191:ARG:HD3	1.73	0.53
1:A:800:ARG:HH11	3:C:149:VAL:CA	2.21	0.53
2:B:121:LEU:CA	2:B:128:PHE:CG	2.89	0.53
1:D:553:MLY:O	4:7:48:GLY:CA	2.56	0.53
1:D:579:PHE:HE1	1:D:581:LEU:HD13	1.72	0.53
3:F:35:ARG:HA	3:F:39:GLN:O	2.07	0.53
1:G:732:ILE:H	1:G:733:PRO:HD2	1.74	0.53
1:J:109:ARG:O	1:J:114:MET:N	2.37	0.53
1:J:721:LYS:C	1:J:736:GLN:OE1	2.46	0.53
1:A:295:MLY:HE2	1:A:332:MET:HE1	1.91	0.53
1:A:529:PRO:HB2	4:4:354:GLN:HA	1.91	0.53
1:D:42:HIS:HB3	1:D:45:GLN:O	2.09	0.53
1:D:404:PRO:CG	1:D:417:GLU:HG3	2.38	0.53
1:D:584:TYR:CD1	1:D:585:ALA:N	2.77	0.53
1:D:724:TYR:CA	1:D:782:MLY:HH21	2.38	0.53
2:E:114:LYS:O	2:E:147:ASN:ND2	2.41	0.53
2:E:162:ASP:O	2:K:21:GLU:HB3	2.08	0.53
1:G:730:SER:HB2	3:I:109:HIS:CE1	2.43	0.53
1:G:818:TYR:CD1	2:H:127:ARG:CZ	2.79	0.53
1:J:32:PHE:CD1	1:J:83:PRO:HD3	2.43	0.53
1:J:295:MLY:CG	1:J:332:MET:HE1	2.39	0.53
1:J:404:PRO:CG	1:J:417:GLU:HG3	2.38	0.53
1:J:765:VAL:HG12	1:J:766:PHE:N	2.22	0.53
1:J:834:LEU:HD11	2:K:54:MET:HG3	1.90	0.53
4:V:185:LEU:HD23	4:V:306:TYR:OH	2.09	0.53
1:A:791:GLN:O	1:A:794:CYS:HB2	2.08	0.53
1:D:135:TYR:CD2	1:D:191:ARG:HG2	2.44	0.53
1:D:277:PHE:CG	1:D:278:GLN:N	2.76	0.53
1:D:510:TRP:CZ3	1:D:711:PHE:HE2	2.26	0.53
1:D:830:PRO:HD2	2:E:67:MET:HE2	1.90	0.53
1:G:32:PHE:CD1	1:G:83:PRO:HD3	2.44	0.53
1:G:251:ARG:HB2	1:G:264:ASP:HB2	1.91	0.53
1:G:553:MLY:O	4:8:48:GLY:CA	2.56	0.53
1:G:728:ASN:ND2	3:I:109:HIS:O	2.41	0.53
1:J:571:ALA:O	1:J:572:LYS:CB	2.56	0.53
1:J:584:TYR:CD1	1:J:585:ALA:N	2.77	0.53
1:J:599:ASN:CG	1:J:649:VAL:H	2.12	0.53
1:J:642:LYS:CG	4:7:22:ALA:CA	2.80	0.53
1:J:661:MET:O	1:J:665:ARG:HG3	2.09	0.53
4:3:185:LEU:HD23	4:3:306:TYR:OH	2.09	0.53
4:4:185:LEU:HD23	4:4:306:TYR:OH	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:22:LYS:O	1:A:26:GLU:N	2.30	0.53
1:A:42:HIS:HB3	1:A:45:GLN:O	2.09	0.53
1:D:135:TYR:HD2	1:D:191:ARG:HD3	1.73	0.53
1:G:149:GLN:OE1	1:G:762:HIS:HB3	2.09	0.53
1:G:277:PHE:CG	1:G:278:GLN:N	2.76	0.53
1:G:817:GLN:HB3	2:H:127:ARG:NH1	2.17	0.53
1:J:22:LYS:O	1:J:26:GLU:N	2.29	0.53
1:J:218:LEU:N	1:J:221:GLN:HG2	2.24	0.53
2:K:121:LEU:CA	2:K:128:PHE:CG	2.89	0.53
1:A:156:PHE:HD1	1:A:195:TYR:CD1	2.27	0.53
1:A:217:THR:C	1:A:221:GLN:NE2	2.62	0.53
1:A:493:HIS:ND1	1:A:514:ASP:OD2	2.41	0.53
1:A:539:GLU:OE2	4:6:45:VAL:C	2.48	0.53
1:A:579:PHE:CD2	1:A:592:ILE:HD11	2.40	0.53
1:A:739:ASP:CB	1:A:742:LYS:CB	2.81	0.53
1:D:32:PHE:CD1	1:D:83:PRO:HD3	2.43	0.53
1:D:642:LYS:HG2	4:5:22:ALA:C	2.27	0.53
1:D:661:MET:O	1:D:665:ARG:HG3	2.09	0.53
1:D:793:ARG:NE	3:F:147:MET:HG2	2.23	0.53
1:G:292:MET:CE	1:G:309:PRO:HA	2.39	0.53
1:G:636:LYS:HB2	4:6:334:GLU:OE1	2.09	0.53
1:G:797:PHE:CE2	3:I:126:LEU:CD2	2.92	0.53
1:G:798:LEU:HD21	3:I:126:LEU:HG	1.90	0.53
2:H:114:LYS:O	2:H:147:ASN:ND2	2.41	0.53
1:J:295:MLY:HE2	1:J:332:MET:HE1	1.91	0.53
1:J:404:PRO:HG3	1:J:417:GLU:HG3	1.91	0.53
2:K:114:LYS:O	2:K:147:ASN:ND2	2.41	0.53
3:L:53:PRO:HB2	3:L:55:LYS:HG3	1.91	0.53
1:A:502:GLU:OE1	1:A:763:THR:CA	2.57	0.53
1:D:599:ASN:CG	1:D:649:VAL:H	2.12	0.53
1:D:796:GLY:CA	3:F:40:ASN:OD1	2.52	0.53
2:E:114:LYS:N	2:E:146:GLY:O	2.40	0.53
3:F:92:ARG:HA	3:F:139:TYR:OH	2.08	0.53
1:G:218:LEU:N	1:G:221:GLN:HG2	2.24	0.53
1:G:295:MLY:HE2	1:G:332:MET:HE1	1.91	0.53
3:I:53:PRO:HB2	3:I:55:LYS:HG3	1.91	0.53
1:J:251:ARG:HB2	1:J:264:ASP:HB2	1.91	0.53
1:J:529:PRO:HB2	4:7:354:GLN:HA	1.91	0.53
1:J:612:GLN:HE22	1:J:627:GLY:HA2	1.66	0.53
2:K:129:THR:O	2:K:133:ILE:HG13	2.09	0.53
4:5:185:LEU:HD23	4:5:306:TYR:OH	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:X:287:ILE:HG22	4:Z:204:ALA:HB3	1.91	0.53
1:A:32:PHE:CD1	1:A:83:PRO:HD3	2.44	0.53
1:A:135:TYR:CD2	1:A:191:ARG:HG2	2.44	0.53
1:A:732:ILE:H	1:A:733:PRO:HD2	1.74	0.53
1:D:493:HIS:ND1	1:D:514:ASP:OD2	2.41	0.53
1:D:834:LEU:HD13	2:E:51:PHE:CD1	2.39	0.53
2:E:129:THR:O	2:E:133:ILE:HG13	2.09	0.53
1:G:534:SER:C	4:6:351:THR:CA	2.48	0.53
1:G:642:LYS:HG2	4:6:22:ALA:C	2.27	0.53
1:G:721:LYS:C	1:G:736:GLN:OE1	2.46	0.53
1:J:418:THR:CB	1:J:421:GLU:HG3	2.37	0.53
4:1:185:LEU:HD23	4:1:306:TYR:OH	2.09	0.53
4:Z:185:LEU:HD23	4:Z:306:TYR:OH	2.09	0.53
1:A:599:ASN:CG	1:A:649:VAL:H	2.12	0.52
1:A:661:MET:O	1:A:665:ARG:HG3	2.09	0.52
1:D:154:HIS:CE1	1:D:156:PHE:HD2	2.27	0.52
1:D:218:LEU:N	1:D:221:GLN:HG2	2.24	0.52
1:D:404:PRO:HG3	1:D:417:GLU:HG3	1.91	0.52
1:D:494:HIS:O	1:D:498:LEU:HB2	2.09	0.52
1:D:556:ASP:HB3	4:7:43:VAL:HG12	1.91	0.52
1:D:642:LYS:CG	4:5:22:ALA:CA	2.80	0.52
1:D:732:ILE:H	1:D:733:PRO:HD2	1.74	0.52
1:D:800:ARG:CG	3:F:149:VAL:HG22	2.37	0.52
1:G:579:PHE:CD2	1:G:592:ILE:HD11	2.39	0.52
1:G:634:GLY:N	4:6:25:ASP:O	2.31	0.52
1:J:197:ALA:O	1:J:201:ALA:HB2	2.09	0.52
1:J:510:TRP:CD2	1:J:768:MLY:CH1	2.92	0.52
1:J:707:CYS:HG	1:J:714:ARG:HH12	1.45	0.52
4:2:185:LEU:HD23	4:2:306:TYR:OH	2.09	0.52
4:3:180:LEU:HD22	4:3:267:ILE:HD11	1.92	0.52
4:V:287:ILE:HG22	4:X:204:ALA:HB3	1.91	0.52
1:A:555:TYR:N	4:6:48:GLY:N	2.58	0.52
1:D:538:GLU:HG3	4:5:352:PHE:CA	2.38	0.52
1:D:791:GLN:O	1:D:794:CYS:HB2	2.08	0.52
1:G:63:MLY:HG3	1:G:64:THR:H	1.75	0.52
1:G:404:PRO:HG3	1:G:417:GLU:HG3	1.91	0.52
1:G:584:TYR:CD1	1:G:585:ALA:N	2.77	0.52
1:G:599:ASN:CG	1:G:649:VAL:H	2.12	0.52
1:G:642:LYS:CG	4:6:22:ALA:HA	2.37	0.52
4:0:287:ILE:HG22	4:2:204:ALA:HB3	1.91	0.52
4:1:285:CYS:O	4:1:290:ARG:NH1	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:2:180:LEU:HD22	4:2:267:ILE:HD11	1.92	0.52
4:2:288:ASP:CA	4:4:204:ALA:HB2	2.31	0.52
4:6:185:LEU:HD23	4:6:306:TYR:OH	2.09	0.52
4:7:287:ILE:HG22	4:V:204:ALA:HB3	1.91	0.52
4:8:185:LEU:HD23	4:8:306:TYR:OH	2.09	0.52
4:W:185:LEU:HD23	4:W:306:TYR:OH	2.09	0.52
1:A:277:PHE:CG	1:A:278:GLN:N	2.76	0.52
1:A:732:ILE:HG23	1:A:747:LEU:CD1	1.04	0.52
1:D:418:THR:CB	1:D:421:GLU:HG3	2.37	0.52
1:D:636:LYS:HB2	4:5:334:GLU:OE1	2.09	0.52
1:D:725:ARG:HG3	1:D:733:PRO:CA	2.36	0.52
1:G:84:MLY:CH1	1:G:720:PHE:N	2.72	0.52
1:J:84:MLY:HH11	1:J:720:PHE:N	2.24	0.52
1:J:135:TYR:CD2	1:J:191:ARG:HG2	2.44	0.52
1:J:220:ASP:O	1:J:224:SER:N	2.27	0.52
1:J:277:PHE:CG	1:J:278:GLN:N	2.76	0.52
1:J:732:ILE:HG23	1:J:747:LEU:CD1	1.05	0.52
1:J:797:PHE:CG	3:L:149:VAL:CG1	2.80	0.52
2:K:114:LYS:HA	2:K:147:ASN:HD22	1.74	0.52
4:6:180:LEU:HD22	4:6:267:ILE:HD11	1.92	0.52
4:7:285:CYS:O	4:7:290:ARG:NH1	2.43	0.52
4:W:285:CYS:O	4:W:290:ARG:NH1	2.43	0.52
4:X:285:CYS:O	4:X:290:ARG:NH1	2.43	0.52
4:Y:185:LEU:HD23	4:Y:306:TYR:OH	2.09	0.52
4:Y:285:CYS:O	4:Y:290:ARG:NH1	2.43	0.52
4:Z:285:CYS:O	4:Z:290:ARG:NH1	2.43	0.52
1:A:504:MLY:HB2	1:A:762:HIS:NE2	2.24	0.52
1:A:636:LYS:HB2	4:4:334:GLU:OE1	2.08	0.52
1:A:798:LEU:HD22	3:C:126:LEU:HD11	1.90	0.52
3:C:104:GLY:HA2	3:C:137:ILE:HD11	1.91	0.52
1:D:128:PRO:O	1:D:129:TYR:HB2	2.09	0.52
1:D:538:GLU:CG	4:5:351:THR:C	2.74	0.52
1:J:98:HIS:HB3	1:J:100:PRO:CD	2.25	0.52
1:J:156:PHE:HD1	1:J:195:TYR:CD1	2.27	0.52
1:J:642:LYS:CA	4:7:22:ALA:C	2.70	0.52
4:5:180:LEU:HD22	4:5:267:ILE:HD11	1.92	0.52
4:5:287:ILE:HG22	4:7:204:ALA:HB3	1.91	0.52
4:6:285:CYS:O	4:6:290:ARG:NH1	2.43	0.52
4:7:185:LEU:HD23	4:7:306:TYR:OH	2.09	0.52
4:W:180:LEU:HD22	4:W:267:ILE:HD11	1.92	0.52
1:A:63:MLY:HG3	1:A:64:THR:H	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:109:ARG:HD3	1:A:117:THR:HB	1.92	0.52
1:A:556:ASP:HB3	4:6:43:VAL:HG12	1.91	0.52
1:D:732:ILE:H	1:D:733:PRO:CD	2.23	0.52
1:G:217:THR:C	1:G:221:GLN:NE2	2.62	0.52
1:G:530:MET:HG2	4:6:354:GLN:HB2	0.57	0.52
1:J:759:ALA:O	1:J:766:PHE:N	2.32	0.52
1:J:795:ARG:HD3	3:L:35:ARG:NH2	1.91	0.52
1:J:795:ARG:CB	3:L:35:ARG:NH2	2.73	0.52
2:K:112:ILE:C	2:K:147:ASN:O	2.42	0.52
3:L:104:GLY:HA2	3:L:137:ILE:HD11	1.92	0.52
3:L:110:VAL:HG13	3:L:114:LEU:HD12	1.92	0.52
4:5:285:CYS:O	4:5:290:ARG:NH1	2.43	0.52
4:V:180:LEU:HD22	4:V:267:ILE:HD11	1.92	0.52
4:Y:180:LEU:HD22	4:Y:267:ILE:HD11	1.92	0.52
1:A:154:HIS:CE1	1:A:156:PHE:HD2	2.27	0.52
1:A:404:PRO:HG3	1:A:417:GLU:HG3	1.91	0.52
1:A:494:HIS:O	1:A:498:LEU:HB2	2.09	0.52
1:A:732:ILE:H	1:A:733:PRO:CD	2.23	0.52
1:A:788:THR:CG2	3:C:42:THR:HG21	2.40	0.52
1:A:795:ARG:HG2	3:C:118:MET:HE3	1.90	0.52
3:F:104:GLY:HA2	3:F:137:ILE:HD11	1.92	0.52
1:G:41:VAL:HG13	1:G:42:HIS:N	2.25	0.52
1:G:42:HIS:HB3	1:G:45:GLN:O	2.09	0.52
1:G:109:ARG:HD3	1:G:117:THR:HB	1.92	0.52
1:G:510:TRP:CH2	1:G:768:MLY:HH11	2.39	0.52
1:G:732:ILE:HG23	1:G:747:LEU:CD1	1.04	0.52
2:H:114:LYS:HA	2:H:147:ASN:HD22	1.75	0.52
1:J:556:ASP:HB3	4:V:43:VAL:HG12	1.91	0.52
4:0:180:LEU:HD22	4:0:267:ILE:HD11	1.92	0.52
4:1:180:LEU:HD22	4:1:267:ILE:HD11	1.92	0.52
4:2:287:ILE:HG22	4:4:204:ALA:HB3	1.91	0.52
4:4:180:LEU:HD22	4:4:267:ILE:HD11	1.92	0.52
4:8:285:CYS:O	4:8:290:ARG:NH1	2.43	0.52
4:X:180:LEU:HD22	4:X:267:ILE:HD11	1.92	0.52
1:A:212:GLY:O	1:A:213:LYS:HB2	2.10	0.52
1:A:800:ARG:HB3	3:C:149:VAL:HG23	1.73	0.52
3:C:52:ASN:HB2	3:C:53:PRO:CD	2.28	0.52
3:C:53:PRO:HB2	3:C:55:LYS:HG3	1.91	0.52
3:C:92:ARG:HA	3:C:139:TYR:OH	2.09	0.52
1:D:41:VAL:HG13	1:D:42:HIS:N	2.25	0.52
1:D:156:PHE:HD1	1:D:195:TYR:CD1	2.28	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:491:PHE:HD1	1:D:671:PHE:CE2	2.27	0.52
1:D:538:GLU:HA	4:5:349:LEU:CB	2.40	0.52
1:G:40:VAL:HG13	1:G:41:VAL:O	2.10	0.52
1:G:128:PRO:O	1:G:129:TYR:HB2	2.09	0.52
1:G:135:TYR:CD2	1:G:191:ARG:HG2	2.44	0.52
1:G:154:HIS:CE1	1:G:156:PHE:HD2	2.26	0.52
1:G:529:PRO:HB2	4:6:354:GLN:HA	1.92	0.52
1:G:793:ARG:HH11	3:I:40:ASN:HD21	1.56	0.52
1:J:41:VAL:HG13	1:J:42:HIS:N	2.25	0.52
1:J:42:HIS:HB3	1:J:45:GLN:O	2.09	0.52
1:J:530:MET:HG2	4:7:354:GLN:HB2	0.57	0.52
1:J:817:GLN:HG3	2:K:128:PHE:CZ	2.45	0.52
4:0:185:LEU:HD23	4:0:306:TYR:OH	2.09	0.52
4:2:285:CYS:O	4:2:290:ARG:NH1	2.43	0.52
4:3:287:ILE:HG22	4:5:204:ALA:HB3	1.91	0.52
1:A:218:LEU:CD2	1:A:222:ILE:CG1	2.85	0.52
1:A:491:PHE:HD1	1:A:671:PHE:CE2	2.27	0.52
1:A:795:ARG:CD	3:C:43:ASN:OD1	2.58	0.52
1:A:798:LEU:HD11	3:C:126:LEU:HG	1.90	0.52
1:D:839:MLY:HH11	2:E:159:HIS:HB3	1.87	0.52
3:F:53:PRO:HB2	3:F:55:LYS:HG3	1.91	0.52
1:G:156:PHE:HD1	1:G:195:TYR:CD1	2.27	0.52
1:G:197:ALA:O	1:G:201:ALA:HB2	2.09	0.52
1:G:491:PHE:HD1	1:G:671:PHE:CE2	2.27	0.52
1:J:555:TYR:N	4:V:48:GLY:N	2.58	0.52
1:J:642:LYS:HG2	4:7:21:PHE:C	2.29	0.52
4:7:180:LEU:HD22	4:7:267:ILE:HD11	1.92	0.52
4:8:287:ILE:HG22	4:W:204:ALA:HB3	1.91	0.52
4:V:285:CYS:O	4:V:290:ARG:NH1	2.43	0.52
4:Z:180:LEU:HD22	4:Z:267:ILE:HD11	1.92	0.52
1:A:251:ARG:HB2	1:A:264:ASP:HB2	1.91	0.52
1:D:63:MLY:HG3	1:D:64:THR:H	1.75	0.52
1:D:251:ARG:HB2	1:D:264:ASP:HB2	1.91	0.52
1:D:830:PRO:CD	2:E:67:MET:HE2	2.38	0.52
3:F:110:VAL:HG13	3:F:114:LEU:HD12	1.91	0.52
1:J:128:PRO:O	1:J:129:TYR:HB2	2.09	0.52
1:J:154:HIS:CE1	1:J:156:PHE:HD2	2.26	0.52
4:0:285:CYS:O	4:0:290:ARG:NH1	2.43	0.52
4:8:180:LEU:HD22	4:8:267:ILE:HD11	1.92	0.52
4:W:287:ILE:HG22	4:Y:204:ALA:HB3	1.91	0.52
1:A:40:VAL:HG13	1:A:41:VAL:O	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:292:MET:CE	1:A:309:PRO:HA	2.39	0.52
1:A:797:PHE:CD1	3:C:149:VAL:HG12	2.20	0.52
2:B:129:THR:O	2:B:133:ILE:HG13	2.09	0.52
1:D:41:VAL:HG21	1:D:76:GLN:HG3	1.92	0.52
1:D:109:ARG:HD3	1:D:117:THR:HB	1.92	0.52
1:D:195:TYR:CE2	1:D:199:ILE:CD1	2.93	0.52
1:D:642:LYS:HG2	4:5:21:PHE:C	2.30	0.52
1:D:733:PRO:O	1:D:737:PHE:CE1	2.53	0.52
1:G:481:ASN:N	1:G:481:ASN:ND2	2.51	0.52
1:G:494:HIS:O	1:G:498:LEU:HB2	2.09	0.52
1:G:556:ASP:HB3	4:8:43:VAL:HG12	1.92	0.52
1:J:90:ASP:OD2	1:J:764:MLY:HH21	2.08	0.52
1:J:135:TYR:HD2	1:J:191:ARG:CD	2.23	0.52
1:J:232:PHE:CE1	1:J:287:ILE:HD13	2.44	0.52
1:J:491:PHE:HD1	1:J:671:PHE:CE2	2.27	0.52
1:J:510:TRP:CE2	1:J:768:MLY:HH13	2.45	0.52
1:J:553:MLY:CE	4:V:45:VAL:CA	2.49	0.52
1:J:636:LYS:HB2	4:7:334:GLU:OE1	2.09	0.52
1:J:642:LYS:HB2	4:7:24:ASP:O	1.89	0.52
3:L:100:GLY:O	3:L:138:ASN:HA	2.10	0.52
1:A:135:TYR:HD2	1:A:191:ARG:CD	2.23	0.51
1:A:538:GLU:HA	4:4:349:LEU:CB	2.39	0.51
1:A:578:HIS:O	1:A:579:PHE:HB3	2.11	0.51
1:A:642:LYS:CG	4:4:22:ALA:HA	2.38	0.51
1:A:725:ARG:O	1:A:729:ALA:HA	2.10	0.51
2:B:114:LYS:O	2:B:147:ASN:ND2	2.41	0.51
1:D:40:VAL:HG13	1:D:41:VAL:O	2.10	0.51
1:D:410:ASN:CG	4:5:334:GLU:C	2.65	0.51
1:D:555:TYR:N	4:7:48:GLY:N	2.58	0.51
2:E:114:LYS:HA	2:E:147:ASN:HD22	1.74	0.51
1:G:221:GLN:HB2	1:G:449:LEU:HD11	1.92	0.51
2:H:129:THR:O	2:H:133:ILE:HG13	2.09	0.51
3:I:110:VAL:HG13	3:I:114:LEU:HD12	1.91	0.51
1:J:40:VAL:HG13	1:J:41:VAL:O	2.10	0.51
1:J:221:GLN:HB2	1:J:449:LEU:HD11	1.92	0.51
1:J:292:MET:CE	1:J:309:PRO:HA	2.40	0.51
1:J:539:GLU:OE2	4:V:45:VAL:C	2.47	0.51
4:4:287:ILE:HG22	4:6:204:ALA:HB3	1.91	0.51
1:D:221:GLN:HB2	1:D:449:LEU:HD11	1.92	0.51
1:D:813:ILE:CB	2:E:127:ARG:NH1	2.73	0.51
1:G:93:MET:CG	1:G:716:LEU:HD12	2.39	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:727:LEU:O	3:I:113:THR:CB	2.58	0.51
1:J:63:MLY:HG3	1:J:64:THR:H	1.75	0.51
1:J:494:HIS:O	1:J:498:LEU:HB2	2.09	0.51
1:J:538:GLU:HA	4:7:349:LEU:CB	2.40	0.51
1:A:97:LEU:CD2	1:A:712:PRO:CB	2.88	0.51
1:A:408:VAL:CG1	4:4:332:PRO:HB3	2.40	0.51
1:A:501:GLU:C	1:A:762:HIS:CE1	2.84	0.51
1:A:530:MET:HG2	4:4:354:GLN:HB2	0.57	0.51
1:A:530:MET:CE	4:4:354:GLN:HG3	2.35	0.51
2:B:114:LYS:HA	2:B:147:ASN:HD22	1.74	0.51
1:D:295:MLY:HE2	1:D:332:MET:HE1	1.91	0.51
3:F:100:GLY:O	3:F:138:ASN:HA	2.11	0.51
1:G:232:PHE:CE1	1:G:287:ILE:HD13	2.45	0.51
1:G:559:LEU:HD23	1:G:559:LEU:C	2.31	0.51
1:G:762:HIS:CD2	1:G:762:HIS:N	2.78	0.51
1:J:195:TYR:CE2	1:J:199:ILE:CD1	2.93	0.51
1:A:221:GLN:HB2	1:A:449:LEU:HD11	1.92	0.51
1:A:232:PHE:CE1	1:A:287:ILE:HD13	2.45	0.51
1:A:546:THR:CG2	1:A:548:THR:HB	2.41	0.51
1:A:592:ILE:O	1:A:592:ILE:HG22	2.11	0.51
1:D:248:MLY:N	1:D:463:ASP:O	2.44	0.51
1:D:642:LYS:CA	4:5:22:ALA:C	2.71	0.51
1:G:538:GLU:HA	4:6:349:LEU:CB	2.40	0.51
1:G:546:THR:CG2	1:G:548:THR:HB	2.41	0.51
1:J:248:MLY:N	1:J:463:ASP:O	2.44	0.51
1:J:640:LYS:CA	1:J:645:SER:OG	2.58	0.51
1:J:818:TYR:CD1	2:K:127:ARG:NH1	2.78	0.51
4:1:287:ILE:HG22	4:3:204:ALA:HB3	1.91	0.51
4:3:285:CYS:O	4:3:290:ARG:NH1	2.43	0.51
1:A:195:TYR:CE2	1:A:199:ILE:CD1	2.93	0.51
1:D:232:PHE:CE1	1:D:287:ILE:HD13	2.45	0.51
1:D:538:GLU:CD	4:5:355:MET:HE3	2.29	0.51
1:G:195:TYR:CE2	1:G:199:ILE:CD1	2.93	0.51
1:G:411:GLU:H	4:6:333:PRO:CG	2.24	0.51
1:G:418:THR:O	1:G:422:VAL:HG23	2.11	0.51
1:G:578:HIS:O	1:G:579:PHE:HB3	2.11	0.51
3:I:100:GLY:O	3:I:138:ASN:HA	2.11	0.51
3:I:104:GLY:HA2	3:I:137:ILE:HD11	1.92	0.51
1:J:13:ALA:C	1:J:15:PRO:HD2	2.31	0.51
1:J:212:GLY:O	1:J:213:LYS:HB2	2.11	0.51
1:J:418:THR:O	1:J:422:VAL:HG23	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:578:HIS:O	1:J:579:PHE:HB3	2.11	0.51
1:J:687:GLU:O	1:J:691:VAL:HG23	2.11	0.51
4:4:285:CYS:O	4:4:290:ARG:NH1	2.43	0.51
1:A:38:VAL:CG1	1:A:39:PHE:N	2.74	0.51
1:A:41:VAL:HG13	1:A:42:HIS:N	2.25	0.51
1:A:248:MLY:N	1:A:463:ASP:O	2.44	0.51
1:A:559:LEU:HD23	1:A:559:LEU:C	2.31	0.51
1:A:814:PHE:CA	2:B:127:ARG:NH2	2.67	0.51
1:D:197:ALA:O	1:D:201:ALA:HB2	2.10	0.51
2:E:112:ILE:HG23	2:E:147:ASN:HB3	1.93	0.51
1:G:248:MLY:N	1:G:463:ASP:O	2.44	0.51
1:G:675:ILE:CG2	1:G:676:ILE:N	2.74	0.51
1:G:826:VAL:HG21	2:H:88:LEU:HD21	1.93	0.51
4:6:287:ILE:HG22	4:8:204:ALA:HB3	1.91	0.51
1:A:418:THR:O	1:A:422:VAL:HG23	2.11	0.51
1:A:757:GLN:HG3	1:A:771:LEU:CD1	2.30	0.51
1:D:237:THR:O	1:D:240:ASN:O	2.29	0.51
1:D:400:ALA:HB1	1:D:606:THR:HG22	1.92	0.51
1:D:411:GLU:H	4:5:333:PRO:CG	2.24	0.51
1:G:38:VAL:CG1	1:G:39:PHE:N	2.74	0.51
1:G:41:VAL:HG21	1:G:76:GLN:HG3	1.93	0.51
1:G:311:ASP:HB2	1:G:312:TYR:CE1	2.46	0.51
1:J:90:ASP:CG	1:J:764:MLY:CH2	2.79	0.51
1:J:202:SER:HB2	1:J:207:LYS:NZ	2.26	0.51
1:J:592:ILE:HG22	1:J:592:ILE:O	2.10	0.51
1:J:818:TYR:OH	2:K:127:ARG:NH2	2.35	0.51
2:K:114:LYS:N	2:K:146:GLY:O	2.40	0.51
1:A:400:ALA:HB1	1:A:606:THR:HG22	1.92	0.51
1:A:631:GLU:C	4:4:25:ASP:HB2	2.31	0.51
1:D:13:ALA:C	1:D:15:PRO:HD2	2.31	0.51
1:D:135:TYR:HD2	1:D:191:ARG:CD	2.23	0.51
1:D:217:THR:C	1:D:221:GLN:NE2	2.62	0.51
1:D:553:MLY:CE	4:7:45:VAL:CA	2.49	0.51
1:D:592:ILE:O	1:D:592:ILE:HG22	2.10	0.51
1:G:13:ALA:C	1:G:15:PRO:HD2	2.31	0.51
1:G:400:ALA:HB1	1:G:606:THR:HG22	1.93	0.51
1:G:631:GLU:C	4:6:25:ASP:HB2	2.31	0.51
1:G:725:ARG:O	1:G:729:ALA:HA	2.10	0.51
1:J:41:VAL:HG21	1:J:76:GLN:HG3	1.93	0.51
1:J:742:LYS:O	1:J:745:GLU:HB2	2.10	0.51
1:A:506:GLU:OE1	1:A:761:GLY:N	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:110:VAL:HG13	3:C:114:LEU:HD12	1.92	0.51
1:D:202:SER:HB2	1:D:207:LYS:NZ	2.26	0.51
1:D:530:MET:HG2	4:5:354:GLN:HB2	0.57	0.51
1:D:687:GLU:O	1:D:691:VAL:HG23	2.11	0.51
1:D:815:CYS:O	2:E:90:GLY:CA	2.59	0.51
2:E:121:LEU:HA	2:E:128:PHE:CD2	2.46	0.51
1:G:267:THR:HG21	1:G:438:PHE:HE2	1.76	0.51
1:J:649:VAL:HA	1:J:649:VAL:HG23	1.83	0.51
4:7:288:ASP:CA	4:V:204:ALA:HB2	2.31	0.51
1:A:128:PRO:O	1:A:129:TYR:HB2	2.09	0.51
1:A:197:ALA:O	1:A:201:ALA:HB2	2.10	0.51
1:A:311:ASP:HB2	1:A:312:TYR:CE1	2.46	0.51
1:D:38:VAL:CG1	1:D:39:PHE:N	2.74	0.51
1:D:632:GLY:HA3	1:D:643:GLY:N	2.17	0.51
1:D:725:ARG:O	1:D:729:ALA:HA	2.10	0.51
1:G:212:GLY:O	1:G:213:LYS:HB2	2.10	0.51
2:H:114:LYS:N	2:H:146:GLY:O	2.40	0.51
1:J:169:ASP:N	1:J:169:ASP:OD1	2.44	0.51
1:J:768:MLY:HH21	1:J:772:LEU:HD13	1.93	0.51
1:A:556:ASP:CA	4:6:49:GLN:O	2.52	0.50
1:A:640:LYS:CA	1:A:645:SER:OG	2.58	0.50
1:A:646:PHE:CE2	1:A:652:LEU:CD2	2.87	0.50
1:A:675:ILE:CG2	1:A:676:ILE:N	2.74	0.50
1:A:822:SER:HB3	2:B:88:LEU:CD2	2.41	0.50
1:D:212:GLY:O	1:D:213:LYS:HB2	2.11	0.50
1:D:218:LEU:N	1:D:221:GLN:CG	2.74	0.50
1:D:578:HIS:O	1:D:579:PHE:HB3	2.10	0.50
1:G:429:LEU:O	1:G:433:VAL:HG23	2.11	0.50
1:G:797:PHE:CD2	3:I:126:LEU:CD2	2.93	0.50
1:J:109:ARG:HD3	1:J:117:THR:HB	1.92	0.50
1:J:408:VAL:CG1	4:7:332:PRO:HB3	2.40	0.50
1:J:632:GLY:HA3	1:J:643:GLY:N	2.17	0.50
1:J:733:PRO:O	1:J:737:PHE:CE1	2.53	0.50
1:A:41:VAL:HG21	1:A:76:GLN:HG3	1.92	0.50
1:A:687:GLU:O	1:A:691:VAL:HG23	2.11	0.50
1:D:546:THR:CG2	1:D:548:THR:HB	2.41	0.50
1:D:559:LEU:HD23	1:D:559:LEU:C	2.31	0.50
1:D:631:GLU:C	4:5:25:ASP:HB2	2.31	0.50
1:D:818:TYR:CG	2:E:89:LYS:CB	2.93	0.50
1:D:818:TYR:HB3	2:E:90:GLY:N	2.26	0.50
1:G:135:TYR:HD2	1:G:191:ARG:CD	2.23	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:218:LEU:N	1:G:221:GLN:CG	2.74	0.50
1:G:730:SER:CB	3:I:109:HIS:CE1	2.94	0.50
1:J:218:LEU:N	1:J:221:GLN:CG	2.74	0.50
1:J:237:THR:O	1:J:240:ASN:O	2.29	0.50
1:A:629:GLU:CB	1:A:645:SER:N	2.74	0.50
1:A:759:ALA:O	1:A:766:PHE:N	2.32	0.50
1:D:169:ASP:OD1	1:D:169:ASP:N	2.44	0.50
1:D:418:THR:O	1:D:422:VAL:HG23	2.11	0.50
1:D:723:ARG:C	1:D:782:MLY:NZ	2.65	0.50
1:D:742:LYS:O	1:D:745:GLU:HB2	2.10	0.50
1:G:202:SER:HB2	1:G:207:LYS:NZ	2.26	0.50
1:G:237:THR:O	1:G:240:ASN:O	2.29	0.50
1:G:555:TYR:N	4:8:48:GLY:N	2.59	0.50
1:J:411:GLU:H	4:7:333:PRO:CG	2.25	0.50
1:J:646:PHE:HE2	1:J:652:LEU:CG	2.25	0.50
1:J:725:ARG:O	1:J:729:ALA:HA	2.10	0.50
1:J:732:ILE:H	1:J:733:PRO:CD	2.23	0.50
1:J:823:PHE:HE1	2:K:156:VAL:O	1.88	0.50
1:A:13:ALA:C	1:A:15:PRO:HD2	2.31	0.50
1:A:169:ASP:OD1	1:A:169:ASP:N	2.44	0.50
1:A:267:THR:HG21	1:A:438:PHE:HE2	1.76	0.50
1:A:817:GLN:CG	2:B:127:ARG:HG2	2.41	0.50
1:A:839:MLY:HD3	2:B:159:HIS:CB	2.40	0.50
1:D:154:HIS:CD2	1:D:155:ILE:H	2.30	0.50
1:G:538:GLU:OE1	4:6:351:THR:HB	2.12	0.50
1:G:732:ILE:H	1:G:733:PRO:CD	2.23	0.50
1:G:797:PHE:CE2	3:I:126:LEU:HD23	2.45	0.50
1:G:800:ARG:CZ	3:I:149:VAL:HG22	2.30	0.50
1:J:154:HIS:CD2	1:J:155:ILE:H	2.30	0.50
1:J:278:GLN:HG3	1:J:318:GLY:H	1.75	0.50
1:J:311:ASP:HB2	1:J:312:TYR:CE1	2.46	0.50
1:J:346:ASP:O	1:J:349:THR:HB	2.12	0.50
1:J:629:GLU:CB	1:J:645:SER:N	2.73	0.50
1:J:631:GLU:C	4:7:25:ASP:HB2	2.31	0.50
1:J:733:PRO:CA	1:J:737:PHE:CE1	2.95	0.50
3:C:100:GLY:O	3:C:138:ASN:HA	2.11	0.50
1:D:311:ASP:HB2	1:D:312:TYR:CE1	2.46	0.50
1:D:346:ASP:O	1:D:349:THR:HB	2.11	0.50
1:D:429:LEU:O	1:D:433:VAL:HG23	2.11	0.50
1:D:646:PHE:HE2	1:D:652:LEU:CG	2.25	0.50
1:G:687:GLU:O	1:G:691:VAL:HG23	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:733:PRO:O	1:G:737:PHE:CE1	2.53	0.50
1:G:742:LYS:O	1:G:745:GLU:HB2	2.10	0.50
1:A:715:VAL:O	1:A:764:MLY:HB3	2.12	0.50
1:A:732:ILE:O	1:A:736:GLN:HG3	2.12	0.50
1:D:507:GLY:O	1:D:761:GLY:C	2.49	0.50
1:D:640:LYS:CA	1:D:645:SER:OG	2.58	0.50
1:D:715:VAL:O	1:D:764:MLY:HB3	2.12	0.50
1:D:732:ILE:HG23	1:D:747:LEU:HD12	0.94	0.50
1:G:149:GLN:OE1	1:G:762:HIS:CB	2.59	0.50
1:G:592:ILE:HG22	1:G:592:ILE:O	2.10	0.50
1:G:640:LYS:CA	1:G:645:SER:OG	2.58	0.50
1:G:715:VAL:O	1:G:764:MLY:HB3	2.12	0.50
1:J:400:ALA:HB1	1:J:606:THR:HG22	1.93	0.50
1:J:538:GLU:CD	4:7:355:MET:HE3	2.30	0.50
1:J:792:ALA:CB	3:L:40:ASN:CB	2.52	0.50
2:K:112:ILE:HG23	2:K:147:ASN:HB3	1.93	0.50
1:A:218:LEU:N	1:A:221:GLN:CG	2.74	0.50
1:A:237:THR:O	1:A:240:ASN:O	2.29	0.50
1:A:601:ASP:N	1:A:602:PRO:CD	2.75	0.50
1:A:742:LYS:O	1:A:745:GLU:HB2	2.10	0.50
1:D:278:GLN:HG3	1:D:318:GLY:H	1.75	0.50
1:D:629:GLU:CA	1:D:643:GLY:C	2.73	0.50
1:D:795:ARG:HB3	3:F:35:ARG:HD3	1.91	0.50
1:D:798:LEU:HD11	3:F:126:LEU:CD2	2.19	0.50
1:G:218:LEU:CD2	1:G:222:ILE:CG1	2.85	0.50
1:G:291:ILE:HA	1:G:331:LEU:CD1	2.39	0.50
1:G:646:PHE:CE2	1:G:652:LEU:CD2	2.87	0.50
1:J:429:LEU:O	1:J:433:VAL:HG23	2.12	0.50
1:J:546:THR:CG2	1:J:548:THR:HB	2.41	0.50
1:J:559:LEU:HD23	1:J:559:LEU:C	2.31	0.50
1:J:839:MLY:HB2	1:J:840:PRO:HD3	1.94	0.50
4:0:288:ASP:CA	4:2:204:ALA:HB2	2.31	0.50
4:7:318:THR:HA	4:7:327:ILE:HG12	1.94	0.50
1:A:202:SER:HB2	1:A:207:LYS:NZ	2.26	0.50
1:A:471:ASP:HB3	1:A:573:GLY:O	2.12	0.50
1:A:576:GLU:CG	1:A:577:ALA:N	2.43	0.50
1:A:733:PRO:CA	1:A:737:PHE:CE1	2.95	0.50
1:A:769:ALA:N	1:A:771:LEU:CB	2.74	0.50
1:D:109:ARG:O	1:D:114:MET:N	2.37	0.50
1:D:408:VAL:CG1	4:5:332:PRO:HB3	2.41	0.50
1:D:471:ASP:HB3	1:D:573:GLY:O	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:346:ASP:O	1:G:349:THR:HB	2.11	0.50
1:G:707:CYS:C	1:G:714:ARG:NH2	2.52	0.50
1:G:733:PRO:CA	1:G:737:PHE:CE1	2.95	0.50
1:G:795:ARG:HH21	3:I:116:GLU:HB3	1.77	0.50
1:J:732:ILE:O	1:J:736:GLN:HG3	2.12	0.50
2:K:117:LEU:HG	2:K:147:ASN:HB3	1.93	0.50
4:4:70:PRO:HG3	4:4:81:ASP:HB3	1.94	0.50
1:A:95:THR:HG1	1:A:769:ALA:HA	1.76	0.50
1:A:409:GLY:N	1:A:636:LYS:CD	2.70	0.50
1:A:530:MET:HA	4:4:354:GLN:CD	2.11	0.50
1:A:547:ASP:O	1:A:550:PHE:HB3	2.12	0.50
1:A:553:MLY:HG3	4:6:44:MET:O	2.07	0.50
1:D:539:GLU:OE2	4:7:45:VAL:C	2.47	0.50
1:D:733:PRO:CA	1:D:737:PHE:CE1	2.94	0.50
1:G:471:ASP:HB3	1:G:573:GLY:O	2.12	0.50
1:G:839:MLY:N	1:G:840:PRO:CD	2.75	0.50
1:J:38:VAL:CG1	1:J:39:PHE:N	2.74	0.50
1:J:217:THR:C	1:J:221:GLN:NE2	2.62	0.50
4:8:318:THR:HA	4:8:327:ILE:HG12	1.94	0.50
1:A:411:GLU:H	4:4:333:PRO:CG	2.24	0.49
1:A:505:MLY:HB2	1:A:761:GLY:CA	2.42	0.49
1:D:291:ILE:HA	1:D:331:LEU:CD1	2.39	0.49
1:D:538:GLU:OE1	4:5:351:THR:HB	2.12	0.49
2:E:140:PHE:HB3	2:E:144:VAL:HG12	1.94	0.49
2:H:137:TRP:CA	2:H:145:ALA:CB	2.82	0.49
1:J:251:ARG:O	1:J:263:ALA:HA	2.12	0.49
1:J:642:LYS:CG	4:7:22:ALA:HA	2.37	0.49
1:J:642:LYS:HA	4:7:22:ALA:C	2.33	0.49
1:J:675:ILE:CG2	1:J:676:ILE:N	2.74	0.49
4:3:318:THR:HA	4:3:327:ILE:HG12	1.94	0.49
4:5:318:THR:HA	4:5:327:ILE:HG12	1.95	0.49
4:6:318:THR:HA	4:6:327:ILE:HG12	1.94	0.49
1:A:51:THR:C	1:A:62:VAL:HG13	2.32	0.49
1:A:756:THR:O	1:A:758:TYR:N	2.46	0.49
1:A:818:TYR:HB2	2:B:89:LYS:C	2.31	0.49
2:B:117:LEU:CG	2:B:147:ASN:OD1	2.52	0.49
2:B:140:PHE:HB3	2:B:144:VAL:HG12	1.94	0.49
1:D:769:ALA:C	1:D:770:GLY:C	2.69	0.49
2:E:162:ASP:HB2	2:K:20:ASP:HA	1.94	0.49
1:G:169:ASP:N	1:G:169:ASP:OD1	2.44	0.49
1:G:278:GLN:HG3	1:G:318:GLY:H	1.75	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:632:GLY:HA3	1:G:643:GLY:N	2.17	0.49
1:G:756:THR:O	1:G:758:TYR:N	2.45	0.49
1:J:192:VAL:O	1:J:195:TYR:HB3	2.12	0.49
1:J:538:GLU:OE1	4:7:351:THR:HB	2.12	0.49
4:W:318:THR:HA	4:W:327:ILE:HG12	1.94	0.49
4:Z:70:PRO:HG3	4:Z:81:ASP:HB3	1.94	0.49
1:A:154:HIS:CD2	1:A:155:ILE:H	2.30	0.49
1:A:715:VAL:HG12	1:A:716:LEU:O	2.13	0.49
2:B:112:ILE:HG23	2:B:147:ASN:HB3	1.93	0.49
1:D:192:VAL:O	1:D:195:TYR:HB3	2.13	0.49
1:D:251:ARG:O	1:D:263:ALA:HA	2.12	0.49
1:D:725:ARG:NE	1:D:733:PRO:CB	1.95	0.49
1:D:732:ILE:O	1:D:736:GLN:HG3	2.12	0.49
1:D:817:GLN:CD	2:E:127:ARG:CZ	2.70	0.49
1:G:543:PRO:CD	4:6:146:GLY:O	2.60	0.49
1:G:751:GLY:H	3:I:114:LEU:CD1	2.25	0.49
1:G:757:GLN:CD	1:G:772:LEU:CG	2.75	0.49
2:H:112:ILE:HG23	2:H:147:ASN:HB3	1.93	0.49
1:J:214:MET:HA	1:J:340:ILE:CD1	2.41	0.49
1:J:595:TRP:N	1:J:595:TRP:CD1	2.80	0.49
1:J:739:ASP:OD1	1:J:740:SER:N	2.45	0.49
1:J:756:THR:O	1:J:758:TYR:N	2.45	0.49
1:J:768:MLY:CE	1:J:772:LEU:CD2	2.90	0.49
1:J:795:ARG:NE	3:L:35:ARG:HH12	2.10	0.49
4:1:318:THR:HA	4:1:327:ILE:HG12	1.94	0.49
4:4:318:THR:HA	4:4:327:ILE:HG12	1.94	0.49
4:V:318:THR:HA	4:V:327:ILE:HG12	1.94	0.49
4:X:253:GLU:HA	4:X:256:ARG:CG	2.42	0.49
1:A:20:SER:HB3	1:A:23:GLU:OE1	2.13	0.49
1:A:278:GLN:HG3	1:A:318:GLY:H	1.75	0.49
1:A:291:ILE:HA	1:A:331:LEU:CD1	2.39	0.49
1:A:786:ILE:HD13	3:C:90:GLY:HA2	1.93	0.49
1:A:839:MLY:HB2	1:A:840:PRO:HD3	1.94	0.49
2:B:114:LYS:N	2:B:146:GLY:O	2.40	0.49
1:D:601:ASP:N	1:D:602:PRO:CD	2.75	0.49
1:D:831:TRP:HZ3	2:E:50:THR:HG21	1.77	0.49
2:E:93:PRO:O	2:E:97:ILE:HG13	2.13	0.49
1:G:84:MLY:HH11	1:G:715:VAL:HG12	1.76	0.49
1:J:128:PRO:O	1:J:683:PRO:HB3	2.12	0.49
1:J:471:ASP:HB3	1:J:573:GLY:O	2.12	0.49
1:J:543:PRO:CD	4:7:146:GLY:O	2.61	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:601:ASP:N	1:J:602:PRO:CD	2.75	0.49
1:J:715:VAL:O	1:J:764:MLY:HB3	2.12	0.49
4:0:70:PRO:HG3	4:0:81:ASP:HB3	1.94	0.49
4:2:70:PRO:HG3	4:2:81:ASP:HB3	1.94	0.49
4:6:70:PRO:HG3	4:6:81:ASP:HB3	1.94	0.49
4:Y:318:THR:HA	4:Y:327:ILE:HG12	1.94	0.49
1:A:543:PRO:CD	4:4:146:GLY:O	2.61	0.49
1:A:795:ARG:CD	3:C:35:ARG:CZ	2.76	0.49
1:D:543:PRO:CD	4:5:146:GLY:O	2.61	0.49
1:D:715:VAL:HG12	1:D:716:LEU:O	2.12	0.49
2:E:162:ASP:HB3	2:K:20:ASP:CB	2.37	0.49
1:G:290:GLN:HG2	1:G:331:LEU:CA	2.43	0.49
1:G:530:MET:HA	4:6:354:GLN:CD	2.11	0.49
1:G:601:ASP:N	1:G:602:PRO:CD	2.75	0.49
1:G:642:LYS:CB	4:6:24:ASP:O	2.60	0.49
1:G:715:VAL:HG12	1:G:716:LEU:O	2.12	0.49
2:H:93:PRO:O	2:H:97:ILE:HG13	2.12	0.49
1:J:97:LEU:HD13	1:J:97:LEU:N	2.28	0.49
1:J:237:THR:HG22	1:J:238:VAL:N	2.28	0.49
1:J:291:ILE:HA	1:J:331:LEU:CD1	2.39	0.49
1:J:310:TYR:CE2	1:J:320:ILE:CD1	2.94	0.49
4:0:124:PHE:CZ	4:0:132:MET:HG3	2.48	0.49
4:2:318:THR:HA	4:2:327:ILE:HG12	1.94	0.49
4:4:124:PHE:CZ	4:4:132:MET:HG3	2.48	0.49
4:8:124:PHE:CZ	4:8:132:MET:HG3	2.48	0.49
4:W:124:PHE:CZ	4:W:132:MET:HG3	2.48	0.49
1:A:312:TYR:N	1:A:312:TYR:CD1	2.80	0.49
1:A:642:LYS:HG2	4:4:21:PHE:C	2.30	0.49
2:B:121:LEU:HA	2:B:128:PHE:CD2	2.46	0.49
1:D:173:GLN:OE1	1:D:668:HIS:HB3	2.13	0.49
1:D:214:MET:HA	1:D:340:ILE:CD1	2.42	0.49
1:D:251:ARG:HB2	1:D:264:ASP:HB3	1.95	0.49
1:D:332:MET:O	1:D:336:SER:OG	2.27	0.49
1:D:642:LYS:CG	4:5:22:ALA:HA	2.37	0.49
1:D:739:ASP:OD1	1:D:740:SER:N	2.45	0.49
2:E:117:LEU:HG	2:E:147:ASN:HB3	1.93	0.49
1:G:732:ILE:O	1:G:736:GLN:HG3	2.12	0.49
3:I:50:LEU:O	3:I:55:LYS:HB2	2.13	0.49
1:J:218:LEU:HA	1:J:221:GLN:HG3	1.71	0.49
1:J:544:LYS:HD2	4:7:147:ARG:CB	2.36	0.49
1:J:715:VAL:HG12	1:J:716:LEU:O	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:114:LYS:HG3	2:K:137:TRP:CZ2	2.48	0.49
4:2:124:PHE:CZ	4:2:132:MET:HG3	2.48	0.49
4:6:124:PHE:CZ	4:6:132:MET:HG3	2.48	0.49
4:X:318:THR:HA	4:X:327:ILE:HG12	1.94	0.49
4:Z:124:PHE:CZ	4:Z:132:MET:HG3	2.48	0.49
1:A:173:GLN:OE1	1:A:668:HIS:HB3	2.13	0.49
1:A:354:LEU:HD12	1:A:354:LEU:HA	1.56	0.49
1:A:429:LEU:O	1:A:433:VAL:HG23	2.12	0.49
1:A:538:GLU:OE1	4:4:351:THR:HB	2.12	0.49
1:A:739:ASP:OD1	1:A:740:SER:N	2.45	0.49
1:A:834:LEU:HD13	2:B:54:MET:HG3	1.86	0.49
1:D:128:PRO:O	1:D:683:PRO:HB3	2.12	0.49
1:D:290:GLN:HG2	1:D:331:LEU:CA	2.43	0.49
1:D:507:GLY:HA2	1:D:762:HIS:CD2	2.47	0.49
1:D:538:GLU:HA	4:5:351:THR:H	1.77	0.49
1:D:732:ILE:HG21	1:D:747:LEU:CD1	0.64	0.49
1:D:822:SER:OG	2:E:88:LEU:HA	2.13	0.49
2:E:114:LYS:HG3	2:E:137:TRP:CZ2	2.48	0.49
1:G:154:HIS:CD2	1:G:155:ILE:H	2.30	0.49
1:G:642:LYS:HG2	4:6:21:PHE:C	2.30	0.49
1:G:642:LYS:HA	4:6:22:ALA:C	2.33	0.49
1:J:20:SER:HB3	1:J:23:GLU:OE1	2.13	0.49
2:K:121:LEU:O	2:K:128:PHE:CG	2.61	0.49
4:0:253:GLU:HA	4:0:256:ARG:CG	2.42	0.49
4:7:124:PHE:CZ	4:7:132:MET:HG3	2.48	0.49
4:8:70:PRO:HG3	4:8:81:ASP:HB3	1.94	0.49
4:8:198:TYR:CZ	4:8:248:ILE:HG13	2.48	0.49
4:W:198:TYR:CZ	4:W:248:ILE:HG13	2.48	0.49
1:A:720:PHE:CD2	1:A:744:SER:HB3	2.48	0.49
1:D:64:THR:CG2	1:D:65:GLU:N	2.75	0.49
1:D:237:THR:HG22	1:D:238:VAL:N	2.28	0.49
1:D:292:MET:HE1	1:D:309:PRO:HD3	1.95	0.49
1:D:310:TYR:CE2	1:D:320:ILE:CD1	2.94	0.49
1:D:642:LYS:HA	4:5:22:ALA:C	2.33	0.49
1:D:756:THR:O	1:D:758:TYR:N	2.45	0.49
1:D:793:ARG:HH21	3:F:147:MET:HB3	1.77	0.49
2:E:128:PHE:O	2:E:133:ILE:HD11	2.13	0.49
1:G:20:SER:HB3	1:G:23:GLU:OE1	2.12	0.49
1:G:51:THR:C	1:G:62:VAL:HG13	2.32	0.49
1:G:768:MLY:HD3	1:G:772:LEU:HB2	1.94	0.49
1:J:312:TYR:N	1:J:312:TYR:CD1	2.81	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:753:VAL:CA	1:J:780:ASP:OD2	2.54	0.49
1:J:768:MLY:HH11	1:J:772:LEU:HD22	1.78	0.49
4:1:198:TYR:CZ	4:1:248:ILE:HG13	2.48	0.49
4:X:70:PRO:HG3	4:X:81:ASP:HB3	1.94	0.49
4:Y:124:PHE:CZ	4:Y:132:MET:HG3	2.48	0.49
4:Z:318:THR:HA	4:Z:327:ILE:HG12	1.94	0.49
1:A:97:LEU:HD13	1:A:97:LEU:N	2.28	0.49
1:A:103:LEU:C	1:A:103:LEU:HD12	2.33	0.49
1:A:168:THR:HG22	1:A:169:ASP:OD1	2.12	0.49
1:A:192:VAL:O	1:A:195:TYR:HB3	2.13	0.49
1:A:251:ARG:O	1:A:263:ALA:HA	2.12	0.49
1:A:346:ASP:O	1:A:349:THR:HB	2.11	0.49
1:A:839:MLY:N	1:A:840:PRO:CD	2.75	0.49
1:D:51:THR:C	1:D:62:VAL:HG13	2.32	0.49
1:D:831:TRP:CZ3	2:E:50:THR:CB	2.96	0.49
1:G:41:VAL:CG1	1:G:42:HIS:N	2.75	0.49
1:G:192:VAL:O	1:G:195:TYR:HB3	2.13	0.49
1:G:237:THR:HG22	1:G:238:VAL:N	2.28	0.49
2:H:114:LYS:HG3	2:H:137:TRP:CZ2	2.48	0.49
1:J:51:THR:C	1:J:62:VAL:HG13	2.32	0.49
1:J:64:THR:CG2	1:J:65:GLU:N	2.75	0.49
1:J:173:GLN:OE1	1:J:668:HIS:HB3	2.13	0.49
1:J:251:ARG:HB2	1:J:264:ASP:HB3	1.95	0.49
3:L:50:LEU:O	3:L:55:LYS:HB2	2.13	0.49
4:0:318:THR:HA	4:0:327:ILE:HG12	1.94	0.49
4:1:213:LYS:O	4:1:217:CYS:HB2	2.13	0.49
4:3:70:PRO:HG3	4:3:81:ASP:HB3	1.94	0.49
4:6:198:TYR:CZ	4:6:248:ILE:HG13	2.48	0.49
4:X:124:PHE:CZ	4:X:132:MET:HG3	2.48	0.49
4:Y:198:TYR:CZ	4:Y:248:ILE:HG13	2.48	0.49
1:A:128:PRO:O	1:A:683:PRO:HB3	2.12	0.49
1:A:218:LEU:HD22	1:A:222:ILE:HG13	1.95	0.49
1:A:768:MLY:O	1:A:771:LEU:HB3	2.13	0.49
2:B:114:LYS:HG3	2:B:137:TRP:CZ2	2.48	0.49
3:C:50:LEU:O	3:C:55:LYS:HB2	2.13	0.49
1:D:20:SER:HB3	1:D:23:GLU:OE1	2.13	0.49
1:D:547:ASP:O	1:D:550:PHE:HB3	2.12	0.49
1:D:769:ALA:CB	1:D:770:GLY:N	2.75	0.49
1:D:830:PRO:CB	2:E:67:MET:HE1	2.41	0.49
1:D:831:TRP:CE2	2:E:47:LEU:CB	2.93	0.49
1:D:839:MLY:N	1:D:840:PRO:CD	2.75	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:50:LEU:O	3:F:55:LYS:HB2	2.13	0.49
1:G:95:THR:OG1	1:G:713:SER:CB	2.55	0.49
1:G:547:ASP:O	1:G:550:PHE:HB3	2.12	0.49
1:J:290:GLN:HG2	1:J:331:LEU:CA	2.43	0.49
1:J:405:ARG:HB2	1:J:414:THR:OG1	2.13	0.49
1:J:720:PHE:CD2	1:J:744:SER:HB3	2.48	0.49
1:J:798:LEU:HD21	3:L:122:GLU:O	2.12	0.49
1:J:831:TRP:HH2	2:K:34:ILE:CG2	2.24	0.49
2:K:93:PRO:O	2:K:97:ILE:HG13	2.12	0.49
4:5:70:PRO:HG3	4:5:81:ASP:HB3	1.94	0.49
4:5:124:PHE:CZ	4:5:132:MET:HG3	2.48	0.49
1:A:93:MET:HE2	1:A:715:VAL:HA	1.94	0.48
1:A:732:ILE:HG23	1:A:747:LEU:HD12	0.95	0.48
1:A:795:ARG:NE	3:C:43:ASN:OD1	2.10	0.48
1:A:813:ILE:HG22	2:B:127:ARG:HD2	1.25	0.48
1:D:168:THR:HG22	1:D:169:ASP:OD1	2.12	0.48
1:D:267:THR:HG21	1:D:438:PHE:HE2	1.76	0.48
1:D:793:ARG:O	1:D:797:PHE:N	2.39	0.48
1:D:839:MLY:HB2	1:D:840:PRO:HD3	1.94	0.48
1:G:128:PRO:O	1:G:683:PRO:HB3	2.12	0.48
1:G:134:VAL:C	1:G:136:ASN:H	2.16	0.48
1:G:168:THR:HG22	1:G:169:ASP:OD1	2.12	0.48
1:G:248:MLY:HE2	1:G:250:ILE:HD11	1.95	0.48
1:G:739:ASP:OD1	1:G:740:SER:N	2.46	0.48
1:G:839:MLY:HB2	1:G:840:PRO:HD3	1.94	0.48
1:J:84:MLY:CH1	1:J:715:VAL:HG11	2.17	0.48
1:J:530:MET:HE3	4:7:354:GLN:CB	2.43	0.48
4:1:70:PRO:HG3	4:1:81:ASP:HB3	1.94	0.48
4:1:124:PHE:CZ	4:1:132:MET:HG3	2.48	0.48
4:3:124:PHE:CZ	4:3:132:MET:HG3	2.48	0.48
4:3:198:TYR:CZ	4:3:248:ILE:HG13	2.48	0.48
4:V:124:PHE:CZ	4:V:132:MET:HG3	2.48	0.48
1:A:237:THR:HG22	1:A:238:VAL:N	2.28	0.48
1:A:290:GLN:HG2	1:A:331:LEU:CA	2.43	0.48
1:A:310:TYR:CE2	1:A:320:ILE:CD1	2.94	0.48
1:A:530:MET:HE3	4:4:355:MET:SD	2.53	0.48
1:A:542:PHE:CD2	4:4:143:TYR:CD1	3.02	0.48
2:B:130:PRO:O	2:B:131:GLU:C	2.52	0.48
1:G:405:ARG:HB2	1:G:414:THR:OG1	2.13	0.48
1:G:556:ASP:CA	4:8:49:GLN:O	2.51	0.48
1:G:836:PHE:CE2	2:H:160:GLY:HA3	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:117:LEU:HG	2:H:147:ASN:HB3	1.93	0.48
1:J:215:GLN:H	1:J:340:ILE:CD1	2.20	0.48
1:J:817:GLN:CD	2:K:127:ARG:CD	2.58	0.48
2:K:128:PHE:O	2:K:133:ILE:HD11	2.13	0.48
4:4:198:TYR:CZ	4:4:248:ILE:HG13	2.48	0.48
4:5:198:TYR:CZ	4:5:248:ILE:HG13	2.48	0.48
4:7:70:PRO:HG3	4:7:81:ASP:HB3	1.94	0.48
4:W:70:PRO:HG3	4:W:81:ASP:HB3	1.94	0.48
1:A:642:LYS:HA	4:4:22:ALA:C	2.34	0.48
2:B:93:PRO:O	2:B:97:ILE:HG13	2.13	0.48
1:D:292:MET:CE	1:D:309:PRO:HA	2.39	0.48
1:D:404:PRO:HD2	1:D:415:MLY:O	2.13	0.48
1:D:724:TYR:CZ	1:D:778:MET:CB	2.97	0.48
1:G:93:MET:CE	1:G:763:THR:O	2.60	0.48
1:G:530:MET:HE3	4:6:355:MET:SD	2.53	0.48
1:G:757:GLN:HE22	1:G:772:LEU:CD2	2.27	0.48
1:G:797:PHE:HB2	3:I:149:VAL:CG1	2.43	0.48
1:J:87:MLY:HD3	1:J:87:MLY:HH12	1.61	0.48
1:J:404:PRO:HD2	1:J:415:MLY:O	2.13	0.48
1:J:538:GLU:HA	4:7:351:THR:H	1.77	0.48
1:J:739:ASP:CB	1:J:742:LYS:CB	2.81	0.48
1:J:839:MLY:N	1:J:840:PRO:CD	2.75	0.48
1:A:499:GLU:OE1	1:A:499:GLU:HA	2.13	0.48
1:D:724:TYR:CA	1:D:782:MLY:CH1	2.90	0.48
1:G:251:ARG:O	1:G:263:ALA:HA	2.12	0.48
1:G:759:ALA:O	1:G:766:PHE:N	2.32	0.48
2:H:128:PHE:O	2:H:133:ILE:HD11	2.13	0.48
1:J:136:ASN:O	1:J:139:VAL:N	2.47	0.48
1:J:168:THR:HG22	1:J:169:ASP:OD1	2.12	0.48
1:J:410:ASN:HD22	4:7:336:LYS:HE2	1.78	0.48
1:J:547:ASP:O	1:J:550:PHE:HB3	2.12	0.48
1:J:732:ILE:HG21	1:J:747:LEU:CD1	0.63	0.48
1:J:817:GLN:HG2	2:K:127:ARG:CD	2.42	0.48
2:K:130:PRO:O	2:K:131:GLU:C	2.52	0.48
4:V:70:PRO:HG3	4:V:81:ASP:HB3	1.94	0.48
1:A:406:VAL:CG1	1:A:407:GLY:N	2.77	0.48
2:B:117:LEU:HG	2:B:147:ASN:HB3	1.93	0.48
1:D:405:ARG:HB2	1:D:414:THR:OG1	2.13	0.48
1:D:436:MLY:HE3	1:D:626:TYR:HE1	1.77	0.48
1:D:530:MET:HE3	4:5:354:GLN:CG	2.32	0.48
1:D:544:LYS:HD2	4:5:147:ARG:CB	2.36	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:173:GLN:OE1	1:G:668:HIS:HB3	2.13	0.48
1:G:310:TYR:CE2	1:G:320:ILE:CD1	2.94	0.48
1:G:409:GLY:N	1:G:636:LYS:CD	2.71	0.48
1:G:538:GLU:HA	4:6:351:THR:H	1.77	0.48
1:G:617:MLY:O	1:G:620:ALA:HB3	2.14	0.48
1:G:720:PHE:CD2	1:G:744:SER:HB3	2.48	0.48
1:G:723:ARG:HH11	1:G:723:ARG:HG3	1.78	0.48
1:G:800:ARG:NH1	3:I:149:VAL:CG2	2.26	0.48
1:J:289:TYR:OH	1:J:315:VAL:O	2.27	0.48
4:1:253:GLU:HA	4:1:256:ARG:CG	2.42	0.48
4:2:120:THR:HG21	4:2:370:VAL:HG11	1.95	0.48
4:8:213:LYS:O	4:8:217:CYS:HB2	2.13	0.48
4:8:253:GLU:HA	4:8:256:ARG:CG	2.42	0.48
1:A:10:PHE:CD2	1:A:17:LEU:HD23	2.49	0.48
1:A:544:LYS:HD2	4:4:147:ARG:CB	2.36	0.48
2:B:112:ILE:CG2	2:B:147:ASN:O	2.62	0.48
2:B:128:PHE:O	2:B:133:ILE:HD11	2.13	0.48
1:D:103:LEU:C	1:D:103:LEU:HD12	2.33	0.48
1:D:314:TYR:CZ	1:D:362:GLY:HA2	2.48	0.48
1:D:617:MLY:O	1:D:620:ALA:HB3	2.14	0.48
1:D:642:LYS:CB	4:5:24:ASP:O	2.59	0.48
1:D:838:ILE:C	1:D:840:PRO:HD2	2.34	0.48
1:G:64:THR:CG2	1:G:65:GLU:N	2.75	0.48
1:G:499:GLU:OE1	1:G:499:GLU:HA	2.13	0.48
1:J:41:VAL:CG1	1:J:42:HIS:N	2.76	0.48
1:J:103:LEU:C	1:J:103:LEU:HD12	2.33	0.48
1:J:267:THR:HG21	1:J:438:PHE:HE2	1.76	0.48
1:J:314:TYR:CZ	1:J:362:GLY:HA2	2.48	0.48
4:2:198:TYR:CZ	4:2:248:ILE:HG13	2.48	0.48
4:3:213:LYS:O	4:3:217:CYS:HB2	2.13	0.48
4:6:120:THR:HG21	4:6:370:VAL:HG11	1.95	0.48
4:7:198:TYR:CZ	4:7:248:ILE:HG13	2.48	0.48
4:7:213:LYS:O	4:7:217:CYS:HB2	2.13	0.48
4:V:250:ILE:HG23	4:V:253:GLU:HG2	1.96	0.48
1:A:64:THR:CG2	1:A:65:GLU:N	2.75	0.48
1:A:405:ARG:HB2	1:A:414:THR:OG1	2.13	0.48
1:A:506:GLU:OE2	1:A:760:PHE:HD2	1.97	0.48
1:D:106:LEU:HD12	1:D:117:THR:HG21	1.96	0.48
1:D:550:PHE:CE2	1:D:592:ILE:CG2	2.97	0.48
1:D:689:GLU:O	1:D:689:GLU:HG2	2.14	0.48
1:D:720:PHE:CD2	1:D:744:SER:HB3	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:103:LEU:C	1:G:103:LEU:HD12	2.33	0.48
1:G:728:ASN:ND2	3:I:110:VAL:HA	2.18	0.48
1:G:739:ASP:CB	1:G:742:LYS:CB	2.81	0.48
1:J:10:PHE:CD2	1:J:17:LEU:HD23	2.49	0.48
1:J:617:MLY:O	1:J:620:ALA:HB3	2.14	0.48
1:J:707:CYS:CB	1:J:714:ARG:NH2	2.73	0.48
4:7:250:ILE:HG23	4:7:253:GLU:HG2	1.96	0.48
4:V:213:LYS:O	4:V:217:CYS:HB2	2.13	0.48
4:Y:253:GLU:HA	4:Y:256:ARG:CG	2.42	0.48
1:D:790:THR:HA	3:F:87:PHE:CZ	2.47	0.48
1:G:10:PHE:CD2	1:G:17:LEU:HD23	2.49	0.48
1:G:312:TYR:N	1:G:312:TYR:CD1	2.81	0.48
1:J:664:LEU:HD12	1:J:664:LEU:HA	1.52	0.48
1:J:723:ARG:HH11	1:J:723:ARG:HG3	1.78	0.48
2:K:137:TRP:CA	2:K:145:ALA:CB	2.82	0.48
4:0:198:TYR:CZ	4:0:248:ILE:HG13	2.48	0.48
4:6:213:LYS:O	4:6:217:CYS:HB2	2.13	0.48
4:X:250:ILE:HG23	4:X:253:GLU:HG2	1.96	0.48
4:Y:70:PRO:HG3	4:Y:81:ASP:HB3	1.94	0.48
4:Z:198:TYR:CZ	4:Z:248:ILE:HG13	2.48	0.48
1:A:765:VAL:CG1	1:A:766:PHE:N	2.77	0.48
1:D:723:ARG:HH11	1:D:723:ARG:HG3	1.79	0.48
1:D:806:MET:SD	3:F:17:PHE:HE2	2.37	0.48
1:D:818:TYR:CD2	2:E:89:LYS:O	2.63	0.48
1:G:97:LEU:HD13	1:G:97:LEU:N	2.28	0.48
1:G:635:GLY:HA3	4:6:334:GLU:CG	2.30	0.48
1:G:823:PHE:CZ	2:H:156:VAL:HG12	2.48	0.48
1:G:838:ILE:C	1:G:840:PRO:HD2	2.34	0.48
2:H:130:PRO:O	2:H:131:GLU:C	2.52	0.48
2:H:140:PHE:HB3	2:H:144:VAL:HG12	1.95	0.48
1:J:768:MLY:HE2	1:J:772:LEU:HD23	1.95	0.48
4:0:250:ILE:HG23	4:0:253:GLU:HG2	1.96	0.48
4:1:120:THR:HG21	4:1:370:VAL:HG11	1.95	0.48
4:2:250:ILE:HG23	4:2:253:GLU:HG2	1.96	0.48
4:4:120:THR:HG21	4:4:370:VAL:HG11	1.95	0.48
4:6:250:ILE:HG23	4:6:253:GLU:HG2	1.96	0.48
4:V:198:TYR:CZ	4:V:248:ILE:HG13	2.48	0.48
4:W:288:ASP:CA	4:Y:204:ALA:HB2	2.31	0.48
4:X:198:TYR:CZ	4:X:248:ILE:HG13	2.48	0.48
4:Y:213:LYS:O	4:Y:217:CYS:HB2	2.13	0.48
4:Z:250:ILE:HG23	4:Z:253:GLU:HG2	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:248:MLY:HE2	1:A:250:ILE:HD11	1.95	0.48
1:A:410:ASN:HD22	4:4:336:LYS:HE2	1.78	0.48
1:A:546:THR:CG2	1:A:547:ASP:N	2.77	0.48
1:A:550:PHE:CE2	1:A:592:ILE:CG2	2.97	0.48
1:A:617:MLY:O	1:A:620:ALA:HB3	2.14	0.48
1:A:664:LEU:HD12	1:A:664:LEU:HA	1.53	0.48
1:A:689:GLU:HG2	1:A:689:GLU:O	2.14	0.48
1:A:723:ARG:HH11	1:A:723:ARG:HG3	1.78	0.48
1:D:312:TYR:N	1:D:312:TYR:CD1	2.81	0.48
1:D:578:HIS:HB3	1:D:592:ILE:CD1	2.38	0.48
1:D:792:ALA:HB2	3:F:40:ASN:O	2.10	0.48
1:D:830:PRO:HG2	2:E:67:MET:HE3	0.48	0.48
1:J:134:VAL:C	1:J:136:ASN:H	2.16	0.48
1:J:757:GLN:OE1	1:J:773:GLY:HA2	2.14	0.48
2:K:121:LEU:HA	2:K:128:PHE:CD2	2.46	0.48
4:0:120:THR:HG21	4:0:370:VAL:HG11	1.95	0.48
4:1:250:ILE:HG23	4:1:253:GLU:HG2	1.96	0.48
4:4:250:ILE:HG23	4:4:253:GLU:HG2	1.96	0.48
4:5:250:ILE:HG23	4:5:253:GLU:HG2	1.96	0.48
4:8:120:THR:HG21	4:8:370:VAL:HG11	1.95	0.48
4:V:253:GLU:HA	4:V:256:ARG:CG	2.42	0.48
1:A:602:PRO:O	1:A:603:LEU:HD12	2.14	0.47
1:A:640:LYS:HD2	1:A:646:PHE:O	2.14	0.47
1:D:10:PHE:CD2	1:D:17:LEU:HD23	2.49	0.47
1:D:542:PHE:CD2	4:5:143:TYR:CD1	3.02	0.47
1:D:546:THR:CG2	1:D:547:ASP:N	2.77	0.47
1:D:568:PRO:HD3	1:D:579:PHE:HA	1.96	0.47
2:E:137:TRP:CA	2:E:145:ALA:CB	2.82	0.47
2:E:160:GLY:O	2:E:161:GLU:HG2	2.14	0.47
1:G:530:MET:CE	4:6:354:GLN:HG3	2.34	0.47
1:G:544:LYS:HD2	4:6:147:ARG:CB	2.36	0.47
1:G:707:CYS:CB	1:G:714:ARG:NH1	2.45	0.47
2:H:121:LEU:O	2:H:128:PHE:CG	2.61	0.47
1:J:84:MLY:HH12	1:J:715:VAL:HG12	1.84	0.47
1:J:542:PHE:CD2	4:7:143:TYR:CD1	3.02	0.47
1:J:550:PHE:CE2	1:J:592:ILE:CG2	2.97	0.47
1:J:636:LYS:O	4:7:144:ALA:HB1	2.14	0.47
1:J:768:MLY:CE	1:J:772:LEU:HD23	2.44	0.47
2:K:112:ILE:CG2	2:K:147:ASN:O	2.62	0.47
4:3:120:THR:HG21	4:3:370:VAL:HG11	1.95	0.47
4:3:250:ILE:HG23	4:3:253:GLU:HG2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:8:250:ILE:HG23	4:8:253:GLU:HG2	1.96	0.47
4:W:213:LYS:O	4:W:217:CYS:HB2	2.13	0.47
4:W:250:ILE:HG23	4:W:253:GLU:HG2	1.96	0.47
4:Y:250:ILE:HG23	4:Y:253:GLU:HG2	1.96	0.47
1:A:218:LEU:HA	1:A:221:GLN:H	1.79	0.47
1:A:501:GLU:CA	1:A:762:HIS:CE1	2.97	0.47
1:A:783:LEU:HA	1:A:786:ILE:HB	1.96	0.47
2:B:160:GLY:O	2:B:161:GLU:HG2	2.14	0.47
1:D:97:LEU:HD13	1:D:97:LEU:N	2.28	0.47
1:D:154:HIS:CE1	1:D:156:PHE:CE2	3.02	0.47
1:D:602:PRO:O	1:D:603:LEU:HD12	2.14	0.47
2:E:144:VAL:HG12	2:E:153:ILE:HD13	1.92	0.47
1:G:410:ASN:HD22	4:6:336:LYS:HE2	1.79	0.47
1:G:550:PHE:CE2	1:G:592:ILE:CG2	2.97	0.47
1:G:564:ASN:HD22	1:G:582:VAL:HB	1.79	0.47
1:G:629:GLU:CA	1:G:643:GLY:C	2.73	0.47
1:G:640:LYS:HD2	1:G:646:PHE:O	2.14	0.47
1:G:701:LEU:HA	1:G:701:LEU:HD12	1.55	0.47
1:G:795:ARG:HB2	3:I:35:ARG:CZ	2.44	0.47
1:G:826:VAL:HG21	2:H:88:LEU:CD2	2.43	0.47
1:J:218:LEU:CD2	1:J:222:ILE:CG1	2.86	0.47
1:J:765:VAL:CG1	1:J:766:PHE:N	2.77	0.47
4:5:120:THR:HG21	4:5:370:VAL:HG11	1.95	0.47
4:X:213:LYS:O	4:X:217:CYS:HB2	2.13	0.47
4:X:287:ILE:CB	4:Z:204:ALA:H	2.13	0.47
4:Y:120:THR:HG21	4:Y:370:VAL:HG11	1.95	0.47
4:Z:120:THR:HG21	4:Z:370:VAL:HG11	1.95	0.47
1:A:314:TYR:CZ	1:A:362:GLY:HA2	2.48	0.47
1:A:538:GLU:HA	4:4:351:THR:H	1.78	0.47
1:G:314:TYR:CZ	1:G:362:GLY:HA2	2.48	0.47
1:G:546:THR:CG2	1:G:547:ASP:N	2.77	0.47
1:G:793:ARG:O	1:G:797:PHE:N	2.39	0.47
1:J:546:THR:CG2	1:J:547:ASP:N	2.77	0.47
1:J:564:ASN:HD22	1:J:582:VAL:HB	1.79	0.47
4:0:213:LYS:O	4:0:217:CYS:HB2	2.13	0.47
4:Z:213:LYS:O	4:Z:217:CYS:HB2	2.13	0.47
1:A:122:PHE:CE2	1:A:700:VAL:HA	2.49	0.47
1:A:595:TRP:N	1:A:595:TRP:CD1	2.80	0.47
1:D:188:ASN:ND2	1:D:674:CYS:SG	2.88	0.47
1:D:410:ASN:HD22	4:5:336:LYS:HE2	1.78	0.47
1:D:564:ASN:HD22	1:D:582:VAL:HB	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:765:VAL:CG1	1:D:766:PHE:N	2.77	0.47
1:D:834:LEU:CD2	2:E:50:THR:HG22	2.44	0.47
1:G:22:LYS:O	1:G:26:GLU:N	2.29	0.47
1:G:93:MET:CE	1:G:764:MLY:CG	2.88	0.47
1:G:154:HIS:CE1	1:G:156:PHE:CE2	3.02	0.47
1:G:408:VAL:HG22	1:G:636:LYS:HG2	1.51	0.47
1:G:725:ARG:CG	1:G:733:PRO:HA	2.43	0.47
1:G:798:LEU:CD1	3:I:126:LEU:HD23	2.12	0.47
2:H:160:GLY:O	2:H:161:GLU:HG2	2.15	0.47
1:J:214:MET:C	1:J:340:ILE:CD1	2.82	0.47
1:J:436:MLY:HE3	1:J:626:TYR:HE1	1.77	0.47
1:J:786:ILE:CD1	3:L:86:ASP:HB3	2.45	0.47
2:K:140:PHE:HB3	2:K:144:VAL:HG12	1.94	0.47
3:L:53:PRO:O	3:L:55:LYS:HG3	2.15	0.47
4:5:213:LYS:O	4:5:217:CYS:HB2	2.13	0.47
4:V:162:ASN:OD1	4:V:277:THR:HG22	2.15	0.47
1:A:136:ASN:O	1:A:139:VAL:N	2.47	0.47
1:A:154:HIS:CE1	1:A:156:PHE:CE2	3.02	0.47
1:A:176:LEU:N	1:A:176:LEU:CD1	2.74	0.47
1:A:404:PRO:HD2	1:A:415:MLY:O	2.13	0.47
1:A:646:PHE:HE2	1:A:652:LEU:CG	2.24	0.47
1:A:838:ILE:C	1:A:840:PRO:HD2	2.35	0.47
2:B:139:ALA:C	2:B:141:PRO:HD3	2.33	0.47
1:D:636:LYS:O	4:5:144:ALA:HB1	2.14	0.47
1:G:106:LEU:HD12	1:G:117:THR:HG21	1.96	0.47
1:G:295:MLY:HG3	1:G:332:MET:HE2	1.94	0.47
1:G:602:PRO:O	1:G:603:LEU:HD12	2.14	0.47
1:G:664:LEU:HD12	1:G:664:LEU:HA	1.53	0.47
1:G:819:ASN:CB	2:H:92:ASP:HB2	2.41	0.47
2:H:112:ILE:CG2	2:H:147:ASN:O	2.62	0.47
1:J:629:GLU:CA	1:J:643:GLY:C	2.73	0.47
4:2:213:LYS:O	4:2:217:CYS:HB2	2.13	0.47
4:3:162:ASN:OD1	4:3:277:THR:HG22	2.15	0.47
4:5:288:ASP:CA	4:7:204:ALA:HB2	2.31	0.47
4:7:162:ASN:OD1	4:7:277:THR:HG22	2.15	0.47
4:8:162:ASN:OD1	4:8:277:THR:HG22	2.15	0.47
1:A:214:MET:C	1:A:340:ILE:CD1	2.82	0.47
1:D:499:GLU:OE1	1:D:499:GLU:HA	2.13	0.47
1:D:640:LYS:HD2	1:D:646:PHE:O	2.15	0.47
1:D:715:VAL:HG11	1:D:720:PHE:CD1	2.50	0.47
2:E:130:PRO:O	2:E:131:GLU:C	2.52	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:122:PHE:CE2	1:G:700:VAL:HA	2.50	0.47
1:G:292:MET:HE1	1:G:309:PRO:HD3	1.97	0.47
1:G:542:PHE:CD2	4:6:143:TYR:CD1	3.03	0.47
1:J:188:ASN:ND2	1:J:674:CYS:SG	2.88	0.47
1:J:406:VAL:CG1	1:J:407:GLY:N	2.77	0.47
1:J:689:GLU:O	1:J:689:GLU:HG2	2.14	0.47
1:J:838:ILE:C	1:J:840:PRO:HD2	2.35	0.47
4:4:213:LYS:O	4:4:217:CYS:HB2	2.13	0.47
4:7:120:THR:HG21	4:7:370:VAL:HG11	1.95	0.47
4:W:120:THR:HG21	4:W:370:VAL:HG11	1.95	0.47
4:X:162:ASN:OD1	4:X:277:THR:HG22	2.15	0.47
4:Y:162:ASN:OD1	4:Y:277:THR:HG22	2.15	0.47
4:Z:162:ASN:OD1	4:Z:277:THR:HG22	2.15	0.47
1:A:400:ALA:HB1	1:A:606:THR:CG2	2.45	0.47
1:A:505:MLY:HB2	1:A:761:GLY:HA2	1.96	0.47
1:A:732:ILE:CG2	1:A:747:LEU:CD1	0.65	0.47
1:D:214:MET:C	1:D:340:ILE:CD1	2.82	0.47
1:D:248:MLY:HE2	1:D:250:ILE:HD11	1.96	0.47
1:D:311:ASP:CB	1:D:312:TYR:CE1	2.98	0.47
1:D:524:GLU:HB3	1:D:528:MLY:HG2	1.97	0.47
1:D:642:LYS:HB2	4:5:24:ASP:O	1.88	0.47
1:D:675:ILE:CG2	1:D:676:ILE:N	2.74	0.47
1:D:724:TYR:HD1	1:D:727:LEU:CD1	2.27	0.47
1:D:783:LEU:HA	1:D:786:ILE:HB	1.97	0.47
2:E:139:ALA:C	2:E:141:PRO:HD3	2.33	0.47
3:F:53:PRO:O	3:F:55:LYS:HG3	2.14	0.47
1:G:84:MLY:HH11	1:G:719:ASP:C	2.33	0.47
1:G:84:MLY:NZ	1:G:719:ASP:O	2.18	0.47
1:G:214:MET:HA	1:G:340:ILE:CD1	2.41	0.47
1:G:215:GLN:H	1:G:340:ILE:CD1	2.20	0.47
1:G:406:VAL:CG1	1:G:407:GLY:N	2.77	0.47
1:G:418:THR:CB	1:G:421:GLU:HG3	2.37	0.47
1:G:595:TRP:N	1:G:595:TRP:CD1	2.80	0.47
1:G:689:GLU:O	1:G:689:GLU:HG2	2.14	0.47
1:G:695:LEU:HB3	1:G:701:LEU:HD22	1.97	0.47
1:G:765:VAL:CG1	1:G:766:PHE:N	2.77	0.47
2:H:121:LEU:HA	2:H:128:PHE:CD2	2.47	0.47
1:J:154:HIS:CE1	1:J:156:PHE:CE2	3.02	0.47
1:J:406:VAL:CG1	1:J:407:GLY:H	2.28	0.47
1:J:510:TRP:CD2	1:J:768:MLY:HH13	2.50	0.47
1:J:519:LEU:N	1:J:519:LEU:CD1	2.77	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:524:GLU:HB3	1:J:528:MLY:HG2	1.97	0.47
1:J:554:LEU:HD12	1:J:554:LEU:HA	1.77	0.47
1:J:568:PRO:HD3	1:J:579:PHE:HA	1.96	0.47
1:J:602:PRO:O	1:J:603:LEU:HD12	2.14	0.47
1:J:749:GLY:O	3:L:114:LEU:HD22	2.12	0.47
2:K:137:TRP:CZ3	2:K:145:ALA:N	2.81	0.47
2:K:139:ALA:C	2:K:141:PRO:HD3	2.33	0.47
4:0:162:ASN:OD1	4:0:277:THR:HG22	2.15	0.47
4:5:162:ASN:OD1	4:5:277:THR:HG22	2.15	0.47
4:6:253:GLU:HA	4:6:256:ARG:CG	2.42	0.47
4:X:120:THR:HG21	4:X:370:VAL:HG11	1.95	0.47
1:A:406:VAL:CG1	1:A:407:GLY:H	2.28	0.47
1:A:538:GLU:OE1	4:4:355:MET:HE3	2.15	0.47
1:A:564:ASN:HD22	1:A:582:VAL:HB	1.79	0.47
1:D:400:ALA:HB1	1:D:606:THR:CG2	2.45	0.47
1:D:496:PHE:CE2	1:D:514:ASP:HA	2.50	0.47
1:D:629:GLU:CB	1:D:645:SER:N	2.74	0.47
1:D:732:ILE:CG2	1:D:747:LEU:CD1	0.65	0.47
1:G:251:ARG:HB2	1:G:264:ASP:HB3	1.95	0.47
1:G:404:PRO:HD2	1:G:415:MLY:O	2.13	0.47
1:G:543:PRO:HD2	4:6:146:GLY:O	2.15	0.47
1:J:496:PHE:CE2	1:J:514:ASP:HA	2.50	0.47
1:J:499:GLU:OE1	1:J:499:GLU:HA	2.13	0.47
1:J:725:ARG:NE	1:J:733:PRO:CB	1.95	0.47
4:3:253:GLU:HA	4:3:256:ARG:CG	2.42	0.47
1:A:524:GLU:HB3	1:A:528:MLY:HG2	1.96	0.47
1:A:732:ILE:HG21	1:A:747:LEU:CD1	0.64	0.47
1:A:768:MLY:CA	1:A:771:LEU:HB2	2.43	0.47
1:A:839:MLY:NZ	2:B:159:HIS:CB	2.62	0.47
1:D:406:VAL:CG1	1:D:407:GLY:N	2.77	0.47
1:D:543:PRO:HD2	4:5:146:GLY:O	2.15	0.47
1:D:695:LEU:HB3	1:D:701:LEU:HD22	1.97	0.47
1:D:809:ARG:NH1	2:E:124:GLY:C	2.68	0.47
2:E:112:ILE:CG2	2:E:147:ASN:O	2.62	0.47
1:G:202:SER:HA	1:G:207:LYS:NZ	2.22	0.47
1:G:406:VAL:CG1	1:G:407:GLY:H	2.28	0.47
1:G:538:GLU:CD	4:6:355:MET:HE1	2.25	0.47
1:G:793:ARG:HB2	3:I:40:ASN:ND2	2.30	0.47
1:G:831:TRP:CZ2	2:H:67:MET:CB	2.98	0.47
1:J:84:MLY:HG2	1:J:719:ASP:OD2	2.14	0.47
1:J:311:ASP:CB	1:J:312:TYR:CE1	2.98	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:400:ALA:HB1	1:J:606:THR:CG2	2.45	0.47
1:J:578:HIS:HB3	1:J:592:ILE:CD1	2.38	0.47
4:2:162:ASN:OD1	4:2:277:THR:HG22	2.15	0.47
1:A:144:ARG:HA	1:A:144:ARG:HD2	1.78	0.47
1:A:202:SER:HA	1:A:207:LYS:NZ	2.22	0.47
1:A:265:ILE:CG2	1:A:266:GLU:N	2.78	0.47
1:A:292:MET:HE1	1:A:309:PRO:HD3	1.97	0.47
1:A:636:LYS:O	4:4:144:ALA:HB1	2.15	0.47
1:A:810:ARG:HG2	1:A:810:ARG:NH1	2.29	0.47
1:D:30:MLY:HB3	1:D:31:PRO:HD2	1.97	0.47
1:D:221:GLN:HG2	1:D:221:GLN:H	1.47	0.47
1:G:188:ASN:ND2	1:G:674:CYS:SG	2.88	0.47
1:J:106:LEU:HD12	1:J:117:THR:HG21	1.96	0.47
1:J:640:LYS:HD2	1:J:646:PHE:O	2.15	0.47
3:L:50:LEU:O	3:L:53:PRO:CD	2.63	0.47
4:4:162:ASN:OD1	4:4:277:THR:HG22	2.15	0.47
4:4:299:MET:HE2	4:4:331:ALA:HB2	1.96	0.47
4:4:324:THR:O	4:6:244:ASP:HA	2.08	0.47
4:V:120:THR:HG21	4:V:370:VAL:HG11	1.95	0.47
1:A:251:ARG:HB2	1:A:264:ASP:HB3	1.95	0.46
2:B:88:LEU:HB3	2:B:91:ALA:HB2	1.97	0.46
3:C:53:PRO:O	3:C:55:LYS:HG3	2.15	0.46
1:D:406:VAL:CG1	1:D:407:GLY:H	2.28	0.46
1:D:556:ASP:CA	4:7:49:GLN:O	2.52	0.46
1:G:214:MET:C	1:G:340:ILE:CD1	2.82	0.46
1:G:559:LEU:HD23	1:G:560:GLY:N	2.30	0.46
1:G:568:PRO:HD3	1:G:579:PHE:HA	1.97	0.46
1:G:640:LYS:HB3	1:G:645:SER:CB	2.42	0.46
1:G:823:PHE:CD1	2:H:157:ILE:HA	2.50	0.46
1:J:122:PHE:CE2	1:J:700:VAL:HA	2.50	0.46
1:J:248:MLY:HE2	1:J:250:ILE:HD11	1.95	0.46
1:J:374:GLN:NE2	1:J:403:TYR:CE1	2.84	0.46
1:J:640:LYS:C	4:7:23:GLY:C	2.74	0.46
1:J:800:ARG:HD2	3:L:149:VAL:CA	2.45	0.46
1:J:839:MLY:HH21	2:K:158:THR:HG22	1.97	0.46
4:2:299:MET:HE2	4:2:331:ALA:HB2	1.97	0.46
4:6:162:ASN:OD1	4:6:277:THR:HG22	2.15	0.46
1:A:188:ASN:ND2	1:A:674:CYS:SG	2.88	0.46
1:A:332:MET:O	1:A:336:SER:OG	2.27	0.46
1:A:640:LYS:HB3	1:A:645:SER:CB	2.42	0.46
1:A:836:PHE:CD2	2:B:160:GLY:C	2.88	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:121:LEU:O	2:B:128:PHE:CG	2.61	0.46
1:D:122:PHE:CE2	1:D:700:VAL:HA	2.50	0.46
1:D:732:ILE:HG23	1:D:747:LEU:CD1	1.04	0.46
1:D:809:ARG:CZ	2:E:124:GLY:HA2	2.35	0.46
1:D:831:TRP:CE3	2:E:34:ILE:HD13	2.50	0.46
1:G:646:PHE:HE2	1:G:652:LEU:CG	2.24	0.46
1:G:715:VAL:HG11	1:G:720:PHE:CD1	2.49	0.46
1:G:724:TYR:HD1	1:G:727:LEU:CD1	2.27	0.46
1:J:42:HIS:O	1:J:45:GLN:O	2.33	0.46
1:J:206:LYS:HD2	1:J:217:THR:CG2	2.17	0.46
1:J:529:PRO:HB2	4:7:354:GLN:HB3	1.98	0.46
1:J:629:GLU:HG2	1:J:643:GLY:C	2.35	0.46
1:J:714:ARG:HD3	1:J:766:PHE:CE2	2.50	0.46
4:1:162:ASN:OD1	4:1:277:THR:HG22	2.15	0.46
4:1:299:MET:HE2	4:1:331:ALA:HB2	1.96	0.46
4:6:299:MET:HE2	4:6:331:ALA:HB2	1.96	0.46
4:8:299:MET:HE2	4:8:331:ALA:HB2	1.95	0.46
4:Y:299:MET:HE2	4:Y:331:ALA:HB2	1.96	0.46
1:A:41:VAL:CG1	1:A:42:HIS:N	2.76	0.46
1:A:42:HIS:O	1:A:45:GLN:O	2.33	0.46
1:A:106:LEU:HD12	1:A:117:THR:HG21	1.96	0.46
1:A:292:MET:HE1	1:A:309:PRO:CG	2.46	0.46
1:A:714:ARG:HD3	1:A:766:PHE:CE2	2.50	0.46
1:A:800:ARG:CZ	3:C:149:VAL:O	2.63	0.46
1:D:42:HIS:O	1:D:45:GLN:O	2.33	0.46
1:D:530:MET:HE3	4:5:354:GLN:CB	2.44	0.46
1:D:540:CYS:N	4:5:349:LEU:HD11	2.31	0.46
1:D:643:GLY:N	4:5:23:GLY:C	2.55	0.46
1:D:715:VAL:CG1	1:D:720:PHE:HB2	2.46	0.46
1:D:809:ARG:NH1	2:E:124:GLY:O	2.48	0.46
1:D:815:CYS:O	2:E:90:GLY:C	2.53	0.46
1:D:831:TRP:CA	2:E:51:PHE:CZ	2.98	0.46
2:E:163:ALA:O	2:K:21:GLU:N	2.47	0.46
1:G:218:LEU:HA	1:G:221:GLN:H	1.79	0.46
1:G:715:VAL:CG1	1:G:720:PHE:HB2	2.45	0.46
3:I:53:PRO:O	3:I:55:LYS:HG3	2.15	0.46
1:J:559:LEU:HD23	1:J:560:GLY:N	2.30	0.46
1:J:715:VAL:CG1	1:J:720:PHE:HB2	2.45	0.46
1:J:800:ARG:CB	3:L:149:VAL:HG23	2.26	0.46
2:K:160:GLY:O	2:K:161:GLU:HG2	2.15	0.46
4:5:6:THR:HG22	4:5:101:HIS:HA	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:7:6:THR:HG22	4:7:101:HIS:HA	1.98	0.46
4:V:6:THR:HG22	4:V:101:HIS:HA	1.97	0.46
1:A:559:LEU:HD23	1:A:560:GLY:N	2.30	0.46
1:A:715:VAL:CG1	1:A:720:PHE:HB2	2.45	0.46
1:A:724:TYR:HD1	1:A:727:LEU:CD1	2.27	0.46
1:D:218:LEU:HA	1:D:221:GLN:H	1.79	0.46
1:D:374:GLN:NE2	1:D:403:TYR:CE1	2.84	0.46
1:D:543:PRO:CD	4:5:143:TYR:O	2.64	0.46
1:D:595:TRP:N	1:D:595:TRP:CD1	2.80	0.46
1:D:640:LYS:HB3	1:D:645:SER:CB	2.42	0.46
1:D:714:ARG:HD3	1:D:766:PHE:CE2	2.50	0.46
1:D:769:ALA:C	1:D:771:LEU:HA	2.36	0.46
1:G:139:VAL:HG12	1:G:143:TYR:HD2	1.81	0.46
1:G:784:ALA:O	1:G:788:THR:CA	2.62	0.46
1:J:82:PRO:HG2	1:J:85:TYR:CE2	2.50	0.46
1:J:540:CYS:N	4:7:349:LEU:HD11	2.31	0.46
1:J:797:PHE:CD2	3:L:126:LEU:HD22	2.50	0.46
1:J:797:PHE:CE2	3:L:126:LEU:CD2	2.99	0.46
4:4:287:ILE:CB	4:6:204:ALA:H	2.13	0.46
1:A:87:MLY:HH12	1:A:87:MLY:HD3	1.61	0.46
1:A:136:ASN:HA	1:A:137:PRO:HD3	1.50	0.46
1:A:374:GLN:NE2	1:A:403:TYR:CE1	2.84	0.46
1:A:543:PRO:HD2	4:4:146:GLY:O	2.15	0.46
1:A:568:PRO:HD3	1:A:579:PHE:HA	1.97	0.46
1:A:834:LEU:CD1	2:B:54:MET:CG	2.49	0.46
1:A:836:PHE:CB	2:B:161:GLU:HG2	2.37	0.46
1:D:82:PRO:HG2	1:D:85:TYR:CE2	2.51	0.46
1:D:322:VAL:HB	1:D:325:ILE:HG13	1.97	0.46
1:D:332:MET:H	1:D:332:MET:HG2	1.52	0.46
1:D:529:PRO:HB2	4:5:354:GLN:HB3	1.98	0.46
1:D:629:GLU:HG2	1:D:643:GLY:C	2.35	0.46
1:D:797:PHE:CE2	3:F:126:LEU:HD22	2.50	0.46
1:G:311:ASP:CB	1:G:312:TYR:CE1	2.98	0.46
1:G:659:MLY:HD2	1:G:659:MLY:HH22	1.42	0.46
1:J:84:MLY:HH11	1:J:720:PHE:CA	2.45	0.46
1:J:218:LEU:HA	1:J:221:GLN:H	1.79	0.46
1:J:292:MET:HE1	1:J:309:PRO:CG	2.46	0.46
1:J:793:ARG:O	1:J:797:PHE:N	2.39	0.46
4:V:366:GLY:O	4:V:369:ILE:HG22	2.16	0.46
4:W:253:GLU:HA	4:W:256:ARG:CG	2.42	0.46
4:X:6:THR:HG22	4:X:101:HIS:HA	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:326:ASP:O	1:A:330:GLU:HG2	2.16	0.46
1:A:411:GLU:H	4:4:333:PRO:HB2	1.80	0.46
1:A:543:PRO:CD	4:4:143:TYR:O	2.63	0.46
1:A:783:LEU:N	1:A:783:LEU:CD1	2.79	0.46
1:D:206:LYS:HD3	1:D:217:THR:OG1	2.16	0.46
1:D:265:ILE:CG2	1:D:266:GLU:N	2.78	0.46
1:D:448:GLN:C	1:D:450:ASP:H	2.19	0.46
1:D:640:LYS:C	4:5:23:GLY:C	2.74	0.46
1:G:374:GLN:NE2	1:G:403:TYR:CE1	2.84	0.46
1:G:400:ALA:HB1	1:G:606:THR:CG2	2.45	0.46
1:G:524:GLU:HB3	1:G:528:MLY:HG2	1.96	0.46
1:G:636:LYS:O	4:6:144:ALA:HB1	2.14	0.46
1:G:835:PHE:O	1:G:839:MLY:N	2.49	0.46
4:7:366:GLY:O	4:7:369:ILE:HG22	2.16	0.46
1:A:93:MET:CE	1:A:715:VAL:HA	2.45	0.46
1:A:206:LYS:HD3	1:A:217:THR:OG1	2.16	0.46
1:A:311:ASP:CB	1:A:312:TYR:CE1	2.98	0.46
1:A:335:ASP:OD1	1:A:348:MLY:NZ	2.49	0.46
1:A:361:TYR:O	1:A:364:LEU:HB2	2.16	0.46
1:A:640:LYS:C	4:4:23:GLY:C	2.74	0.46
1:A:642:LYS:CB	4:4:24:ASP:O	2.59	0.46
1:A:817:GLN:NE2	2:B:127:ARG:HG2	2.30	0.46
1:D:335:ASP:OD1	1:D:348:MLY:NZ	2.49	0.46
2:E:114:LYS:CG	2:E:146:GLY:HA2	2.46	0.46
1:G:89:GLU:CD	1:G:153:PRO:HD2	2.36	0.46
1:G:136:ASN:HA	1:G:137:PRO:HD3	1.49	0.46
1:G:335:ASP:OD1	1:G:348:MLY:NZ	2.49	0.46
1:G:642:LYS:HA	4:6:21:PHE:C	2.36	0.46
1:G:714:ARG:HD3	1:G:766:PHE:CE2	2.51	0.46
1:G:725:ARG:NE	1:G:733:PRO:CB	1.95	0.46
2:H:88:LEU:HB3	2:H:91:ALA:HB2	1.98	0.46
1:J:30:MLY:HB3	1:J:31:PRO:HD2	1.97	0.46
1:J:194:GLN:HE21	1:J:194:GLN:HB3	1.43	0.46
1:J:206:LYS:HD3	1:J:217:THR:OG1	2.16	0.46
1:J:503:TYR:CZ	1:J:711:PHE:CD2	3.03	0.46
1:J:543:PRO:HD2	4:7:146:GLY:O	2.16	0.46
1:J:642:LYS:HA	4:7:21:PHE:C	2.36	0.46
4:X:299:MET:HE2	4:X:331:ALA:HB2	1.98	0.46
4:X:366:GLY:O	4:X:369:ILE:HG22	2.16	0.46
4:Z:366:GLY:O	4:Z:369:ILE:HG22	2.16	0.46
1:A:629:GLU:CA	1:A:643:GLY:C	2.73	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:642:LYS:HA	4:4:21:PHE:C	2.36	0.46
1:A:695:LEU:HB3	1:A:701:LEU:HD22	1.97	0.46
1:A:725:ARG:NE	1:A:733:PRO:CB	1.95	0.46
1:A:793:ARG:HE	3:C:147:MET:CB	2.29	0.46
2:B:149:ASP:CG	2:B:150:TYR:N	2.49	0.46
1:D:443:ILE:HG22	1:D:444:ARG:N	2.29	0.46
1:D:510:TRP:CZ3	1:D:711:PHE:CE2	3.04	0.46
1:D:767:PHE:C	1:D:771:LEU:HD11	2.36	0.46
1:D:831:TRP:CE2	2:E:47:LEU:HB3	2.50	0.46
1:G:42:HIS:O	1:G:45:GLN:O	2.33	0.46
1:G:278:GLN:HE21	1:G:278:GLN:HB3	1.42	0.46
1:G:361:TYR:O	1:G:364:LEU:HB2	2.16	0.46
1:J:322:VAL:HB	1:J:325:ILE:HG13	1.98	0.46
1:J:695:LEU:HB3	1:J:701:LEU:HD22	1.97	0.46
1:J:795:ARG:HH22	3:L:116:GLU:CD	2.19	0.46
1:J:797:PHE:HE2	3:L:126:LEU:HD23	1.81	0.46
2:K:88:LEU:HB3	2:K:91:ALA:HB2	1.98	0.46
4:0:190:MET:O	4:0:194:THR:HG23	2.16	0.46
4:3:6:THR:HG22	4:3:101:HIS:HA	1.98	0.46
4:3:299:MET:HE2	4:3:331:ALA:HB2	1.97	0.46
4:3:366:GLY:O	4:3:369:ILE:HG22	2.16	0.46
4:5:366:GLY:O	4:5:369:ILE:HG22	2.16	0.46
4:V:190:MET:O	4:V:194:THR:HG23	2.16	0.46
4:W:162:ASN:OD1	4:W:277:THR:HG22	2.15	0.46
1:A:464:ILE:CG2	1:A:465:ALA:N	2.79	0.46
2:B:137:TRP:CA	2:B:145:ALA:HB2	2.37	0.46
1:D:99:GLU:N	1:D:100:PRO:CD	2.79	0.46
1:D:642:LYS:HA	4:5:21:PHE:C	2.36	0.46
1:G:206:LYS:HD3	1:G:217:THR:OG1	2.16	0.46
1:G:326:ASP:O	1:G:330:GLU:HG2	2.16	0.46
1:G:411:GLU:H	4:6:333:PRO:HB2	1.80	0.46
1:J:769:ALA:HB2	1:J:770:GLY:N	2.30	0.46
1:J:798:LEU:HA	1:J:798:LEU:HD12	1.36	0.46
4:3:324:THR:N	4:5:245:GLY:CA	2.69	0.46
1:A:214:MET:HA	1:A:340:ILE:CD1	2.42	0.46
1:A:295:MLY:HG3	1:A:332:MET:HE2	1.95	0.46
1:A:332:MET:H	1:A:332:MET:HG2	1.52	0.46
1:A:418:THR:CG2	1:A:419:VAL:N	2.79	0.46
1:A:418:THR:CB	1:A:421:GLU:HG3	2.37	0.46
1:A:502:GLU:OE2	1:A:764:MLY:O	2.34	0.46
1:A:793:ARG:O	1:A:797:PHE:N	2.40	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:798:LEU:HD13	3:C:126:LEU:HD11	1.98	0.46
3:C:50:LEU:O	3:C:53:PRO:CD	2.63	0.46
1:D:89:GLU:CD	1:D:153:PRO:HD2	2.36	0.46
1:D:136:ASN:O	1:D:139:VAL:N	2.47	0.46
1:D:559:LEU:HD23	1:D:560:GLY:N	2.30	0.46
1:D:810:ARG:HG2	1:D:810:ARG:NH1	2.29	0.46
1:D:822:SER:HB3	2:E:88:LEU:CD2	2.40	0.46
3:F:50:LEU:O	3:F:53:PRO:CD	2.63	0.46
1:G:82:PRO:HG2	1:G:85:TYR:CE2	2.51	0.46
1:G:206:LYS:HD2	1:G:217:THR:CG2	2.17	0.46
1:G:354:LEU:HD12	1:G:354:LEU:HA	1.56	0.46
1:G:543:PRO:CD	4:6:143:TYR:O	2.64	0.46
1:G:821:ARG:NH2	2:H:127:ARG:CD	2.74	0.46
2:H:137:TRP:CZ3	2:H:145:ALA:N	2.81	0.46
1:J:218:LEU:HD22	1:J:222:ILE:HG13	1.95	0.46
1:J:361:TYR:O	1:J:364:LEU:HB2	2.16	0.46
1:J:715:VAL:HG11	1:J:720:PHE:CD1	2.49	0.46
2:K:112:ILE:O	2:K:148:VAL:HA	2.16	0.46
4:7:253:GLU:HA	4:7:256:ARG:CG	2.42	0.46
4:V:223:PHE:CD2	4:V:259:GLU:HG3	2.51	0.46
4:W:32:PRO:HB2	4:W:34:ILE:HD11	1.98	0.46
1:A:501:GLU:HG2	1:A:762:HIS:CE1	2.44	0.45
1:D:664:LEU:HD12	1:D:664:LEU:HA	1.53	0.45
1:D:818:TYR:HB3	2:E:89:LYS:HB2	1.99	0.45
1:G:332:MET:O	1:G:336:SER:OG	2.27	0.45
1:G:448:GLN:C	1:G:450:ASP:H	2.19	0.45
1:G:464:ILE:CG2	1:G:465:ALA:N	2.79	0.45
1:G:728:ASN:HD21	3:I:109:HIS:C	2.20	0.45
1:J:292:MET:HE1	1:J:309:PRO:HD3	1.98	0.45
1:J:330:GLU:O	1:J:333:ALA:HB3	2.16	0.45
1:J:783:LEU:N	1:J:783:LEU:CD1	2.78	0.45
3:L:52:ASN:CB	3:L:53:PRO:CD	2.92	0.45
4:1:190:MET:O	4:1:194:THR:HG23	2.16	0.45
4:4:253:GLU:HA	4:4:256:ARG:CG	2.42	0.45
4:7:223:PHE:CD2	4:7:259:GLU:HG3	2.51	0.45
4:8:324:THR:N	4:W:245:GLY:CA	2.69	0.45
4:V:288:ASP:CA	4:X:204:ALA:HB2	2.31	0.45
4:Y:32:PRO:HB2	4:Y:34:ILE:HD11	1.98	0.45
4:Z:6:THR:HG22	4:Z:101:HIS:HA	1.98	0.45
1:A:30:MLY:HB3	1:A:31:PRO:HD2	1.97	0.45
1:A:82:PRO:HG2	1:A:85:TYR:CE2	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:629:GLU:HG2	1:A:643:GLY:C	2.35	0.45
1:A:637:LYS:HD2	4:4:144:ALA:HB3	1.21	0.45
1:D:724:TYR:N	1:D:782:MLY:CH2	2.80	0.45
1:D:726:VAL:H	1:D:782:MLY:HH21	1.80	0.45
1:D:818:TYR:CD2	2:E:89:LYS:CB	2.99	0.45
1:G:30:MLY:HB3	1:G:31:PRO:HD2	1.97	0.45
1:G:436:MLY:HE3	1:G:626:TYR:HE1	1.77	0.45
1:J:56:GLU:HB2	1:J:59:MLY:CB	2.30	0.45
1:J:84:MLY:HH23	1:J:716:LEU:O	2.12	0.45
1:J:265:ILE:CG2	1:J:266:GLU:N	2.79	0.45
1:J:335:ASP:OD1	1:J:348:MLY:NZ	2.49	0.45
1:J:642:LYS:NZ	4:7:340:TRP:O	2.50	0.45
1:J:815:CYS:SG	2:K:92:ASP:OD1	2.74	0.45
4:0:6:THR:HG22	4:0:101:HIS:HA	1.97	0.45
4:0:366:GLY:O	4:0:369:ILE:HG22	2.16	0.45
4:2:190:MET:O	4:2:194:THR:HG23	2.16	0.45
4:7:190:MET:O	4:7:194:THR:HG23	2.16	0.45
4:X:190:MET:O	4:X:194:THR:HG23	2.16	0.45
4:X:324:THR:N	4:Z:245:GLY:CA	2.69	0.45
1:A:17:LEU:HD12	1:A:17:LEU:HA	1.68	0.45
1:A:476:GLU:OE2	1:A:598:MLY:HH13	2.17	0.45
1:A:667:THR:O	1:A:669:PRO:HD3	2.16	0.45
1:A:723:ARG:CG	1:A:723:ARG:NH1	2.79	0.45
1:A:733:PRO:O	1:A:737:PHE:CE1	2.53	0.45
1:D:136:ASN:HA	1:D:137:PRO:HD3	1.50	0.45
1:D:410:ASN:HA	4:5:334:GLU:HB3	1.29	0.45
1:D:476:GLU:OE2	1:D:598:MLY:HH13	2.16	0.45
1:D:612:GLN:NE2	1:D:627:GLY:H	2.14	0.45
1:G:17:LEU:HA	1:G:17:LEU:HD12	1.67	0.45
1:G:55:MLY:HH23	1:G:60:VAL:HG22	1.99	0.45
1:G:93:MET:SD	1:G:763:THR:CG2	2.94	0.45
1:G:144:ARG:HA	1:G:144:ARG:HD2	1.78	0.45
1:G:186:THR:O	1:G:190:MLY:HG2	2.17	0.45
1:G:322:VAL:HB	1:G:325:ILE:HG13	1.98	0.45
1:G:637:LYS:HD2	4:6:144:ALA:HB3	1.20	0.45
1:G:639:GLY:CA	4:6:344:SER:O	2.40	0.45
2:H:112:ILE:O	2:H:148:VAL:HA	2.16	0.45
1:J:186:THR:O	1:J:190:MLY:HG2	2.17	0.45
1:J:202:SER:HA	1:J:207:LYS:NZ	2.22	0.45
1:J:332:MET:O	1:J:336:SER:OG	2.27	0.45
1:J:448:GLN:C	1:J:450:ASP:H	2.19	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:732:ILE:CG2	1:J:747:LEU:CD1	0.65	0.45
4:1:6:THR:HG22	4:1:101:HIS:HA	1.98	0.45
4:X:223:PHE:CD2	4:X:259:GLU:HG3	2.52	0.45
4:X:288:ASP:CA	4:Z:204:ALA:HB2	2.31	0.45
1:A:139:VAL:HG12	1:A:143:TYR:HD2	1.81	0.45
1:A:206:LYS:CE	1:A:217:THR:HG23	2.29	0.45
1:A:322:VAL:HB	1:A:325:ILE:HG13	1.98	0.45
1:A:496:PHE:CE2	1:A:514:ASP:HA	2.50	0.45
1:A:529:PRO:HB2	4:4:354:GLN:HB3	1.98	0.45
1:A:642:LYS:HB2	4:4:24:ASP:O	1.88	0.45
1:D:330:GLU:O	1:D:333:ALA:HB3	2.17	0.45
1:D:464:ILE:CG2	1:D:465:ALA:N	2.79	0.45
1:D:818:TYR:CD2	2:E:89:LYS:HB3	2.52	0.45
1:D:830:PRO:CB	2:E:51:PHE:CE2	2.95	0.45
1:G:265:ILE:CG2	1:G:266:GLU:N	2.79	0.45
1:G:540:CYS:C	4:6:349:LEU:HD21	2.36	0.45
1:G:540:CYS:N	4:6:349:LEU:HD11	2.31	0.45
1:G:629:GLU:CB	1:G:645:SER:N	2.74	0.45
1:G:823:PHE:HE1	2:H:156:VAL:O	1.89	0.45
2:H:114:LYS:CG	2:H:146:GLY:HA2	2.46	0.45
1:J:17:LEU:HA	1:J:17:LEU:HD12	1.67	0.45
1:J:534:SER:HB2	4:7:354:GLN:HE22	1.56	0.45
1:J:723:ARG:CG	1:J:723:ARG:NH1	2.79	0.45
4:1:32:PRO:HB2	4:1:34:ILE:HD11	1.98	0.45
4:1:366:GLY:O	4:1:369:ILE:HG22	2.16	0.45
4:5:299:MET:HE2	4:5:331:ALA:HB2	1.98	0.45
4:6:32:PRO:HB2	4:6:34:ILE:HD11	1.98	0.45
4:8:6:THR:HG22	4:8:101:HIS:HA	1.98	0.45
4:8:288:ASP:CA	4:W:204:ALA:HB2	2.31	0.45
1:A:89:GLU:CD	1:A:153:PRO:HD2	2.36	0.45
1:A:296:MLY:O	1:A:299:LEU:HB2	2.17	0.45
1:A:411:GLU:H	4:4:333:PRO:CB	2.30	0.45
1:D:97:LEU:HD12	1:D:97:LEU:HA	1.67	0.45
1:D:411:GLU:H	4:5:333:PRO:CB	2.29	0.45
1:D:449:LEU:HD12	1:D:449:LEU:HA	1.60	0.45
2:E:112:ILE:O	2:E:148:VAL:HA	2.17	0.45
1:G:757:GLN:NE2	1:G:772:LEU:CD2	2.80	0.45
1:G:757:GLN:HE22	1:G:772:LEU:HG	1.80	0.45
3:I:50:LEU:O	3:I:53:PRO:CD	2.63	0.45
1:J:89:GLU:CD	1:J:153:PRO:HD2	2.37	0.45
1:J:476:GLU:OE2	1:J:598:MLY:HH13	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:640:LYS:HB3	1:J:645:SER:CB	2.42	0.45
1:J:724:TYR:HD1	1:J:727:LEU:CD1	2.27	0.45
1:J:725:ARG:HA	1:J:732:ILE:HG22	1.99	0.45
4:5:223:PHE:CD2	4:5:259:GLU:HG3	2.51	0.45
4:8:32:PRO:HB2	4:8:34:ILE:HD11	1.98	0.45
4:X:287:ILE:HA	4:Z:202:THR:HG21	1.59	0.45
1:A:55:MLY:HH23	1:A:60:VAL:HG22	1.99	0.45
1:A:179:GLY:O	1:A:185:LYS:HE2	2.17	0.45
1:A:443:ILE:HG22	1:A:444:ARG:N	2.29	0.45
1:D:179:GLY:O	1:D:185:LYS:HE2	2.17	0.45
1:D:642:LYS:NZ	4:5:340:TRP:O	2.50	0.45
1:D:725:ARG:HH21	1:D:733:PRO:HB2	1.81	0.45
1:D:783:LEU:N	1:D:783:LEU:CD1	2.78	0.45
1:G:173:GLN:HG3	1:G:670:HIS:HD2	1.82	0.45
1:G:529:PRO:HB2	4:6:354:GLN:HB3	1.98	0.45
1:G:725:ARG:HH21	1:G:733:PRO:HB2	1.81	0.45
1:G:800:ARG:CD	3:I:149:VAL:HG22	2.41	0.45
1:J:173:GLN:HG3	1:J:670:HIS:HD2	1.82	0.45
1:J:530:MET:CE	4:7:354:GLN:HG3	2.35	0.45
1:J:707:CYS:C	1:J:714:ARG:NH2	2.70	0.45
1:J:797:PHE:HD2	3:L:126:LEU:CD2	2.27	0.45
4:0:223:PHE:CD2	4:0:259:GLU:HG3	2.51	0.45
4:0:287:ILE:HA	4:2:202:THR:HG21	1.59	0.45
4:2:6:THR:HG22	4:2:101:HIS:HA	1.98	0.45
4:2:253:GLU:HA	4:2:256:ARG:CG	2.42	0.45
4:2:366:GLY:O	4:2:369:ILE:HG22	2.16	0.45
4:3:32:PRO:HB2	4:3:34:ILE:HD11	1.98	0.45
4:3:190:MET:O	4:3:194:THR:HG23	2.16	0.45
4:5:290:ARG:HH22	4:7:202:THR:CG2	2.17	0.45
4:6:6:THR:HG22	4:6:101:HIS:HA	1.97	0.45
4:Z:223:PHE:CD2	4:Z:259:GLU:HG3	2.52	0.45
1:A:210:GLN:C	1:A:211:SER:HG	2.15	0.45
1:A:448:GLN:C	1:A:450:ASP:H	2.19	0.45
1:A:540:CYS:N	4:4:349:LEU:HD11	2.31	0.45
2:B:112:ILE:O	2:B:148:VAL:HA	2.17	0.45
1:D:103:LEU:HD22	1:D:692:LEU:HG	1.98	0.45
1:D:229:LEU:HD12	1:D:229:LEU:HA	1.75	0.45
1:D:295:MLY:CG	1:D:332:MET:HE1	2.46	0.45
1:D:296:MLY:O	1:D:299:LEU:HB2	2.17	0.45
1:D:326:ASP:O	1:D:330:GLU:HG2	2.16	0.45
1:D:361:TYR:O	1:D:364:LEU:HB2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:822:SER:HB3	2:E:88:LEU:HD21	1.99	0.45
1:D:835:PHE:O	1:D:839:MLY:N	2.49	0.45
1:G:292:MET:HE1	1:G:309:PRO:CG	2.46	0.45
1:G:418:THR:CG2	1:G:419:VAL:N	2.79	0.45
1:G:496:PHE:CE2	1:G:514:ASP:HA	2.50	0.45
1:G:612:GLN:NE2	1:G:627:GLY:H	2.14	0.45
1:G:642:LYS:NZ	4:6:340:TRP:O	2.50	0.45
1:J:179:GLY:O	1:J:185:LYS:HE2	2.17	0.45
1:J:326:ASP:O	1:J:330:GLU:HG2	2.16	0.45
1:J:732:ILE:H	1:J:733:PRO:HD2	1.74	0.45
4:4:366:GLY:O	4:4:369:ILE:HG22	2.16	0.45
4:6:288:ASP:CA	4:8:204:ALA:HB2	2.31	0.45
4:W:6:THR:HG22	4:W:101:HIS:HA	1.98	0.45
4:Y:366:GLY:O	4:Y:369:ILE:HG22	2.16	0.45
1:A:206:LYS:HD2	1:A:217:THR:CG2	2.17	0.45
1:A:278:GLN:HE21	1:A:278:GLN:HB3	1.42	0.45
1:D:14:ALA:N	1:D:15:PRO:HD2	2.32	0.45
1:D:37:SER:O	1:D:38:VAL:HG23	2.17	0.45
1:D:202:SER:HA	1:D:207:LYS:NZ	2.23	0.45
1:D:226:ASN:N	1:D:227:PRO:HD2	2.32	0.45
1:D:725:ARG:CG	1:D:733:PRO:HA	2.43	0.45
1:D:767:PHE:C	1:D:771:LEU:CD1	2.85	0.45
1:G:99:GLU:N	1:G:100:PRO:CD	2.80	0.45
1:G:410:ASN:HA	4:6:334:GLU:HB3	1.28	0.45
1:G:476:GLU:OE2	1:G:598:MLY:HH13	2.17	0.45
1:G:485:GLU:OE1	1:G:583:HIS:ND1	2.49	0.45
1:G:597:GLU:O	1:G:600:MLY:N	2.50	0.45
1:G:747:LEU:C	1:G:749:GLY:H	2.20	0.45
2:K:137:TRP:CA	2:K:145:ALA:HB2	2.37	0.45
4:0:287:ILE:CB	4:2:204:ALA:H	2.13	0.45
4:1:288:ASP:CA	4:3:204:ALA:HB2	2.32	0.45
4:2:287:ILE:HA	4:4:202:THR:HG21	1.59	0.45
4:4:190:MET:O	4:4:194:THR:HG23	2.16	0.45
1:D:186:THR:O	1:D:190:MLY:HG2	2.17	0.45
1:D:597:GLU:O	1:D:600:MLY:N	2.50	0.45
1:D:769:ALA:HB1	1:D:771:LEU:N	2.25	0.45
1:G:176:LEU:N	1:G:176:LEU:CD1	2.75	0.45
1:G:642:LYS:HG3	4:6:23:GLY:CA	2.31	0.45
1:G:725:ARG:CG	1:G:733:PRO:CA	2.95	0.45
2:H:137:TRP:CA	2:H:145:ALA:HB2	2.37	0.45
1:J:408:VAL:HG22	1:J:636:LYS:HG2	1.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:794:CYS:O	1:J:797:PHE:HB3	2.17	0.45
4:0:32:PRO:HB2	4:0:34:ILE:HD11	1.98	0.45
4:2:223:PHE:CD2	4:2:259:GLU:HG3	2.52	0.45
4:4:6:THR:HG22	4:4:101:HIS:HA	1.98	0.45
4:8:223:PHE:CD2	4:8:259:GLU:HG3	2.51	0.45
4:Y:6:THR:HG22	4:Y:101:HIS:HA	1.98	0.45
1:A:106:LEU:HD12	1:A:106:LEU:HA	1.79	0.45
1:A:163:TYR:O	1:A:166:MET:HB3	2.16	0.45
1:A:195:TYR:CE2	1:A:199:ILE:HD12	2.52	0.45
1:A:224:SER:O	1:A:227:PRO:HD2	2.17	0.45
1:A:322:VAL:CG1	1:A:325:ILE:HD11	2.47	0.45
1:A:488:GLN:O	1:A:491:PHE:HB3	2.17	0.45
1:A:519:LEU:N	1:A:519:LEU:CD1	2.77	0.45
1:A:747:LEU:C	1:A:749:GLY:H	2.20	0.45
1:A:839:MLY:CE	2:B:159:HIS:HB3	2.47	0.45
1:D:64:THR:HB	1:D:68:GLU:N	2.33	0.45
1:D:106:LEU:HD12	1:D:106:LEU:HA	1.79	0.45
1:D:675:ILE:HG23	1:D:676:ILE:N	2.32	0.45
1:G:14:ALA:N	1:G:15:PRO:HD2	2.32	0.45
1:G:296:MLY:O	1:G:299:LEU:HB2	2.17	0.45
1:G:408:VAL:CG1	4:6:332:PRO:HB3	2.41	0.45
1:G:640:LYS:C	4:6:23:GLY:C	2.75	0.45
1:G:768:MLY:HD3	1:G:772:LEU:CB	2.47	0.45
1:G:794:CYS:O	1:G:797:PHE:HB3	2.17	0.45
1:J:14:ALA:N	1:J:15:PRO:HD2	2.32	0.45
1:J:37:SER:O	1:J:38:VAL:HG23	2.17	0.45
1:J:322:VAL:CG1	1:J:325:ILE:HD11	2.47	0.45
1:J:553:MLY:NZ	4:V:45:VAL:CA	2.58	0.45
1:J:597:GLU:O	1:J:600:MLY:N	2.50	0.45
1:J:642:LYS:CB	4:7:24:ASP:O	2.60	0.45
1:J:667:THR:O	1:J:669:PRO:HD3	2.16	0.45
1:J:797:PHE:CE2	3:L:126:LEU:HD23	2.52	0.45
1:J:831:TRP:CZ3	2:K:34:ILE:HD11	2.36	0.45
4:4:223:PHE:CD2	4:4:259:GLU:HG3	2.51	0.45
4:6:223:PHE:CD2	4:6:259:GLU:HG3	2.51	0.45
4:6:324:THR:O	4:8:244:ASP:HA	2.09	0.45
4:8:366:GLY:O	4:8:369:ILE:HG22	2.16	0.45
4:V:287:ILE:CB	4:X:204:ALA:H	2.13	0.45
4:W:223:PHE:CD2	4:W:259:GLU:HG3	2.51	0.45
4:W:287:ILE:HA	4:Y:202:THR:HG21	1.59	0.45
4:Z:32:PRO:HB2	4:Z:34:ILE:HD11	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:37:SER:O	1:A:38:VAL:HG23	2.17	0.44
1:A:99:GLU:N	1:A:100:PRO:CD	2.80	0.44
1:A:229:LEU:HD12	1:A:229:LEU:HA	1.75	0.44
1:A:346:ASP:O	1:A:350:ALA:N	2.46	0.44
1:A:597:GLU:O	1:A:600:MLY:N	2.50	0.44
1:A:642:LYS:NZ	4:4:340:TRP:O	2.50	0.44
1:D:41:VAL:CG1	1:D:42:HIS:N	2.75	0.44
1:D:139:VAL:HG12	1:D:143:TYR:HD2	1.81	0.44
1:D:486:MLY:HH22	1:D:527:GLU:CD	2.37	0.44
1:D:568:PRO:CG	1:D:578:HIS:H	2.30	0.44
2:E:137:TRP:CZ3	2:E:145:ALA:N	2.81	0.44
1:G:64:THR:HB	1:G:68:GLU:N	2.32	0.44
1:G:667:THR:O	1:G:669:PRO:HD3	2.16	0.44
1:J:226:ASN:N	1:J:227:PRO:HD2	2.32	0.44
1:J:464:ILE:CG2	1:J:465:ALA:N	2.80	0.44
1:J:673:ARG:HA	1:J:673:ARG:HD2	1.79	0.44
1:J:732:ILE:HG23	1:J:747:LEU:HD12	0.95	0.44
1:J:829:TRP:HA	1:J:830:PRO:HD2	1.86	0.44
4:0:223:PHE:HB3	4:0:259:GLU:OE2	2.18	0.44
4:0:299:MET:HE2	4:0:331:ALA:HB2	1.99	0.44
4:2:223:PHE:HB3	4:2:259:GLU:OE2	2.18	0.44
4:3:223:PHE:HB3	4:3:259:GLU:OE2	2.18	0.44
4:4:32:PRO:HB2	4:4:34:ILE:HD11	1.98	0.44
4:5:190:MET:O	4:5:194:THR:HG23	2.16	0.44
4:5:223:PHE:HB3	4:5:259:GLU:OE2	2.18	0.44
4:X:32:PRO:HB2	4:X:34:ILE:HD11	1.98	0.44
4:Z:223:PHE:HB3	4:Z:259:GLU:OE2	2.18	0.44
1:A:48:VAL:HA	1:A:104:TYR:OH	2.17	0.44
1:A:64:THR:HB	1:A:68:GLU:N	2.33	0.44
1:A:186:THR:O	1:A:190:MLY:HG2	2.17	0.44
1:A:711:PHE:HB3	1:A:766:PHE:HB3	1.99	0.44
1:A:794:CYS:O	1:A:797:PHE:HB3	2.17	0.44
1:D:163:TYR:O	1:D:166:MET:HB3	2.17	0.44
1:D:278:GLN:HE21	1:D:278:GLN:HB3	1.42	0.44
1:D:640:LYS:C	1:D:645:SER:HG	2.09	0.44
2:E:121:LEU:O	2:E:128:PHE:CG	2.61	0.44
1:G:155:ILE:HG22	1:G:156:PHE:N	2.33	0.44
1:G:411:GLU:H	4:6:333:PRO:CB	2.29	0.44
1:G:485:GLU:HA	1:G:584:TYR:HE2	1.83	0.44
1:G:488:GLN:O	1:G:491:PHE:HB3	2.17	0.44
1:G:519:LEU:N	1:G:519:LEU:CD1	2.77	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:823:PHE:CE2	2:H:140:PHE:CZ	3.05	0.44
1:J:64:THR:HB	1:J:68:GLU:N	2.33	0.44
1:J:689:GLU:HA	1:J:692:LEU:HB2	2.00	0.44
4:1:223:PHE:HB3	4:1:259:GLU:OE2	2.18	0.44
4:4:324:THR:N	4:6:245:GLY:CA	2.69	0.44
4:5:32:PRO:HB2	4:5:34:ILE:HD11	1.98	0.44
4:7:32:PRO:HB2	4:7:34:ILE:HD11	1.98	0.44
4:7:223:PHE:HB3	4:7:259:GLU:OE2	2.18	0.44
4:V:287:ILE:HA	4:X:202:THR:HG21	1.59	0.44
4:W:366:GLY:O	4:W:369:ILE:HG22	2.16	0.44
4:X:223:PHE:HB3	4:X:259:GLU:OE2	2.18	0.44
4:Z:190:MET:O	4:Z:194:THR:HG23	2.16	0.44
1:A:97:LEU:HD12	1:A:97:LEU:HA	1.67	0.44
1:A:725:ARG:HH21	1:A:733:PRO:HB2	1.81	0.44
1:D:488:GLN:O	1:D:491:PHE:HB3	2.17	0.44
1:D:689:GLU:HA	1:D:692:LEU:HB2	1.99	0.44
1:D:708:ARG:O	1:D:710:GLY:N	2.50	0.44
1:D:723:ARG:O	1:D:782:MLY:HD2	1.99	0.44
1:D:794:CYS:O	1:D:797:PHE:HB3	2.16	0.44
2:E:129:THR:HG23	2:E:132:GLU:OE1	2.17	0.44
1:G:179:GLY:O	1:G:185:LYS:HE2	2.17	0.44
1:G:530:MET:CB	4:6:354:GLN:CB	2.96	0.44
1:G:629:GLU:HG2	1:G:643:GLY:C	2.35	0.44
2:H:112:ILE:O	2:H:148:VAL:N	2.50	0.44
1:J:408:VAL:HA	1:J:636:LYS:HG3	1.03	0.44
1:J:486:MLY:HH22	1:J:527:GLU:CD	2.37	0.44
1:J:488:GLN:O	1:J:491:PHE:HB3	2.17	0.44
1:J:543:PRO:CD	4:7:143:TYR:O	2.64	0.44
1:J:639:GLY:H	4:7:344:SER:HB3	1.83	0.44
1:J:725:ARG:HH21	1:J:733:PRO:HB2	1.82	0.44
1:J:817:GLN:CB	2:K:127:ARG:HD2	2.47	0.44
4:1:223:PHE:CD2	4:1:259:GLU:HG3	2.52	0.44
4:3:288:ASP:CA	4:5:204:ALA:HB2	2.31	0.44
4:6:190:MET:O	4:6:194:THR:HG23	2.16	0.44
4:V:32:PRO:HB2	4:V:34:ILE:HD11	1.98	0.44
4:V:223:PHE:HB3	4:V:259:GLU:OE2	2.18	0.44
4:Y:223:PHE:CD2	4:Y:259:GLU:HG3	2.52	0.44
1:A:502:GLU:CD	1:A:763:THR:N	2.56	0.44
1:A:793:ARG:HH21	3:C:147:MET:CE	2.28	0.44
1:D:292:MET:HE3	1:D:309:PRO:CA	2.44	0.44
1:D:809:ARG:NH2	2:E:124:GLY:HA3	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:768:MLY:CD	1:G:772:LEU:HB2	2.47	0.44
1:J:296:MLY:O	1:J:299:LEU:HB2	2.17	0.44
1:J:410:ASN:HA	4:7:334:GLU:HB3	1.29	0.44
4:3:223:PHE:CD2	4:3:259:GLU:HG3	2.52	0.44
4:4:223:PHE:HB3	4:4:259:GLU:OE2	2.18	0.44
4:6:223:PHE:HB3	4:6:259:GLU:OE2	2.18	0.44
4:W:287:ILE:CB	4:Y:204:ALA:H	2.13	0.44
1:A:103:LEU:HD22	1:A:692:LEU:HG	1.98	0.44
1:A:193:ILE:HD11	1:A:250:ILE:CD1	2.48	0.44
1:A:485:GLU:HA	1:A:584:TYR:HE2	1.83	0.44
1:A:701:LEU:HA	1:A:701:LEU:HD12	1.55	0.44
1:D:292:MET:HE1	1:D:309:PRO:CG	2.48	0.44
1:D:322:VAL:CG1	1:D:325:ILE:HD11	2.47	0.44
1:D:725:ARG:CG	1:D:733:PRO:CA	2.95	0.44
1:D:747:LEU:C	1:D:749:GLY:H	2.21	0.44
1:G:37:SER:O	1:G:38:VAL:HG23	2.17	0.44
1:G:103:LEU:HD22	1:G:692:LEU:HG	1.98	0.44
1:G:136:ASN:O	1:G:139:VAL:N	2.47	0.44
1:G:214:MET:CA	1:G:340:ILE:HD11	2.45	0.44
1:G:320:ILE:O	1:G:320:ILE:HG22	2.18	0.44
1:G:723:ARG:CG	1:G:723:ARG:NH1	2.79	0.44
2:H:129:THR:HG23	2:H:132:GLU:OE1	2.17	0.44
1:J:99:GLU:N	1:J:100:PRO:CD	2.80	0.44
1:J:155:ILE:HG22	1:J:156:PHE:N	2.33	0.44
1:J:195:TYR:CE2	1:J:199:ILE:HD12	2.52	0.44
1:J:443:ILE:HG22	1:J:444:ARG:N	2.29	0.44
1:J:540:CYS:C	4:7:349:LEU:HD21	2.36	0.44
1:J:568:PRO:CG	1:J:578:HIS:H	2.30	0.44
1:J:692:LEU:O	1:J:696:ARG:HG3	2.18	0.44
1:J:725:ARG:CG	1:J:733:PRO:CA	2.95	0.44
1:J:795:ARG:HH22	3:L:43:ASN:HB2	1.82	0.44
2:K:129:THR:HG23	2:K:132:GLU:OE1	2.17	0.44
4:0:290:ARG:HH22	4:2:202:THR:CG2	2.17	0.44
4:Y:223:PHE:HB3	4:Y:259:GLU:OE2	2.18	0.44
4:Z:299:MET:HE2	4:Z:331:ALA:HB2	2.00	0.44
1:A:14:ALA:N	1:A:15:PRO:HD2	2.32	0.44
1:A:123:CYS:CB	1:A:158:ILE:HD13	2.48	0.44
1:A:173:GLN:HG3	1:A:670:HIS:HD2	1.82	0.44
1:A:485:GLU:OE2	1:A:584:TYR:N	2.50	0.44
1:A:516:GLY:O	1:A:518:ASP:N	2.51	0.44
1:A:641:LYS:CE	1:A:647:GLN:CB	2.74	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:692:LEU:O	1:A:696:ARG:HG3	2.18	0.44
1:A:835:PHE:O	1:A:839:MLY:N	2.49	0.44
1:D:541:MET:HB3	4:5:345:ILE:HG22	2.00	0.44
1:D:692:LEU:O	1:D:696:ARG:HG3	2.18	0.44
1:D:725:ARG:CZ	1:D:733:PRO:CB	2.83	0.44
1:D:768:MLY:O	1:D:771:LEU:HD12	0.62	0.44
1:G:195:TYR:CE2	1:G:199:ILE:HD12	2.52	0.44
1:G:692:LEU:O	1:G:696:ARG:HG3	2.18	0.44
1:G:725:ARG:CZ	1:G:733:PRO:CB	2.83	0.44
3:I:119:THR:O	3:I:123:VAL:HG23	2.18	0.44
1:J:163:TYR:O	1:J:166:MET:HB3	2.17	0.44
1:J:485:GLU:OE1	1:J:583:HIS:ND1	2.49	0.44
1:J:516:GLY:O	1:J:518:ASP:N	2.51	0.44
2:K:114:LYS:CG	2:K:146:GLY:HA2	2.46	0.44
3:L:122:GLU:HA	3:L:125:GLU:OE1	2.18	0.44
4:1:193:LEU:O	4:1:198:TYR:HD2	2.01	0.44
4:2:32:PRO:HB2	4:2:34:ILE:HD11	1.98	0.44
4:4:287:ILE:HA	4:6:202:THR:HG21	1.59	0.44
4:6:290:ARG:HH22	4:8:202:THR:CG2	2.17	0.44
4:7:299:MET:HE2	4:7:331:ALA:HB2	2.00	0.44
4:8:223:PHE:HB3	4:8:259:GLU:OE2	2.18	0.44
4:Y:190:MET:O	4:Y:194:THR:HG23	2.16	0.44
1:A:226:ASN:N	1:A:227:PRO:HD2	2.32	0.44
1:A:439:LEU:N	1:A:439:LEU:CD1	2.81	0.44
1:A:632:GLY:HA3	1:A:643:GLY:N	2.17	0.44
1:A:725:ARG:CG	1:A:733:PRO:CA	2.95	0.44
1:D:418:THR:CG2	1:D:419:VAL:N	2.79	0.44
1:D:642:LYS:HG3	4:5:23:GLY:CA	2.31	0.44
1:G:175:ILE:C	1:G:176:LEU:HD12	2.38	0.44
1:G:224:SER:O	1:G:227:PRO:HD2	2.17	0.44
1:G:322:VAL:CG1	1:G:325:ILE:HD11	2.47	0.44
1:G:493:HIS:O	1:G:496:PHE:HB3	2.18	0.44
1:G:675:ILE:HG23	1:G:676:ILE:N	2.32	0.44
1:G:728:ASN:ND2	3:I:109:HIS:C	2.71	0.44
1:G:732:ILE:HG21	1:G:747:LEU:CD1	0.64	0.44
3:I:69:LEU:HB3	3:I:70:PRO:HD3	1.99	0.44
3:I:122:GLU:HA	3:I:125:GLU:OE1	2.18	0.44
1:J:91:MET:CE	1:J:119:SER:HB2	2.48	0.44
1:J:139:VAL:HG12	1:J:143:TYR:HD2	1.81	0.44
1:J:439:LEU:N	1:J:439:LEU:CD1	2.81	0.44
1:J:476:GLU:CD	1:J:476:GLU:H	2.21	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:725:ARG:CG	1:J:733:PRO:HA	2.43	0.44
1:J:747:LEU:C	1:J:749:GLY:H	2.20	0.44
1:J:818:TYR:CB	2:K:90:GLY:HA3	2.37	0.44
3:L:50:LEU:O	3:L:53:PRO:HG2	2.18	0.44
4:4:193:LEU:O	4:4:198:TYR:HD2	2.01	0.44
4:6:366:GLY:O	4:6:369:ILE:HG22	2.16	0.44
4:8:190:MET:O	4:8:194:THR:HG23	2.16	0.44
4:W:190:MET:O	4:W:194:THR:HG23	2.16	0.44
4:W:223:PHE:HB3	4:W:259:GLU:OE2	2.18	0.44
1:A:504:MLY:CB	1:A:762:HIS:NE2	2.80	0.44
1:A:530:MET:CB	4:4:354:GLN:CB	2.95	0.44
1:A:675:ILE:HG23	1:A:676:ILE:N	2.32	0.44
1:A:715:VAL:HG12	1:A:720:PHE:HB2	2.00	0.44
1:A:793:ARG:HH21	3:C:147:MET:CG	2.31	0.44
1:D:123:CYS:CB	1:D:158:ILE:HD13	2.48	0.44
1:D:266:GLU:OE1	1:D:659:MLY:NZ	2.51	0.44
1:D:485:GLU:OE1	1:D:583:HIS:ND1	2.49	0.44
1:D:508:ILE:HG12	1:D:766:PHE:HE1	1.33	0.44
1:D:541:MET:HG2	4:5:345:ILE:HG22	2.00	0.44
1:D:667:THR:O	1:D:669:PRO:HD3	2.16	0.44
1:D:788:THR:HG22	3:F:81:GLN:HE22	1.83	0.44
1:D:813:ILE:CG2	2:E:127:ARG:NH1	2.76	0.44
1:G:163:TYR:O	1:G:166:MET:HB3	2.17	0.44
1:G:330:GLU:O	1:G:333:ALA:HB3	2.17	0.44
2:H:139:ALA:C	2:H:141:PRO:HD3	2.33	0.44
3:I:50:LEU:O	3:I:53:PRO:HG2	2.18	0.44
3:I:101:THR:HA	3:I:137:ILE:O	2.18	0.44
1:J:103:LEU:HD22	1:J:692:LEU:HG	1.98	0.44
1:J:123:CYS:CB	1:J:158:ILE:HD13	2.48	0.44
1:J:136:ASN:HA	1:J:137:PRO:HD3	1.50	0.44
1:J:411:GLU:H	4:7:333:PRO:CB	2.30	0.44
1:J:810:ARG:HG2	1:J:810:ARG:NH1	2.29	0.44
3:L:101:THR:HA	3:L:137:ILE:O	2.18	0.44
4:2:287:ILE:N	4:4:202:THR:CG2	2.77	0.44
4:6:220:ALA:HB3	4:6:223:PHE:CD1	2.53	0.44
4:6:287:ILE:HA	4:8:202:THR:HG21	1.59	0.44
4:Z:253:GLU:HA	4:Z:256:ARG:CG	2.42	0.44
1:A:123:CYS:HB2	1:A:158:ILE:HD13	2.00	0.44
1:A:174:SER:OG	1:A:669:PRO:HA	2.18	0.44
1:A:175:ILE:C	1:A:176:LEU:HD12	2.38	0.44
1:A:639:GLY:H	4:4:344:SER:HB3	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:753:VAL:HG12	1:A:775:LEU:CD1	2.47	0.44
1:A:831:TRP:CG	2:B:51:PHE:CZ	3.03	0.44
1:D:195:TYR:CE2	1:D:199:ILE:HD12	2.52	0.44
1:D:206:LYS:CE	1:D:217:THR:HG23	2.29	0.44
1:D:218:LEU:HD22	1:D:222:ILE:HG13	1.95	0.44
1:D:346:ASP:O	1:D:350:ALA:N	2.46	0.44
1:D:439:LEU:N	1:D:439:LEU:CD1	2.81	0.44
1:D:485:GLU:OE2	1:D:584:TYR:N	2.50	0.44
1:D:711:PHE:HB3	1:D:766:PHE:HB3	1.99	0.44
1:D:798:LEU:HA	1:D:798:LEU:HD12	1.36	0.44
2:E:137:TRP:CA	2:E:145:ALA:HB2	2.37	0.44
3:F:122:GLU:HA	3:F:125:GLU:OE1	2.18	0.44
1:G:14:ALA:N	1:G:15:PRO:CD	2.81	0.44
1:G:193:ILE:HD11	1:G:250:ILE:CD1	2.48	0.44
1:G:226:ASN:HB2	1:G:227:PRO:CD	2.48	0.44
1:G:439:LEU:N	1:G:439:LEU:CD1	2.81	0.44
1:G:798:LEU:HD22	3:I:126:LEU:CD1	2.41	0.44
1:J:55:MLY:HH23	1:J:60:VAL:HG22	1.99	0.44
1:J:84:MLY:HH11	1:J:719:ASP:C	2.39	0.44
1:J:144:ARG:HA	1:J:144:ARG:HD2	1.78	0.44
1:J:193:ILE:HD11	1:J:250:ILE:CD1	2.48	0.44
1:J:206:LYS:CE	1:J:217:THR:HG23	2.29	0.44
1:J:308:ASN:HA	1:J:309:PRO:HD2	1.88	0.44
1:J:493:HIS:O	1:J:496:PHE:HB3	2.18	0.44
1:J:599:ASN:CG	1:J:649:VAL:CB	2.80	0.44
1:J:675:ILE:HG23	1:J:676:ILE:N	2.33	0.44
1:J:836:PHE:CD2	2:K:160:GLY:C	2.87	0.44
4:7:205:GLU:O	4:7:208:ILE:HG22	2.18	0.44
4:8:220:ALA:HB3	4:8:223:PHE:CD1	2.53	0.44
4:8:287:ILE:HA	4:W:202:THR:HG21	1.59	0.44
4:W:220:ALA:HB3	4:W:223:PHE:CD1	2.53	0.44
4:X:205:GLU:O	4:X:208:ILE:HG22	2.18	0.44
4:Y:171:LEU:HA	4:Y:172:PRO:HD2	1.84	0.44
1:A:217:THR:HG22	1:A:218:LEU:N	2.33	0.43
1:A:391:GLY:HA3	1:A:616:VAL:HG23	2.00	0.43
1:A:787:ILE:HG23	1:A:791:GLN:HG3	2.00	0.43
2:B:137:TRP:CZ3	2:B:145:ALA:N	2.81	0.43
1:D:40:VAL:HG23	1:D:76:GLN:O	2.18	0.43
1:D:48:VAL:HA	1:D:104:TYR:OH	2.17	0.43
1:D:134:VAL:C	1:D:136:ASN:H	2.16	0.43
1:D:485:GLU:HA	1:D:584:TYR:HE2	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:516:GLY:O	1:D:518:ASP:N	2.51	0.43
1:D:530:MET:CB	4:5:354:GLN:CB	2.95	0.43
1:D:540:CYS:C	4:5:349:LEU:HD21	2.36	0.43
1:D:724:TYR:C	1:D:782:MLY:CH1	2.79	0.43
1:G:107:MLY:CB	1:G:686:MET:HE2	2.37	0.43
1:G:123:CYS:CB	1:G:158:ILE:HD13	2.48	0.43
1:G:309:PRO:C	1:G:311:ASP:H	2.22	0.43
1:G:578:HIS:HB3	1:G:592:ILE:CD1	2.38	0.43
1:G:639:GLY:H	4:6:344:SER:HB3	1.83	0.43
1:J:129:TYR:HD1	1:J:129:TYR:HA	1.65	0.43
1:J:576:GLU:CG	1:J:577:ALA:N	2.44	0.43
3:L:69:LEU:HB3	3:L:70:PRO:HD3	1.99	0.43
4:2:193:LEU:O	4:2:198:TYR:HD2	2.01	0.43
4:V:299:MET:HE2	4:V:331:ALA:HB2	2.00	0.43
4:W:193:LEU:O	4:W:198:TYR:HD2	2.01	0.43
1:A:201:ALA:O	1:A:202:SER:OG	2.36	0.43
1:A:534:SER:CB	4:4:351:THR:HA	2.48	0.43
1:A:753:VAL:HG12	1:A:775:LEU:CG	2.47	0.43
1:D:55:MLY:HH23	1:D:60:VAL:HG22	1.99	0.43
1:D:64:THR:CG2	1:D:65:GLU:H	2.32	0.43
1:D:123:CYS:HB2	1:D:158:ILE:HD13	2.00	0.43
1:D:173:GLN:HG3	1:D:670:HIS:HD2	1.82	0.43
1:D:400:ALA:CB	1:D:606:THR:HG22	2.48	0.43
1:D:639:GLY:H	4:5:344:SER:HB3	1.83	0.43
2:E:88:LEU:HB3	2:E:91:ALA:HB2	1.98	0.43
1:G:322:VAL:CG1	1:G:325:ILE:HG13	2.48	0.43
1:J:174:SER:OG	1:J:669:PRO:HA	2.18	0.43
1:J:246:PHE:HB3	1:J:270:LEU:HD12	2.01	0.43
1:J:391:GLY:HA3	1:J:616:VAL:HG23	2.00	0.43
1:J:541:MET:HB3	4:7:345:ILE:HG22	2.01	0.43
1:J:835:PHE:O	1:J:839:MLY:N	2.49	0.43
4:3:193:LEU:O	4:3:198:TYR:HD2	2.01	0.43
4:3:287:ILE:CB	4:5:204:ALA:H	2.13	0.43
4:4:220:ALA:HB3	4:4:223:PHE:CD1	2.53	0.43
4:5:253:GLU:HA	4:5:256:ARG:CG	2.42	0.43
1:A:348:MLY:HH12	1:A:348:MLY:HD2	1.82	0.43
1:A:436:MLY:HE3	1:A:626:TYR:HE1	1.77	0.43
1:A:496:PHE:HB2	1:A:515:PHE:CD2	2.53	0.43
1:A:549:SER:C	4:6:45:VAL:O	2.56	0.43
1:A:747:LEU:C	1:A:749:GLY:N	2.71	0.43
2:B:129:THR:HG23	2:B:132:GLU:OE1	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:50:LEU:O	3:C:53:PRO:HG2	2.18	0.43
3:C:119:THR:O	3:C:123:VAL:HG23	2.18	0.43
3:C:122:GLU:HA	3:C:125:GLU:OE1	2.18	0.43
1:D:193:ILE:HD11	1:D:250:ILE:CD1	2.48	0.43
1:D:322:VAL:CG1	1:D:325:ILE:HG13	2.48	0.43
1:D:747:LEU:C	1:D:749:GLY:N	2.72	0.43
2:E:112:ILE:O	2:E:148:VAL:N	2.50	0.43
3:F:101:THR:HA	3:F:137:ILE:O	2.18	0.43
1:G:48:VAL:HA	1:G:104:TYR:OH	2.18	0.43
1:G:266:GLU:OE1	1:G:659:MLY:NZ	2.51	0.43
1:G:391:GLY:HA3	1:G:616:VAL:HG23	2.01	0.43
1:G:486:MLY:HH22	1:G:527:GLU:CD	2.37	0.43
1:G:692:LEU:HD23	1:G:692:LEU:HA	1.84	0.43
1:G:725:ARG:CZ	1:G:737:PHE:CZ	3.01	0.43
1:G:787:ILE:HG23	1:G:791:GLN:HG3	2.00	0.43
1:G:834:LEU:HD11	2:H:51:PHE:CD1	2.52	0.43
1:J:48:VAL:HA	1:J:104:TYR:OH	2.18	0.43
1:J:322:VAL:HA	1:J:323:PRO:HD3	1.87	0.43
1:J:409:GLY:N	1:J:636:LYS:CD	2.70	0.43
1:J:496:PHE:HB2	1:J:515:PHE:CD2	2.53	0.43
1:J:711:PHE:HB3	1:J:766:PHE:HB3	2.00	0.43
1:J:813:ILE:HG23	2:K:128:PHE:CZ	2.53	0.43
4:O:205:GLU:O	4:O:208:ILE:HG22	2.18	0.43
4:6:193:LEU:O	4:6:198:TYR:HD2	2.01	0.43
4:V:193:LEU:O	4:V:198:TYR:HD2	2.01	0.43
4:Y:220:ALA:HB3	4:Y:223:PHE:CD1	2.53	0.43
1:A:14:ALA:N	1:A:15:PRO:CD	2.81	0.43
1:A:109:ARG:CD	1:A:117:THR:HB	2.48	0.43
1:A:322:VAL:CG1	1:A:325:ILE:HG13	2.49	0.43
1:A:642:LYS:HG3	4:4:23:GLY:CA	2.32	0.43
1:A:725:ARG:CZ	1:A:737:PHE:CZ	3.01	0.43
1:D:166:MET:CE	1:D:254:PHE:CD2	3.01	0.43
1:D:292:MET:CE	1:D:309:PRO:CA	2.97	0.43
1:D:530:MET:CE	4:5:354:GLN:HG3	2.35	0.43
1:D:726:VAL:CA	1:D:782:MLY:HH13	2.45	0.43
1:D:793:ARG:HE	3:F:147:MET:CG	2.31	0.43
1:G:201:ALA:O	1:G:202:SER:OG	2.36	0.43
1:G:568:PRO:CG	1:G:578:HIS:H	2.29	0.43
1:G:783:LEU:N	1:G:783:LEU:CD1	2.78	0.43
1:G:795:ARG:HE	3:I:118:MET:CE	2.31	0.43
1:J:266:GLU:OE1	1:J:659:MLY:NZ	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:541:MET:HG2	4:7:345:ILE:HG22	2.00	0.43
1:J:790:THR:N	3:L:87:PHE:HE2	2.12	0.43
4:2:220:ALA:HB3	4:2:223:PHE:CD1	2.53	0.43
4:3:149:THR:HA	4:3:165:ILE:O	2.19	0.43
4:4:149:THR:HA	4:4:165:ILE:O	2.19	0.43
4:7:149:THR:HA	4:7:165:ILE:O	2.19	0.43
1:A:40:VAL:HG23	1:A:76:GLN:O	2.19	0.43
1:A:86:ASP:OD2	1:A:87:MLY:HH22	2.19	0.43
1:A:129:TYR:HD1	1:A:129:TYR:HA	1.65	0.43
1:A:295:MLY:CE	1:A:332:MET:CE	2.96	0.43
1:A:320:ILE:O	1:A:320:ILE:HG22	2.18	0.43
1:A:476:GLU:H	1:A:476:GLU:CD	2.22	0.43
1:A:486:MLY:HH22	1:A:527:GLU:CD	2.37	0.43
1:A:529:PRO:HB3	4:4:354:GLN:HA	1.99	0.43
1:A:537:GLU:OE1	4:4:350:SER:HA	2.19	0.43
1:A:540:CYS:C	4:4:349:LEU:HD21	2.36	0.43
1:A:568:PRO:CG	1:A:578:HIS:H	2.30	0.43
3:C:101:THR:HA	3:C:137:ILE:O	2.18	0.43
1:D:155:ILE:HG22	1:D:156:PHE:N	2.33	0.43
1:D:224:SER:O	1:D:227:PRO:HD2	2.17	0.43
1:D:493:HIS:O	1:D:496:PHE:HB3	2.18	0.43
1:D:508:ILE:CG2	1:D:766:PHE:CD1	3.01	0.43
1:D:530:MET:HA	4:5:354:GLN:CD	2.11	0.43
1:D:541:MET:CE	4:5:346:LEU:HD12	2.48	0.43
1:G:92:ALA:HB3	1:G:764:MLY:HH13	1.31	0.43
1:G:174:SER:OG	1:G:669:PRO:HA	2.18	0.43
1:G:217:THR:HG22	1:G:218:LEU:N	2.34	0.43
1:G:218:LEU:HD22	1:G:222:ILE:HG13	1.95	0.43
1:G:226:ASN:N	1:G:227:PRO:HD2	2.32	0.43
1:G:292:MET:CE	1:G:309:PRO:CA	2.97	0.43
1:G:295:MLY:CE	1:G:332:MET:CE	2.97	0.43
1:G:496:PHE:HB2	1:G:515:PHE:CD2	2.53	0.43
1:G:643:GLY:CA	4:6:24:ASP:OD1	2.62	0.43
1:G:689:GLU:HA	1:G:692:LEU:HB2	1.99	0.43
1:G:708:ARG:HA	1:G:714:ARG:NH2	2.33	0.43
3:I:49:ILE:CA	3:I:52:ASN:ND2	2.53	0.43
1:J:166:MET:CE	1:J:254:PHE:HB2	2.47	0.43
1:J:217:THR:HG22	1:J:218:LEU:N	2.34	0.43
1:J:322:VAL:CG1	1:J:325:ILE:HG13	2.49	0.43
1:J:503:TYR:CZ	1:J:711:PHE:CE2	3.05	0.43
1:J:529:PRO:HB3	4:7:354:GLN:HA	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:541:MET:CE	4:7:346:LEU:HD12	2.47	0.43
1:J:757:GLN:OE1	1:J:773:GLY:CA	2.66	0.43
4:0:149:THR:HA	4:0:165:ILE:O	2.19	0.43
4:2:149:THR:HA	4:2:165:ILE:O	2.19	0.43
4:2:205:GLU:O	4:2:208:ILE:HG22	2.18	0.43
4:3:205:GLU:O	4:3:208:ILE:HG22	2.18	0.43
4:Z:205:GLU:O	4:Z:208:ILE:HG22	2.18	0.43
1:A:151:ALA:HB1	1:A:152:PRO:HD2	2.01	0.43
1:A:266:GLU:OE1	1:A:659:MLY:NZ	2.51	0.43
1:A:449:LEU:HD12	1:A:449:LEU:HA	1.60	0.43
1:A:612:GLN:NE2	1:A:627:GLY:H	2.14	0.43
1:A:639:GLY:CA	4:4:344:SER:O	2.40	0.43
1:D:226:ASN:HB2	1:D:227:PRO:CD	2.47	0.43
1:D:246:PHE:HB3	1:D:270:LEU:HD12	2.01	0.43
1:D:391:GLY:HA3	1:D:616:VAL:HG23	2.00	0.43
1:D:723:ARG:CG	1:D:723:ARG:NH1	2.80	0.43
1:D:789:ALA:C	3:F:87:PHE:HE2	2.11	0.43
2:E:163:ALA:CA	2:K:21:GLU:HB3	2.37	0.43
1:G:40:VAL:HG23	1:G:76:GLN:O	2.19	0.43
1:G:332:MET:H	1:G:332:MET:HG2	1.52	0.43
1:G:516:GLY:O	1:G:518:ASP:N	2.51	0.43
1:G:549:SER:C	4:8:45:VAL:O	2.57	0.43
1:G:711:PHE:HB3	1:G:766:PHE:HB3	2.00	0.43
1:J:14:ALA:N	1:J:15:PRO:CD	2.81	0.43
1:J:400:ALA:CB	1:J:606:THR:HG22	2.49	0.43
1:J:530:MET:HA	4:7:354:GLN:CD	2.11	0.43
1:J:537:GLU:OE1	4:7:350:SER:HA	2.19	0.43
1:J:725:ARG:CZ	1:J:737:PHE:CZ	3.01	0.43
1:J:747:LEU:C	1:J:749:GLY:N	2.71	0.43
3:L:119:THR:O	3:L:123:VAL:HG23	2.18	0.43
4:6:149:THR:HA	4:6:165:ILE:O	2.19	0.43
4:V:205:GLU:O	4:V:208:ILE:HG22	2.18	0.43
4:X:149:THR:HA	4:X:165:ILE:O	2.19	0.43
4:X:193:LEU:O	4:X:198:TYR:HD2	2.01	0.43
4:Z:149:THR:HA	4:Z:165:ILE:O	2.19	0.43
1:A:155:ILE:HG22	1:A:156:PHE:N	2.33	0.43
1:A:369:MLY:HH22	1:A:369:MLY:HD3	1.79	0.43
1:A:400:ALA:CB	1:A:606:THR:HG22	2.48	0.43
1:A:442:VAL:O	1:A:445:ILE:HB	2.19	0.43
1:A:541:MET:HB3	4:4:345:ILE:HG22	2.00	0.43
1:A:715:VAL:HG11	1:A:720:PHE:CD1	2.50	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:295:MLY:HG3	1:D:332:MET:HE2	2.00	0.43
1:D:541:MET:HG2	4:5:345:ILE:HG23	2.01	0.43
1:D:712:PRO:HB2	1:D:713:SER:H	1.61	0.43
1:D:725:ARG:CZ	1:D:737:PHE:CE1	3.01	0.43
1:D:789:ALA:O	3:F:87:PHE:HZ	1.98	0.43
1:D:818:TYR:CB	2:E:89:LYS:HB2	2.48	0.43
1:D:822:SER:OG	2:E:87:LYS:O	2.20	0.43
1:G:86:ASP:OD2	1:G:87:MLY:HH22	2.19	0.43
1:G:294:ASN:OD1	1:G:307:THR:HG21	2.19	0.43
1:G:541:MET:HG2	4:6:345:ILE:HG22	2.00	0.43
1:G:725:ARG:CZ	1:G:737:PHE:CE1	3.02	0.43
1:J:64:THR:CG2	1:J:65:GLU:H	2.32	0.43
1:J:123:CYS:HB2	1:J:158:ILE:HD13	2.00	0.43
1:J:224:SER:O	1:J:227:PRO:HD2	2.17	0.43
1:J:485:GLU:OE2	1:J:584:TYR:N	2.50	0.43
1:J:724:TYR:HB3	1:J:727:LEU:CD1	2.48	0.43
1:J:725:ARG:CZ	1:J:737:PHE:CE1	3.02	0.43
4:3:217:CYS:C	4:3:218:TYR:HD1	2.22	0.43
4:7:220:ALA:HB3	4:7:223:PHE:CD1	2.53	0.43
4:7:287:ILE:CB	4:V:204:ALA:H	2.13	0.43
4:8:149:THR:HA	4:8:165:ILE:O	2.19	0.43
1:A:330:GLU:HG2	1:A:330:GLU:H	1.55	0.43
1:A:500:GLN:HB2	1:A:512:PHE:CZ	2.54	0.43
1:A:533:PHE:HD1	1:A:533:PHE:HA	1.79	0.43
1:A:551:MLY:C	4:6:47:MET:HA	2.48	0.43
1:D:14:ALA:N	1:D:15:PRO:CD	2.81	0.43
1:D:17:LEU:HA	1:D:17:LEU:HD12	1.68	0.43
1:D:144:ARG:HA	1:D:144:ARG:HD2	1.78	0.43
1:D:725:ARG:HA	1:D:732:ILE:HG22	1.99	0.43
3:F:69:LEU:HB3	3:F:70:PRO:HD3	1.99	0.43
3:F:119:THR:O	3:F:123:VAL:HG23	2.18	0.43
1:G:500:GLN:HB2	1:G:512:PHE:CZ	2.54	0.43
1:J:169:ASP:O	1:J:170:ARG:HB2	2.19	0.43
1:J:195:TYR:CD2	1:J:199:ILE:HD13	2.54	0.43
1:J:201:ALA:O	1:J:202:SER:OG	2.36	0.43
1:J:292:MET:CE	1:J:309:PRO:CA	2.97	0.43
1:J:309:PRO:C	1:J:311:ASP:H	2.22	0.43
2:K:140:PHE:HA	2:K:141:PRO:HD2	1.57	0.43
4:8:193:LEU:O	4:8:198:TYR:HD2	2.01	0.43
4:V:220:ALA:HB3	4:V:223:PHE:CD1	2.53	0.43
4:Y:193:LEU:O	4:Y:198:TYR:HD2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:294:ASN:OD1	1:A:307:THR:HG21	2.19	0.43
1:A:330:GLU:O	1:A:333:ALA:HB3	2.17	0.43
1:A:408:VAL:HG22	1:A:636:LYS:HG2	1.51	0.43
1:A:485:GLU:OE1	1:A:583:HIS:ND1	2.49	0.43
1:A:502:GLU:HG2	1:A:766:PHE:CE1	2.54	0.43
1:A:578:HIS:HB3	1:A:592:ILE:CD1	2.38	0.43
3:C:69:LEU:HB3	3:C:70:PRO:HD3	1.99	0.43
1:D:174:SER:OG	1:D:669:PRO:HA	2.18	0.43
1:D:529:PRO:HB3	4:5:354:GLN:HA	2.00	0.43
1:G:109:ARG:CD	1:G:117:THR:HB	2.48	0.43
1:G:151:ALA:HB1	1:G:152:PRO:HD2	2.01	0.43
1:G:206:LYS:CE	1:G:217:THR:HG23	2.30	0.43
1:G:442:VAL:O	1:G:445:ILE:HB	2.19	0.43
1:G:445:ILE:HG22	1:G:449:LEU:HD22	2.01	0.43
1:G:725:ARG:HA	1:G:732:ILE:HG22	1.99	0.43
3:I:11:LYS:HE2	3:I:11:LYS:HB3	1.83	0.43
1:J:97:LEU:HA	1:J:97:LEU:HD12	1.67	0.43
1:J:109:ARG:CD	1:J:117:THR:HB	2.49	0.43
1:J:320:ILE:O	1:J:320:ILE:HG22	2.18	0.43
1:J:549:SER:C	4:V:45:VAL:O	2.56	0.43
1:J:783:LEU:HA	1:J:786:ILE:HB	2.00	0.43
4:1:180:LEU:HD11	4:1:261:LEU:HD23	2.01	0.43
4:1:220:ALA:HB3	4:1:223:PHE:CD1	2.53	0.43
4:7:193:LEU:O	4:7:198:TYR:HD2	2.01	0.43
4:V:287:ILE:HD11	4:X:202:THR:HA	1.66	0.43
4:W:149:THR:HA	4:W:165:ILE:O	2.19	0.43
4:X:290:ARG:HH22	4:Z:202:THR:CG2	2.17	0.43
1:A:91:MET:CE	1:A:119:SER:HB2	2.47	0.43
1:A:309:PRO:C	1:A:311:ASP:H	2.22	0.43
1:A:493:HIS:O	1:A:496:PHE:HB3	2.18	0.43
1:A:636:LYS:CB	4:4:334:GLU:OE1	2.67	0.43
1:A:725:ARG:HA	1:A:732:ILE:HG22	1.99	0.43
2:B:140:PHE:CD2	2:B:144:VAL:HG11	2.54	0.43
1:D:169:ASP:O	1:D:170:ARG:HB2	2.19	0.43
1:D:550:PHE:C	4:7:46:GLY:CA	2.87	0.43
1:D:599:ASN:CG	1:D:649:VAL:CB	2.80	0.43
1:D:715:VAL:HG12	1:D:720:PHE:HB2	2.00	0.43
1:D:829:TRP:O	1:D:832:MET:N	2.50	0.43
1:G:195:TYR:CD2	1:G:199:ILE:HD13	2.54	0.43
1:G:213:LYS:HA	1:G:220:ASP:OD2	2.19	0.43
1:G:246:PHE:HB3	1:G:270:LEU:HD12	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:476:GLU:H	1:G:476:GLU:CD	2.21	0.43
1:G:747:LEU:C	1:G:749:GLY:N	2.71	0.43
1:J:442:VAL:O	1:J:445:ILE:HB	2.19	0.43
1:J:568:PRO:O	1:J:570:PRO:HD3	2.19	0.43
4:0:193:LEU:O	4:0:198:TYR:HD2	2.01	0.43
4:1:217:CYS:C	4:1:218:TYR:HD1	2.22	0.43
4:8:324:THR:O	4:W:244:ASP:HA	2.08	0.43
4:W:222:ASP:OD1	4:W:224:GLU:HB3	2.19	0.43
4:Y:149:THR:HA	4:Y:165:ILE:O	2.19	0.43
4:Y:217:CYS:C	4:Y:218:TYR:HD1	2.23	0.43
4:Z:180:LEU:HD11	4:Z:261:LEU:HD23	2.01	0.43
1:A:64:THR:CG2	1:A:65:GLU:H	2.32	0.42
1:A:195:TYR:CD2	1:A:199:ILE:HD13	2.54	0.42
1:A:246:PHE:HB3	1:A:270:LEU:HD12	2.01	0.42
1:A:292:MET:CE	1:A:309:PRO:CA	2.97	0.42
1:A:689:GLU:HA	1:A:692:LEU:HB2	2.00	0.42
1:D:195:TYR:CD2	1:D:199:ILE:HD13	2.54	0.42
1:D:217:THR:HG22	1:D:218:LEU:N	2.34	0.42
1:D:442:VAL:O	1:D:445:ILE:HB	2.19	0.42
1:D:549:SER:C	4:7:45:VAL:O	2.57	0.42
1:D:725:ARG:CZ	1:D:737:PHE:CZ	3.01	0.42
1:D:787:ILE:HG23	1:D:791:GLN:HG3	2.00	0.42
1:G:129:TYR:HD1	1:G:129:TYR:HA	1.65	0.42
1:G:289:TYR:OH	1:G:315:VAL:O	2.27	0.42
1:G:443:ILE:HG22	1:G:444:ARG:N	2.29	0.42
1:G:568:PRO:O	1:G:570:PRO:HD3	2.19	0.42
1:G:715:VAL:HG12	1:G:720:PHE:HB2	2.00	0.42
1:G:829:TRP:O	1:G:832:MET:N	2.50	0.42
3:I:63:ILE:CG2	3:I:64:THR:H	2.32	0.42
1:J:294:ASN:OD1	1:J:307:THR:HG21	2.19	0.42
1:J:406:VAL:O	1:J:412:ALA:HA	2.19	0.42
1:J:530:MET:CB	4:7:354:GLN:CB	2.95	0.42
1:J:541:MET:HG2	4:7:345:ILE:HG23	2.01	0.42
1:J:787:ILE:HG23	1:J:791:GLN:HG3	2.00	0.42
4:0:180:LEU:HD11	4:0:261:LEU:HD23	2.02	0.42
4:0:220:ALA:HB3	4:0:223:PHE:CD1	2.53	0.42
4:2:180:LEU:HD11	4:2:261:LEU:HD23	2.01	0.42
4:4:180:LEU:HD11	4:4:261:LEU:HD23	2.01	0.42
4:4:205:GLU:O	4:4:208:ILE:HG22	2.18	0.42
4:5:180:LEU:HD11	4:5:261:LEU:HD23	2.01	0.42
4:5:220:ALA:HB3	4:5:223:PHE:CD1	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:X:220:ALA:HB3	4:X:223:PHE:CD1	2.53	0.42
4:Z:220:ALA:HB3	4:Z:223:PHE:CD1	2.53	0.42
1:A:62:VAL:O	1:A:69:THR:HA	2.19	0.42
1:A:445:ILE:HG22	1:A:449:LEU:HD22	2.01	0.42
1:A:692:LEU:HA	1:A:692:LEU:HD23	1.84	0.42
1:D:206:LYS:HD2	1:D:217:THR:CG2	2.17	0.42
1:D:496:PHE:HB2	1:D:515:PHE:CD2	2.54	0.42
1:D:673:ARG:HD2	1:D:673:ARG:HA	1.79	0.42
1:D:692:LEU:HD23	1:D:692:LEU:HA	1.84	0.42
1:D:701:LEU:HD12	1:D:701:LEU:HA	1.55	0.42
1:D:834:LEU:HD21	2:E:54:MET:HG2	1.96	0.42
2:E:149:ASP:CG	2:E:150:TYR:N	2.49	0.42
3:F:50:LEU:O	3:F:53:PRO:HG2	2.18	0.42
1:G:64:THR:CG2	1:G:65:GLU:H	2.32	0.42
1:G:141:LEU:HD12	1:G:141:LEU:N	2.32	0.42
1:J:40:VAL:HG23	1:J:76:GLN:O	2.19	0.42
1:J:62:VAL:HG12	1:J:63:MLY:N	2.34	0.42
1:J:84:MLY:CG	1:J:719:ASP:OD2	2.66	0.42
1:J:747:LEU:O	1:J:749:GLY:N	2.52	0.42
2:K:112:ILE:O	2:K:148:VAL:N	2.50	0.42
4:1:149:THR:HA	4:1:165:ILE:O	2.19	0.42
4:2:315:LYS:HD2	4:2:315:LYS:HA	1.92	0.42
4:3:180:LEU:HD11	4:3:261:LEU:HD23	2.02	0.42
4:5:217:CYS:C	4:5:218:TYR:HD1	2.22	0.42
4:6:287:ILE:CB	4:8:204:ALA:H	2.13	0.42
4:7:287:ILE:HA	4:V:202:THR:HG21	1.59	0.42
4:W:217:CYS:C	4:W:218:TYR:HD1	2.22	0.42
4:Y:222:ASP:OD1	4:Y:224:GLU:HB3	2.19	0.42
4:Z:193:LEU:O	4:Z:198:TYR:HD2	2.01	0.42
1:A:402:CYS:C	1:A:404:PRO:HD3	2.39	0.42
1:A:724:TYR:HB3	1:A:727:LEU:CD1	2.48	0.42
1:A:829:TRP:O	1:A:832:MET:N	2.50	0.42
3:C:96:LYS:H	3:C:96:LYS:HG3	1.66	0.42
1:D:62:VAL:HG12	1:D:63:MLY:N	2.35	0.42
1:D:109:ARG:CD	1:D:117:THR:HB	2.49	0.42
1:D:449:LEU:N	1:D:449:LEU:CD1	2.82	0.42
1:D:741:LYS:HG2	1:D:742:LYS:N	2.35	0.42
1:D:829:TRP:HE1	2:E:67:MET:CB	2.26	0.42
2:E:140:PHE:CD2	2:E:144:VAL:HG11	2.54	0.42
1:G:406:VAL:O	1:G:412:ALA:HA	2.19	0.42
1:G:529:PRO:HB3	4:6:354:GLN:HA	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:747:LEU:O	1:G:749:GLY:N	2.52	0.42
1:G:798:LEU:HA	1:G:798:LEU:HD12	1.36	0.42
2:H:144:VAL:HG12	2:H:153:ILE:HD13	1.92	0.42
1:J:278:GLN:HE21	1:J:278:GLN:HB3	1.42	0.42
1:J:445:ILE:HG22	1:J:449:LEU:HD22	2.01	0.42
1:J:449:LEU:N	1:J:449:LEU:CD1	2.81	0.42
4:O:217:CYS:C	4:O:218:TYR:HD1	2.22	0.42
4:4:206:ARG:O	4:4:209:VAL:HG12	2.20	0.42
4:5:324:THR:N	4:7:245:GLY:CA	2.69	0.42
4:6:205:GLU:O	4:6:208:ILE:HG22	2.18	0.42
4:W:315:LYS:HD2	4:W:315:LYS:HA	1.92	0.42
4:X:180:LEU:HD11	4:X:261:LEU:HD23	2.01	0.42
4:Y:180:LEU:HD11	4:Y:261:LEU:HD23	2.01	0.42
1:A:214:MET:CA	1:A:340:ILE:HD11	2.46	0.42
1:A:625:THR:H	1:A:625:THR:HG22	1.48	0.42
1:A:797:PHE:HE2	3:C:126:LEU:CD2	1.91	0.42
1:A:831:TRP:CZ2	2:B:51:PHE:CE1	3.07	0.42
2:B:114:LYS:CG	2:B:146:GLY:HA2	2.46	0.42
1:D:175:ILE:C	1:D:176:LEU:HD12	2.38	0.42
1:D:295:MLY:CE	1:D:332:MET:CE	2.97	0.42
1:D:320:ILE:O	1:D:320:ILE:HG22	2.17	0.42
1:D:445:ILE:HG22	1:D:449:LEU:HD22	2.01	0.42
1:D:733:PRO:CB	1:D:737:PHE:CE1	3.02	0.42
1:D:793:ARG:HG2	3:F:147:MET:HG2	2.01	0.42
1:G:62:VAL:O	1:G:69:THR:HA	2.19	0.42
1:G:123:CYS:HB2	1:G:158:ILE:HD13	2.00	0.42
1:G:173:GLN:HG3	1:G:670:HIS:CD2	2.55	0.42
1:G:551:MLY:C	4:8:47:MET:HA	2.48	0.42
1:G:741:LYS:HG2	1:G:742:LYS:N	2.35	0.42
1:J:86:ASP:OD2	1:J:87:MLY:HH22	2.19	0.42
1:J:173:GLN:HG3	1:J:670:HIS:CD2	2.54	0.42
1:J:485:GLU:HA	1:J:584:TYR:HE2	1.83	0.42
1:J:533:PHE:HD1	1:J:533:PHE:HA	1.79	0.42
1:J:831:TRP:CH2	2:K:34:ILE:CG2	2.95	0.42
3:L:63:ILE:CG2	3:L:64:THR:H	2.33	0.42
4:1:205:GLU:O	4:1:208:ILE:HG22	2.18	0.42
4:4:217:CYS:C	4:4:218:TYR:HD1	2.22	0.42
4:8:205:GLU:O	4:8:208:ILE:HG22	2.18	0.42
4:8:287:ILE:CB	4:W:204:ALA:H	2.13	0.42
4:V:149:THR:HA	4:V:165:ILE:O	2.19	0.42
4:V:222:ASP:OD1	4:V:224:GLU:HB3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:W:196:ARG:HH21	4:W:249:THR:HG23	1.85	0.42
4:Z:217:CYS:C	4:Z:218:TYR:HD1	2.22	0.42
1:A:38:VAL:HG13	1:A:39:PHE:N	2.35	0.42
1:A:501:GLU:HA	1:A:762:HIS:CE1	2.54	0.42
1:A:541:MET:CE	4:4:346:LEU:HD12	2.48	0.42
1:A:712:PRO:HB2	1:A:713:SER:H	1.61	0.42
1:A:744:SER:O	1:A:748:LEU:HD12	2.20	0.42
1:A:747:LEU:O	1:A:749:GLY:N	2.52	0.42
1:D:14:ALA:HB3	1:D:15:PRO:CD	2.45	0.42
1:D:354:LEU:HD12	1:D:354:LEU:HA	1.56	0.42
1:D:476:GLU:CD	1:D:476:GLU:H	2.22	0.42
1:D:519:LEU:HD12	1:D:519:LEU:H	1.83	0.42
1:D:534:SER:CB	4:5:351:THR:HA	2.49	0.42
1:D:723:ARG:HE	1:D:779:ARG:HA	1.84	0.42
2:E:140:PHE:HA	2:E:141:PRO:HD2	1.57	0.42
1:G:346:ASP:O	1:G:350:ALA:N	2.46	0.42
1:G:534:SER:CB	4:6:351:THR:HA	2.50	0.42
1:G:578:HIS:CD2	1:G:592:ILE:H	2.38	0.42
1:G:842:LEU:N	1:G:842:LEU:CD1	2.82	0.42
1:J:93:MET:CA	1:J:714:ARG:HG3	2.44	0.42
1:J:175:ILE:C	1:J:176:LEU:HD12	2.39	0.42
1:J:226:ASN:HB2	1:J:227:PRO:CD	2.47	0.42
1:J:271:GLU:OE1	1:J:274:ARG:NH1	2.53	0.42
1:J:295:MLY:CE	1:J:332:MET:CE	2.97	0.42
1:J:354:LEU:HD12	1:J:354:LEU:HA	1.56	0.42
1:J:534:SER:CB	4:7:351:THR:HA	2.49	0.42
1:J:578:HIS:CD2	1:J:592:ILE:H	2.38	0.42
4:1:196:ARG:HH21	4:1:249:THR:HG23	1.85	0.42
4:4:196:ARG:HH21	4:4:249:THR:HG23	1.85	0.42
4:4:222:ASP:OD1	4:4:224:GLU:HB3	2.20	0.42
4:5:193:LEU:O	4:5:198:TYR:HD2	2.01	0.42
4:5:205:GLU:O	4:5:208:ILE:HG22	2.18	0.42
4:6:217:CYS:C	4:6:218:TYR:HD1	2.22	0.42
4:7:180:LEU:HD11	4:7:261:LEU:HD23	2.01	0.42
4:8:217:CYS:C	4:8:218:TYR:HD1	2.22	0.42
4:V:206:ARG:O	4:V:209:VAL:HG12	2.20	0.42
4:W:205:GLU:O	4:W:208:ILE:HG22	2.18	0.42
4:W:206:ARG:O	4:W:209:VAL:HG12	2.20	0.42
4:X:222:ASP:OD1	4:X:224:GLU:HB3	2.19	0.42
4:Y:205:GLU:O	4:Y:208:ILE:HG22	2.18	0.42
1:A:166:MET:CE	1:A:254:PHE:HB2	2.46	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:169:ASP:O	1:A:170:ARG:HB2	2.19	0.42
1:A:791:GLN:OE1	3:C:116:GLU:HB2	2.20	0.42
2:B:113:LYS:O	2:B:147:ASN:HB2	2.20	0.42
1:D:402:CYS:C	1:D:404:PRO:HD3	2.40	0.42
1:D:409:GLY:N	1:D:636:LYS:CD	2.71	0.42
1:D:725:ARG:HA	1:D:732:ILE:CG2	2.50	0.42
1:D:822:SER:HG	2:E:88:LEU:HA	1.84	0.42
1:D:842:LEU:N	1:D:842:LEU:CD1	2.83	0.42
1:J:62:VAL:O	1:J:69:THR:HA	2.20	0.42
1:J:151:ALA:HB1	1:J:152:PRO:HD2	2.01	0.42
1:J:174:SER:HA	1:J:460:GLY:O	2.20	0.42
1:J:462:LEU:HD11	1:J:464:ILE:CD1	2.50	0.42
4:2:222:ASP:OD1	4:2:224:GLU:HB3	2.20	0.42
4:2:324:THR:HG23	4:4:245:GLY:HA2	1.09	0.42
4:6:180:LEU:HD11	4:6:261:LEU:HD23	2.01	0.42
4:7:222:ASP:OD1	4:7:224:GLU:HB3	2.20	0.42
4:8:222:ASP:OD1	4:8:224:GLU:HB3	2.19	0.42
4:X:206:ARG:O	4:X:209:VAL:HG12	2.20	0.42
4:Z:196:ARG:HH21	4:Z:249:THR:HG23	1.85	0.42
1:A:60:VAL:O	1:A:72:VAL:N	2.51	0.42
1:A:141:LEU:HD12	1:A:141:LEU:N	2.32	0.42
1:A:213:LYS:HA	1:A:220:ASP:OD2	2.19	0.42
1:A:501:GLU:CB	1:A:762:HIS:ND1	2.82	0.42
1:A:568:PRO:O	1:A:570:PRO:HD3	2.19	0.42
1:A:642:LYS:HB3	4:4:24:ASP:HB2	1.37	0.42
1:D:204:GLU:N	1:D:207:LYS:HE3	2.23	0.42
1:D:279:LEU:CB	1:D:280:PRO:HD2	2.49	0.42
1:D:406:VAL:O	1:D:412:ALA:HA	2.20	0.42
1:D:537:GLU:OE1	4:5:350:SER:HA	2.19	0.42
1:D:636:LYS:CB	4:5:334:GLU:OE1	2.68	0.42
1:D:659:MLY:HH22	1:D:659:MLY:HD2	1.42	0.42
1:D:759:ALA:O	1:D:766:PHE:N	2.32	0.42
1:G:166:MET:CE	1:G:254:PHE:HB2	2.46	0.42
1:G:400:ALA:CB	1:G:606:THR:HG22	2.49	0.42
2:H:140:PHE:CD2	2:H:144:VAL:HG11	2.55	0.42
1:J:214:MET:CA	1:J:340:ILE:HD11	2.45	0.42
1:J:418:THR:CG2	1:J:419:VAL:N	2.79	0.42
1:J:795:ARG:HH21	3:L:116:GLU:HB3	1.84	0.42
1:J:826:VAL:O	1:J:828:HIS:N	2.53	0.42
4:3:220:ALA:HB3	4:3:223:PHE:CD1	2.53	0.42
4:5:149:THR:HA	4:5:165:ILE:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:7:217:CYS:C	4:7:218:TYR:HD1	2.22	0.42
4:8:369:ILE:HG23	4:8:370:VAL:N	2.35	0.42
4:V:180:LEU:HD11	4:V:261:LEU:HD23	2.02	0.42
4:V:217:CYS:C	4:V:218:TYR:HD1	2.23	0.42
4:Z:222:ASP:OD1	4:Z:224:GLU:HB3	2.19	0.42
1:A:173:GLN:HG3	1:A:670:HIS:CD2	2.54	0.42
1:A:195:TYR:CE2	1:A:199:ILE:HD13	2.55	0.42
1:A:553:MLY:HE2	4:6:45:VAL:CA	2.38	0.42
1:A:757:GLN:CD	1:A:771:LEU:CD1	2.86	0.42
1:D:174:SER:HA	1:D:460:GLY:O	2.20	0.42
1:D:294:ASN:OD1	1:D:307:THR:HG21	2.19	0.42
1:D:839:MLY:N	1:D:840:PRO:HD2	2.35	0.42
1:G:38:VAL:HG13	1:G:39:PHE:N	2.35	0.42
1:G:633:GLY:HA2	4:6:25:ASP:HA	1.26	0.42
1:G:733:PRO:CB	1:G:737:PHE:CE1	3.02	0.42
1:J:11:GLY:O	1:J:14:ALA:HB3	2.20	0.42
1:J:332:MET:H	1:J:332:MET:HG2	1.52	0.42
1:J:500:GLN:HB2	1:J:512:PHE:CZ	2.54	0.42
1:J:715:VAL:HG12	1:J:720:PHE:HB2	2.00	0.42
2:K:140:PHE:CD2	2:K:144:VAL:HG11	2.54	0.42
4:1:171:LEU:HA	4:1:172:PRO:HD2	1.84	0.42
4:1:206:ARG:O	4:1:209:VAL:HG12	2.20	0.42
4:1:369:ILE:HG23	4:1:370:VAL:N	2.35	0.42
4:2:193:LEU:HD11	4:2:250:ILE:HG13	2.02	0.42
4:5:222:ASP:OD1	4:5:224:GLU:HB3	2.19	0.42
4:6:222:ASP:OD1	4:6:224:GLU:HB3	2.19	0.42
4:W:180:LEU:HD11	4:W:261:LEU:HD23	2.02	0.42
4:W:369:ILE:HG23	4:W:370:VAL:N	2.35	0.42
4:Y:369:ILE:HG23	4:Y:370:VAL:N	2.35	0.42
1:A:406:VAL:O	1:A:412:ALA:HA	2.19	0.42
1:A:797:PHE:CD2	1:A:798:LEU:HD12	2.55	0.42
1:D:215:GLN:H	1:D:340:ILE:CD1	2.21	0.42
1:D:271:GLU:OE1	1:D:274:ARG:NH1	2.53	0.42
1:D:462:LEU:HD11	1:D:464:ILE:CD1	2.50	0.42
1:D:471:ASP:CB	1:D:573:GLY:O	2.68	0.42
1:D:541:MET:CG	4:5:345:ILE:C	2.87	0.42
1:D:578:HIS:CD2	1:D:592:ILE:H	2.38	0.42
1:D:690:LEU:O	1:D:694:GLN:HG3	2.20	0.42
1:D:744:SER:O	1:D:748:LEU:HD12	2.20	0.42
1:G:97:LEU:HD12	1:G:97:LEU:HA	1.67	0.42
1:G:732:ILE:HG23	1:G:747:LEU:HD12	0.95	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:195:TYR:CE2	1:J:199:ILE:HD13	2.55	0.42
4:0:196:ARG:HH21	4:0:249:THR:HG23	1.85	0.42
4:0:206:ARG:O	4:0:209:VAL:HG12	2.20	0.42
4:0:222:ASP:OD1	4:0:224:GLU:HB3	2.19	0.42
4:3:369:ILE:HG23	4:3:370:VAL:N	2.35	0.42
4:5:221:LEU:HA	4:5:312:ARG:HG2	2.02	0.42
4:8:180:LEU:HD11	4:8:261:LEU:HD23	2.01	0.42
4:X:193:LEU:HD11	4:X:250:ILE:HG13	2.02	0.42
4:X:324:THR:HG23	4:Z:245:GLY:HA2	1.09	0.42
4:Y:193:LEU:HD11	4:Y:250:ILE:HG13	2.02	0.42
1:A:110:TYR:O	1:A:113:TRP:N	2.42	0.42
1:A:322:VAL:HA	1:A:323:PRO:HD3	1.87	0.42
1:A:578:HIS:CD2	1:A:592:ILE:H	2.38	0.42
1:A:725:ARG:CZ	1:A:737:PHE:CE1	3.02	0.42
1:D:86:ASP:OD2	1:D:87:MLY:HH22	2.19	0.42
1:D:507:GLY:C	1:D:761:GLY:HA3	2.37	0.42
1:D:747:LEU:O	1:D:749:GLY:N	2.52	0.42
3:F:63:ILE:CG2	3:F:64:THR:H	2.32	0.42
1:G:62:VAL:HG12	1:G:63:MLY:N	2.35	0.42
1:G:568:PRO:CG	1:G:578:HIS:N	2.83	0.42
1:G:732:ILE:CG2	1:G:747:LEU:CD1	0.65	0.42
1:J:84:MLY:HH13	1:J:715:VAL:CG1	2.06	0.42
1:J:754:ASP:HB3	1:J:776:GLU:HG3	1.72	0.42
4:0:193:LEU:HD11	4:0:250:ILE:HG13	2.02	0.42
4:3:221:LEU:HA	4:3:312:ARG:HG2	2.02	0.42
4:5:369:ILE:HG23	4:5:370:VAL:N	2.35	0.42
4:6:196:ARG:HH21	4:6:249:THR:HG23	1.85	0.42
4:6:206:ARG:O	4:6:209:VAL:HG12	2.20	0.42
4:7:206:ARG:O	4:7:209:VAL:HG12	2.20	0.42
4:7:221:LEU:HA	4:7:312:ARG:HG2	2.02	0.42
4:7:369:ILE:HG23	4:7:370:VAL:N	2.35	0.42
4:8:206:ARG:O	4:8:209:VAL:HG12	2.20	0.42
1:A:11:GLY:O	1:A:14:ALA:HB3	2.20	0.41
1:A:462:LEU:HD11	1:A:464:ILE:CD1	2.50	0.41
1:A:659:MLY:HD2	1:A:659:MLY:HH22	1.42	0.41
1:A:826:VAL:O	1:A:828:HIS:N	2.53	0.41
1:A:842:LEU:N	1:A:842:LEU:CD1	2.83	0.41
1:D:151:ALA:HB1	1:D:152:PRO:HD2	2.01	0.41
1:D:466:GLY:CA	1:D:484:ASN:HD21	2.32	0.41
1:D:625:THR:H	1:D:625:THR:HG22	1.48	0.41
1:G:11:GLY:O	1:G:14:ALA:HB3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:60:VAL:O	1:G:72:VAL:N	2.51	0.41
1:G:166:MET:CE	1:G:254:PHE:CD2	3.01	0.41
1:G:169:ASP:O	1:G:170:ARG:HB2	2.19	0.41
1:G:369:MLY:HH22	1:G:369:MLY:HD3	1.79	0.41
1:G:725:ARG:HA	1:G:732:ILE:CG2	2.50	0.41
1:J:725:ARG:HA	1:J:732:ILE:CG2	2.50	0.41
4:2:217:CYS:C	4:2:218:TYR:HD1	2.23	0.41
4:3:193:LEU:HD11	4:3:250:ILE:HG13	2.02	0.41
4:4:315:LYS:HD2	4:4:315:LYS:HA	1.92	0.41
4:4:324:THR:HG23	4:6:245:GLY:HA2	1.09	0.41
4:4:369:ILE:HG23	4:4:370:VAL:N	2.35	0.41
4:7:193:LEU:HD11	4:7:250:ILE:HG13	2.02	0.41
4:8:226:GLU:HG3	4:8:255:PHE:CE2	2.55	0.41
4:V:221:LEU:HA	4:V:312:ARG:HG2	2.02	0.41
4:X:369:ILE:HG23	4:X:370:VAL:N	2.35	0.41
4:Y:206:ARG:O	4:Y:209:VAL:HG12	2.20	0.41
1:A:221:GLN:HG2	1:A:221:GLN:H	1.47	0.41
1:A:330:GLU:OE1	1:A:330:GLU:HA	2.20	0.41
1:A:541:MET:HG2	4:4:345:ILE:HG23	2.01	0.41
1:A:568:PRO:CG	1:A:578:HIS:N	2.84	0.41
1:A:725:ARG:HA	1:A:732:ILE:CG2	2.50	0.41
2:B:140:PHE:HA	2:B:141:PRO:HD2	1.56	0.41
3:C:95:ASP:OD1	3:C:139:TYR:HE1	2.03	0.41
1:D:356:GLY:HA2	1:D:359:MET:HG3	2.02	0.41
1:D:500:GLN:HB2	1:D:512:PHE:CZ	2.54	0.41
1:D:568:PRO:CG	1:D:578:HIS:N	2.83	0.41
1:D:787:ILE:HD13	1:D:787:ILE:HG21	1.67	0.41
1:G:462:LEU:HD11	1:G:464:ILE:CD1	2.50	0.41
1:G:730:SER:OG	3:I:109:HIS:ND1	2.49	0.41
1:G:797:PHE:CD2	1:G:798:LEU:HD12	2.55	0.41
1:G:826:VAL:O	1:G:828:HIS:N	2.53	0.41
3:I:25:ILE:O	3:I:63:ILE:CB	2.66	0.41
3:I:95:ASP:OD1	3:I:139:TYR:HE1	2.03	0.41
1:J:402:CYS:C	1:J:404:PRO:HD3	2.40	0.41
1:J:541:MET:CG	4:7:345:ILE:C	2.87	0.41
1:J:568:PRO:CG	1:J:578:HIS:N	2.83	0.41
1:J:636:LYS:CB	4:7:334:GLU:OE1	2.68	0.41
1:J:690:LEU:O	1:J:694:GLN:HG3	2.20	0.41
4:2:226:GLU:HG3	4:2:255:PHE:CE2	2.56	0.41
4:3:222:ASP:OD1	4:3:224:GLU:HB3	2.20	0.41
4:3:287:ILE:N	4:5:202:THR:CG2	2.77	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:4:193:LEU:HD11	4:4:250:ILE:HG13	2.02	0.41
4:6:193:LEU:HD11	4:6:250:ILE:HG13	2.02	0.41
4:6:315:LYS:HD2	4:6:315:LYS:HA	1.92	0.41
4:6:369:ILE:HG23	4:6:370:VAL:N	2.35	0.41
4:8:193:LEU:HD11	4:8:250:ILE:HG13	2.02	0.41
4:8:287:ILE:HD11	4:W:202:THR:HA	1.66	0.41
4:V:369:ILE:HG23	4:V:370:VAL:N	2.35	0.41
4:W:299:MET:HE2	4:W:331:ALA:HB2	2.01	0.41
4:Y:196:ARG:HH21	4:Y:249:THR:HG23	1.85	0.41
4:Z:193:LEU:HD11	4:Z:250:ILE:HG13	2.02	0.41
1:A:25:ILE:HG23	1:A:29:ASN:HD22	1.85	0.41
1:A:166:MET:CE	1:A:254:PHE:CD2	3.01	0.41
1:A:690:LEU:O	1:A:694:GLN:HG3	2.20	0.41
1:A:795:ARG:CG	3:C:118:MET:HE1	2.50	0.41
1:A:831:TRP:HZ2	2:B:47:LEU:HA	1.85	0.41
1:D:87:MLY:HH12	1:D:87:MLY:HD3	1.61	0.41
1:D:129:TYR:HD1	1:D:129:TYR:HA	1.65	0.41
1:D:135:TYR:CD2	1:D:191:ARG:HD3	2.55	0.41
1:D:554:LEU:HA	1:D:554:LEU:HD12	1.77	0.41
1:D:568:PRO:O	1:D:570:PRO:HD3	2.19	0.41
1:D:641:LYS:CE	1:D:647:GLN:CB	2.75	0.41
1:D:795:ARG:NE	3:F:43:ASN:OD1	2.53	0.41
1:D:799:MET:CE	3:F:32:ASP:CB	2.83	0.41
1:G:136:ASN:O	1:G:138:MLY:N	2.54	0.41
1:G:185:LYS:H	1:G:185:LYS:HG3	1.63	0.41
1:G:541:MET:HB3	4:6:345:ILE:HG22	2.01	0.41
1:G:641:LYS:CE	1:G:647:GLN:CB	2.75	0.41
1:G:775:LEU:HD12	1:G:775:LEU:HA	1.71	0.41
1:J:136:ASN:O	1:J:138:MLY:N	2.54	0.41
1:J:556:ASP:OD1	4:V:50:LYS:CG	2.69	0.41
1:J:797:PHE:CD2	1:J:798:LEU:HD12	2.55	0.41
1:J:821:ARG:CZ	2:K:127:ARG:HD3	2.51	0.41
4:0:226:GLU:HG3	4:0:255:PHE:CE2	2.55	0.41
4:0:369:ILE:HG23	4:0:370:VAL:N	2.35	0.41
4:1:193:LEU:HD11	4:1:250:ILE:HG13	2.02	0.41
4:1:221:LEU:HA	4:1:312:ARG:HG2	2.03	0.41
4:2:206:ARG:O	4:2:209:VAL:HG12	2.20	0.41
4:2:369:ILE:HG23	4:2:370:VAL:N	2.35	0.41
4:3:206:ARG:O	4:3:209:VAL:HG12	2.20	0.41
4:3:287:ILE:HA	4:5:202:THR:HG21	1.59	0.41
4:5:226:GLU:HG3	4:5:255:PHE:CE2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:5:287:ILE:CB	4:7:204:ALA:H	2.13	0.41
4:7:324:THR:HG23	4:V:245:GLY:HA2	1.09	0.41
4:8:315:LYS:HD2	4:8:315:LYS:HA	1.92	0.41
4:V:196:ARG:HH21	4:V:249:THR:HG23	1.85	0.41
4:V:324:THR:HG23	4:X:245:GLY:HA2	1.09	0.41
4:W:193:LEU:HD11	4:W:250:ILE:HG13	2.02	0.41
4:W:226:GLU:HG3	4:W:255:PHE:CE2	2.55	0.41
4:X:217:CYS:C	4:X:218:TYR:HD1	2.23	0.41
4:X:221:LEU:HA	4:X:312:ARG:HG2	2.02	0.41
4:Z:369:ILE:HG23	4:Z:370:VAL:N	2.35	0.41
1:A:62:VAL:HG12	1:A:63:MLY:N	2.35	0.41
1:A:741:LYS:HG2	1:A:742:LYS:N	2.35	0.41
1:D:11:GLY:O	1:D:14:ALA:HB3	2.20	0.41
1:D:812:SER:O	1:D:816:ILE:HG13	2.21	0.41
1:D:822:SER:CB	2:E:88:LEU:HD21	2.47	0.41
1:D:831:TRP:CE2	2:E:51:PHE:CZ	3.09	0.41
2:E:113:LYS:O	2:E:147:ASN:HB2	2.20	0.41
1:G:330:GLU:OE1	1:G:330:GLU:HA	2.20	0.41
1:G:402:CYS:C	1:G:404:PRO:HD3	2.40	0.41
1:G:471:ASP:CB	1:G:573:GLY:O	2.68	0.41
1:G:541:MET:HG2	4:6:345:ILE:HG23	2.01	0.41
1:G:541:MET:CE	4:6:346:LEU:HD12	2.48	0.41
1:G:744:SER:O	1:G:748:LEU:HD12	2.20	0.41
1:J:229:LEU:HD12	1:J:229:LEU:HA	1.76	0.41
1:J:335:ASP:O	1:J:338:ILE:HB	2.20	0.41
1:J:471:ASP:CB	1:J:573:GLY:O	2.68	0.41
4:3:226:GLU:HG3	4:3:255:PHE:CE2	2.55	0.41
4:5:196:ARG:HH21	4:5:249:THR:HG23	1.85	0.41
4:Y:221:LEU:HA	4:Y:312:ARG:HG2	2.02	0.41
1:A:135:TYR:HD2	1:A:191:ARG:CG	2.33	0.41
1:A:839:MLY:N	1:A:840:PRO:HD2	2.35	0.41
2:B:140:PHE:HB3	2:B:144:VAL:HG11	2.03	0.41
2:B:150:TYR:HB3	2:B:151:LYS:HG3	2.03	0.41
1:D:25:ILE:HG23	1:D:29:ASN:HD22	1.85	0.41
1:D:173:GLN:HG3	1:D:670:HIS:CD2	2.55	0.41
1:D:296:MLY:HH11	1:D:348:MLY:CH2	2.48	0.41
1:D:507:GLY:HA3	1:D:762:HIS:N	2.36	0.41
2:E:141:PRO:CB	2:E:142:PRO:HD3	2.48	0.41
1:G:135:TYR:HD2	1:G:191:ARG:CG	2.33	0.41
1:G:174:SER:HA	1:G:460:GLY:O	2.20	0.41
1:G:195:TYR:CE2	1:G:199:ILE:HD13	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:217:THR:CA	1:G:221:GLN:HE21	2.33	0.41
1:G:556:ASP:OD1	4:8:50:LYS:CG	2.68	0.41
1:G:642:LYS:HE2	4:6:344:SER:HA	1.56	0.41
1:G:690:LEU:O	1:G:694:GLN:HG3	2.20	0.41
1:G:810:ARG:HG2	1:G:810:ARG:NH1	2.28	0.41
1:J:14:ALA:HB3	1:J:15:PRO:CD	2.46	0.41
1:J:295:MLY:CE	1:J:332:MET:HE1	2.51	0.41
1:J:296:MLY:HH11	1:J:348:MLY:CH2	2.48	0.41
1:J:320:ILE:O	1:J:320:ILE:CG2	2.68	0.41
1:J:346:ASP:O	1:J:350:ALA:N	2.46	0.41
1:J:464:ILE:HD13	1:J:464:ILE:HG21	1.69	0.41
1:J:612:GLN:NE2	1:J:627:GLY:H	2.14	0.41
1:J:817:GLN:CB	2:K:127:ARG:HH11	2.24	0.41
1:J:829:TRP:O	1:J:832:MET:N	2.50	0.41
2:K:144:VAL:HG12	2:K:153:ILE:HD13	1.92	0.41
4:0:32:PRO:HB2	4:0:34:ILE:CD1	2.51	0.41
4:4:227:MET:O	4:4:230:ALA:HB3	2.21	0.41
4:5:206:ARG:O	4:5:209:VAL:HG12	2.20	0.41
4:7:226:GLU:HG3	4:7:255:PHE:CE2	2.55	0.41
4:8:196:ARG:HH21	4:8:249:THR:HG23	1.85	0.41
4:V:193:LEU:HD11	4:V:250:ILE:HG13	2.02	0.41
4:X:226:GLU:HG3	4:X:255:PHE:CE2	2.55	0.41
4:Z:144:ALA:HB2	4:Z:342:GLY:CA	2.51	0.41
4:Z:206:ARG:O	4:Z:209:VAL:HG12	2.20	0.41
4:Z:226:GLU:HG3	4:Z:255:PHE:CE2	2.55	0.41
1:A:134:VAL:C	1:A:136:ASN:H	2.16	0.41
2:B:144:VAL:HG12	2:B:153:ILE:HD11	1.75	0.41
1:D:62:VAL:O	1:D:69:THR:HA	2.19	0.41
1:D:408:VAL:HG22	1:D:636:LYS:HG2	1.51	0.41
1:D:723:ARG:HH21	1:D:783:LEU:CD1	2.33	0.41
1:D:797:PHE:CD2	1:D:798:LEU:HD12	2.55	0.41
1:D:826:VAL:O	1:D:828:HIS:N	2.53	0.41
1:G:550:PHE:C	4:8:46:GLY:CA	2.88	0.41
1:G:636:LYS:CB	4:6:334:GLU:OE1	2.68	0.41
1:G:839:MLY:N	1:G:840:PRO:HD2	2.35	0.41
1:J:204:GLU:N	1:J:207:LYS:HE3	2.23	0.41
1:J:797:PHE:HB2	3:L:149:VAL:HG13	1.96	0.41
4:0:144:ALA:HB2	4:0:342:GLY:CA	2.51	0.41
4:1:222:ASP:OD1	4:1:224:GLU:HB3	2.19	0.41
4:2:144:ALA:HB2	4:2:342:GLY:CA	2.51	0.41
4:3:290:ARG:HH22	4:5:202:THR:CG2	2.17	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:4:288:ASP:OD1	4:6:204:ALA:HA	2.21	0.41
4:5:193:LEU:HD11	4:5:250:ILE:HG13	2.02	0.41
4:7:227:MET:O	4:7:230:ALA:HB3	2.21	0.41
1:A:49:MLY:HH23	1:A:80:MET:CE	2.51	0.41
1:A:174:SER:HA	1:A:460:GLY:O	2.20	0.41
1:A:541:MET:HG2	4:4:345:ILE:HG22	2.00	0.41
2:B:149:ASP:OD2	2:B:150:TYR:CA	2.64	0.41
1:D:136:ASN:O	1:D:138:MLY:N	2.54	0.41
1:D:330:GLU:HA	1:D:330:GLU:OE1	2.21	0.41
1:D:534:SER:HB2	4:5:354:GLN:HE22	1.56	0.41
2:E:150:TYR:HB3	2:E:151:LYS:HG3	2.03	0.41
3:F:48:LYS:HA	3:F:48:LYS:HD3	1.17	0.41
1:G:56:GLU:HB2	1:G:59:MLY:CB	2.30	0.41
1:G:449:LEU:N	1:G:449:LEU:CD1	2.82	0.41
1:G:831:TRP:CE2	2:H:67:MET:CB	3.01	0.41
1:J:25:ILE:HG23	1:J:29:ASN:HD22	1.85	0.41
1:J:90:ASP:CB	1:J:764:MLY:HH11	2.42	0.41
1:J:610:LEU:N	1:J:610:LEU:CD1	2.84	0.41
1:J:821:ARG:HH12	2:K:127:ARG:CZ	2.33	0.41
1:J:838:ILE:CD1	2:K:54:MET:HE1	2.42	0.41
4:0:288:ASP:OD1	4:2:204:ALA:HA	2.21	0.41
4:1:32:PRO:HB2	4:1:34:ILE:CD1	2.51	0.41
4:2:288:ASP:OD1	4:4:204:ALA:HA	2.21	0.41
4:3:32:PRO:HB2	4:3:34:ILE:CD1	2.51	0.41
4:3:196:ARG:HH21	4:3:249:THR:HG23	1.85	0.41
4:4:226:GLU:HG3	4:4:255:PHE:CE2	2.55	0.41
4:6:226:GLU:HG3	4:6:255:PHE:CE2	2.55	0.41
4:8:144:ALA:HB2	4:8:342:GLY:CA	2.51	0.41
4:V:144:ALA:HB2	4:V:342:GLY:CA	2.51	0.41
4:V:226:GLU:HG3	4:V:255:PHE:CE2	2.55	0.41
4:W:144:ALA:HB2	4:W:342:GLY:CA	2.51	0.41
4:W:324:THR:O	4:Y:244:ASP:HA	2.09	0.41
4:X:144:ALA:HB2	4:X:342:GLY:CA	2.51	0.41
4:Z:221:LEU:HA	4:Z:312:ARG:HG2	2.02	0.41
1:A:107:MLY:CB	1:A:686:MET:HE2	2.40	0.41
1:A:136:ASN:O	1:A:138:MLY:N	2.54	0.41
1:A:193:ILE:HD11	1:A:250:ILE:HD12	2.03	0.41
1:A:711:PHE:O	1:A:714:ARG:NH2	2.54	0.41
1:A:812:SER:O	1:A:816:ILE:HG13	2.21	0.41
3:C:63:ILE:CG2	3:C:64:THR:H	2.33	0.41
1:D:38:VAL:HG13	1:D:39:PHE:N	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:91:MET:CE	1:D:119:SER:HB2	2.48	0.41
1:D:308:ASN:HA	1:D:309:PRO:HD2	1.88	0.41
1:D:322:VAL:HG12	1:D:325:ILE:HG13	2.03	0.41
1:D:629:GLU:HB3	1:D:643:GLY:C	2.41	0.41
1:D:799:MET:SD	3:F:32:ASP:HA	2.51	0.41
1:G:193:ILE:CD1	1:G:250:ILE:HD13	2.51	0.41
1:G:665:ARG:C	1:G:667:THR:N	2.74	0.41
1:G:797:PHE:CD1	3:I:149:VAL:CB	2.85	0.41
1:J:135:TYR:CD2	1:J:191:ARG:HD3	2.55	0.41
1:J:193:ILE:HD11	1:J:250:ILE:HD12	2.03	0.41
1:J:356:GLY:HA2	1:J:359:MET:HG3	2.02	0.41
1:J:629:GLU:HB3	1:J:643:GLY:C	2.41	0.41
1:J:657:LEU:HD12	1:J:657:LEU:O	2.21	0.41
1:J:741:LYS:HG2	1:J:742:LYS:N	2.35	0.41
1:J:744:SER:O	1:J:748:LEU:HD12	2.20	0.41
1:J:812:SER:O	1:J:816:ILE:HG13	2.21	0.41
4:1:226:GLU:HG3	4:1:255:PHE:CE2	2.56	0.41
4:1:288:ASP:OD1	4:3:204:ALA:HA	2.21	0.41
4:5:287:ILE:N	4:7:202:THR:CG2	2.77	0.41
4:6:144:ALA:HB2	4:6:342:GLY:CA	2.51	0.41
4:W:221:LEU:HA	4:W:312:ARG:HG2	2.02	0.41
4:Y:32:PRO:HB2	4:Y:34:ILE:CD1	2.51	0.41
1:A:72:VAL:O	1:A:73:LYS:O	2.39	0.41
1:A:172:ASN:OD1	1:A:457:TYR:HA	2.21	0.41
1:A:193:ILE:CD1	1:A:250:ILE:HD13	2.51	0.41
1:A:194:GLN:HE21	1:A:194:GLN:HB3	1.43	0.41
1:A:217:THR:CA	1:A:221:GLN:HE21	2.33	0.41
1:A:226:ASN:HB2	1:A:227:PRO:CD	2.47	0.41
1:A:303:LEU:O	1:A:304:LEU:HB2	2.21	0.41
1:A:356:GLY:HA2	1:A:359:MET:HG3	2.02	0.41
1:A:471:ASP:CB	1:A:573:GLY:O	2.68	0.41
1:A:732:ILE:HG23	1:A:747:LEU:HD13	1.37	0.41
1:A:793:ARG:HH21	3:C:147:MET:HE2	1.84	0.41
1:A:800:ARG:HD3	3:C:149:VAL:C	2.35	0.41
1:A:800:ARG:NE	3:C:149:VAL:C	2.73	0.41
2:B:111:SER:OG	2:B:148:VAL:CA	2.69	0.41
3:C:56:GLU:OE1	3:C:59:ASN:ND2	2.54	0.41
1:D:195:TYR:CE2	1:D:199:ILE:HD13	2.55	0.41
1:D:242:ASN:OD1	1:D:286:HIS:NE2	2.49	0.41
1:D:309:PRO:C	1:D:311:ASP:H	2.22	0.41
1:D:322:VAL:HB	1:D:325:ILE:HD12	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:398:LEU:HA	1:D:398:LEU:HD12	1.84	0.41
1:D:407:GLY:HA2	1:D:411:GLU:O	2.21	0.41
1:D:493:HIS:O	1:D:496:PHE:N	2.54	0.41
1:G:14:ALA:HB3	1:G:15:PRO:CD	2.46	0.41
1:G:322:VAL:HA	1:G:323:PRO:HD3	1.87	0.41
1:G:335:ASP:O	1:G:338:ILE:HB	2.20	0.41
1:G:356:GLY:HA2	1:G:359:MET:HG3	2.02	0.41
1:G:384:ASP:HA	1:G:394:SER:OG	2.21	0.41
1:G:485:GLU:OE2	1:G:584:TYR:N	2.50	0.41
1:G:534:SER:HB2	4:6:354:GLN:HE22	1.56	0.41
1:G:537:GLU:OE1	4:6:350:SER:HA	2.20	0.41
1:G:717:TYR:OH	1:G:760:PHE:HB3	2.21	0.41
1:G:768:MLY:HG2	1:G:772:LEU:HD23	2.03	0.41
1:G:791:GLN:HB3	3:I:118:MET:CE	2.51	0.41
1:G:812:SER:O	1:G:816:ILE:HG13	2.21	0.41
1:G:832:MET:SD	2:H:84:PHE:CE2	3.06	0.41
2:H:140:PHE:HA	2:H:141:PRO:HD2	1.57	0.41
1:J:107:MLY:N	1:J:686:MET:HE1	2.35	0.41
1:J:322:VAL:HG12	1:J:325:ILE:HG13	2.03	0.41
1:J:330:GLU:HG2	1:J:330:GLU:H	1.54	0.41
1:J:550:PHE:C	4:V:46:GLY:CA	2.88	0.41
1:J:839:MLY:N	1:J:840:PRO:HD2	2.35	0.41
2:K:149:ASP:CG	2:K:150:TYR:N	2.49	0.41
4:0:221:LEU:HA	4:0:312:ARG:HG2	2.02	0.41
4:2:32:PRO:HB2	4:2:34:ILE:CD1	2.51	0.41
4:2:196:ARG:HH21	4:2:249:THR:HG23	1.85	0.41
4:2:227:MET:O	4:2:230:ALA:HB3	2.21	0.41
4:4:144:ALA:HB2	4:4:342:GLY:CA	2.51	0.41
4:5:32:PRO:HB2	4:5:34:ILE:CD1	2.51	0.41
4:5:144:ALA:HB2	4:5:342:GLY:CA	2.51	0.41
4:5:227:MET:O	4:5:230:ALA:HB3	2.21	0.41
4:6:227:MET:O	4:6:230:ALA:HB3	2.21	0.41
4:6:288:ASP:OD1	4:8:204:ALA:HA	2.21	0.41
4:7:144:ALA:HB2	4:7:342:GLY:CA	2.51	0.41
4:V:227:MET:O	4:V:230:ALA:HB3	2.21	0.41
4:W:32:PRO:HB2	4:W:34:ILE:CD1	2.51	0.41
4:Y:144:ALA:HB2	4:Y:342:GLY:CA	2.51	0.41
4:Z:227:MET:O	4:Z:230:ALA:HB3	2.21	0.41
1:A:502:GLU:HG2	1:A:766:PHE:HE1	1.85	0.41
1:A:817:GLN:HG3	2:B:127:ARG:HD3	1.03	0.41
1:D:47:PHE:HE1	1:D:78:PHE:CE1	2.40	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:217:THR:CA	1:D:221:GLN:HE21	2.33	0.41
1:D:335:ASP:O	1:D:338:ILE:HB	2.20	0.41
1:D:723:ARG:C	1:D:782:MLY:CH2	2.89	0.41
1:D:724:TYR:CA	1:D:782:MLY:HH11	2.48	0.41
1:G:91:MET:CE	1:G:119:SER:HB2	2.47	0.41
1:G:172:ASN:OD1	1:G:457:TYR:HA	2.21	0.41
1:G:193:ILE:HD11	1:G:250:ILE:HD12	2.03	0.41
1:G:657:LEU:HD12	1:G:657:LEU:O	2.21	0.41
1:G:712:PRO:HB2	1:G:713:SER:H	1.61	0.41
1:G:795:ARG:HH22	3:I:43:ASN:CB	2.33	0.41
1:G:798:LEU:CD2	3:I:126:LEU:HD11	2.44	0.41
2:H:113:LYS:O	2:H:147:ASN:HB2	2.20	0.41
3:I:56:GLU:OE1	3:I:59:ASN:ND2	2.54	0.41
1:J:193:ILE:CD1	1:J:250:ILE:HD13	2.51	0.41
1:J:322:VAL:HB	1:J:325:ILE:HD12	2.03	0.41
1:J:493:HIS:O	1:J:496:PHE:N	2.54	0.41
1:J:519:LEU:HD12	1:J:519:LEU:H	1.83	0.41
1:J:642:LYS:HE2	4:7:344:SER:HA	1.56	0.41
1:J:701:LEU:HD12	1:J:701:LEU:HA	1.55	0.41
1:J:733:PRO:CB	1:J:737:PHE:CE1	3.02	0.41
1:J:776:GLU:O	1:J:780:ASP:N	2.45	0.41
1:J:793:ARG:HD2	3:L:146:ILE:O	2.21	0.41
1:J:842:LEU:N	1:J:842:LEU:CD1	2.83	0.41
4:1:287:ILE:N	4:3:202:THR:CG2	2.77	0.41
4:3:227:MET:O	4:3:230:ALA:HB3	2.21	0.41
4:4:219:VAL:HG22	4:4:258:PRO:CB	2.52	0.41
4:6:219:VAL:HG22	4:6:258:PRO:CB	2.51	0.41
4:7:32:PRO:HB2	4:7:34:ILE:CD1	2.51	0.41
4:8:221:LEU:HA	4:8:312:ARG:HG2	2.02	0.41
4:X:288:ASP:OD1	4:Z:204:ALA:HA	2.21	0.41
1:A:295:MLY:CG	1:A:332:MET:HE1	2.50	0.40
1:A:335:ASP:O	1:A:338:ILE:HB	2.20	0.40
1:A:410:ASN:HA	4:4:334:GLU:HB3	1.30	0.40
1:A:757:GLN:OE1	1:A:771:LEU:CD1	2.69	0.40
2:B:139:ALA:O	2:B:141:PRO:CD	2.51	0.40
1:D:48:VAL:CG2	1:D:49:MLY:N	2.84	0.40
1:D:135:TYR:HD2	1:D:191:ARG:CG	2.33	0.40
1:D:193:ILE:HD11	1:D:250:ILE:HD12	2.03	0.40
1:D:556:ASP:OD1	4:7:50:LYS:CG	2.69	0.40
1:G:528:MLY:HB2	1:G:529:PRO:HD2	2.03	0.40
1:G:817:GLN:CG	2:H:128:PHE:CE1	3.01	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:835:PHE:CZ	2:H:27:PHE:CE1	3.09	0.40
1:J:330:GLU:OE1	1:J:330:GLU:HA	2.20	0.40
1:J:384:ASP:HA	1:J:394:SER:OG	2.21	0.40
1:J:508:ILE:HD13	1:J:759:ALA:HB2	1.79	0.40
2:K:113:LYS:O	2:K:147:ASN:HB2	2.20	0.40
3:L:48:LYS:HD3	3:L:48:LYS:HA	1.17	0.40
3:L:56:GLU:OE1	3:L:59:ASN:ND2	2.54	0.40
4:0:227:MET:O	4:0:230:ALA:HB3	2.21	0.40
4:1:144:ALA:HB2	4:1:342:GLY:CA	2.51	0.40
4:1:219:VAL:HG22	4:1:258:PRO:CB	2.52	0.40
4:3:144:ALA:HB2	4:3:342:GLY:CA	2.51	0.40
4:5:287:ILE:HA	4:7:202:THR:HG21	1.59	0.40
4:5:288:ASP:OD1	4:7:204:ALA:HA	2.21	0.40
4:6:32:PRO:HB2	4:6:34:ILE:CD1	2.51	0.40
4:8:32:PRO:HB2	4:8:34:ILE:CD1	2.51	0.40
4:W:219:VAL:HG22	4:W:258:PRO:CB	2.52	0.40
4:X:250:ILE:HG22	4:X:254:ARG:HB2	2.04	0.40
4:Z:219:VAL:HG22	4:Z:258:PRO:CB	2.51	0.40
1:A:384:ASP:HA	1:A:394:SER:OG	2.21	0.40
1:A:795:ARG:HH22	3:C:43:ASN:HB2	1.86	0.40
2:B:63:GLU:O	2:B:67:MET:HG3	2.22	0.40
1:D:193:ILE:CD1	1:D:250:ILE:HD13	2.51	0.40
1:D:213:LYS:HA	1:D:220:ASP:OD2	2.19	0.40
1:D:320:ILE:O	1:D:320:ILE:CG2	2.68	0.40
1:D:348:MLY:HH12	1:D:348:MLY:HD2	1.82	0.40
1:D:528:MLY:HB2	1:D:529:PRO:HD2	2.03	0.40
3:F:56:GLU:OE1	3:F:59:ASN:ND2	2.54	0.40
1:G:25:ILE:HG23	1:G:29:ASN:HD22	1.85	0.40
1:G:110:TYR:O	1:G:113:TRP:N	2.42	0.40
1:G:464:ILE:HG22	1:G:465:ALA:H	1.87	0.40
1:G:493:HIS:O	1:G:496:PHE:N	2.54	0.40
1:G:739:ASP:OD1	1:G:739:ASP:C	2.58	0.40
1:G:795:ARG:NH2	3:I:116:GLU:HB3	2.36	0.40
1:G:795:ARG:NH2	3:I:43:ASN:OD1	1.62	0.40
1:J:88:ILE:HG22	1:J:90:ASP:C	2.42	0.40
1:J:172:ASN:OD1	1:J:457:TYR:HA	2.21	0.40
1:J:303:LEU:O	1:J:304:LEU:HB2	2.21	0.40
4:1:120:THR:HG21	4:1:370:VAL:CG1	2.52	0.40
4:2:219:VAL:HG22	4:2:258:PRO:CB	2.51	0.40
4:4:221:LEU:HA	4:4:312:ARG:HG2	2.02	0.40
4:5:120:THR:HG21	4:5:370:VAL:CG1	2.52	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:V:120:THR:HG21	4:V:370:VAL:CG1	2.52	0.40
4:W:120:THR:HG21	4:W:370:VAL:CG1	2.51	0.40
4:Y:219:VAL:HG22	4:Y:258:PRO:CB	2.52	0.40
4:Y:226:GLU:HG3	4:Y:255:PHE:CE2	2.55	0.40
4:Y:227:MET:O	4:Y:230:ALA:HB3	2.21	0.40
1:A:464:ILE:HG22	1:A:465:ALA:H	1.87	0.40
1:A:798:LEU:HD12	1:A:798:LEU:HA	1.37	0.40
2:B:112:ILE:O	2:B:148:VAL:N	2.50	0.40
1:D:60:VAL:O	1:D:72:VAL:N	2.51	0.40
1:D:201:ALA:O	1:D:202:SER:OG	2.36	0.40
1:D:237:THR:CG2	1:D:238:VAL:N	2.85	0.40
1:D:657:LEU:O	1:D:657:LEU:HD12	2.21	0.40
1:G:303:LEU:O	1:G:304:LEU:HB2	2.21	0.40
1:G:407:GLY:HA2	1:G:411:GLU:O	2.21	0.40
1:G:768:MLY:HD3	1:G:772:LEU:HD23	1.87	0.40
1:J:38:VAL:HG13	1:J:39:PHE:N	2.35	0.40
1:J:528:MLY:HB2	1:J:529:PRO:HD2	2.03	0.40
1:J:544:LYS:N	4:7:146:GLY:O	2.55	0.40
1:J:659:MLY:HD2	1:J:659:MLY:HH22	1.42	0.40
3:L:95:ASP:OD1	3:L:139:TYR:HE1	2.04	0.40
4:2:221:LEU:HA	4:2:312:ARG:HG2	2.02	0.40
4:3:219:VAL:HG22	4:3:258:PRO:CB	2.51	0.40
4:6:221:LEU:HA	4:6:312:ARG:HG2	2.02	0.40
4:6:324:THR:HG23	4:8:245:GLY:HA2	1.09	0.40
4:7:196:ARG:HH21	4:7:249:THR:HG23	1.85	0.40
4:8:287:ILE:N	4:W:202:THR:CG2	2.77	0.40
4:X:196:ARG:HH21	4:X:249:THR:HG23	1.85	0.40
4:X:287:ILE:N	4:Z:202:THR:CG2	2.77	0.40
1:A:817:GLN:CB	2:B:127:ARG:CZ	2.69	0.40
3:C:84:PHE:HB3	3:C:147:MET:HE1	2.04	0.40
1:D:64:THR:OG1	1:D:68:GLU:HB3	2.22	0.40
1:D:88:ILE:HG22	1:D:90:ASP:C	2.42	0.40
1:D:172:ASN:OD1	1:D:457:TYR:HA	2.21	0.40
1:D:176:LEU:N	1:D:176:LEU:CD1	2.75	0.40
1:D:303:LEU:O	1:D:304:LEU:HB2	2.21	0.40
1:D:507:GLY:HA2	1:D:762:HIS:NE2	2.36	0.40
1:D:610:LEU:N	1:D:610:LEU:CD1	2.84	0.40
1:D:717:TYR:OH	1:D:760:PHE:HB3	2.21	0.40
1:D:813:ILE:HG22	2:E:127:ARG:NH1	2.08	0.40
1:G:93:MET:SD	1:G:764:MLY:HH23	2.61	0.40
1:G:305:ILE:HG22	1:G:312:TYR:OH	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:47:PHE:HE1	1:J:78:PHE:CE1	2.40	0.40
1:J:648:THR:CG2	1:J:651:ALA:CB	2.92	0.40
1:J:717:TYR:OH	1:J:760:PHE:HB3	2.21	0.40
3:L:62:ALA:O	3:L:63:ILE:CB	2.63	0.40
4:1:227:MET:O	4:1:230:ALA:HB3	2.21	0.40
4:6:120:THR:HG21	4:6:370:VAL:CG1	2.52	0.40
4:8:219:VAL:HG22	4:8:258:PRO:CB	2.52	0.40
4:8:227:MET:O	4:8:230:ALA:HB3	2.21	0.40
4:8:250:ILE:HG22	4:8:254:ARG:HB2	2.04	0.40
4:8:288:ASP:OD1	4:W:204:ALA:HA	2.21	0.40
4:W:250:ILE:HG22	4:W:254:ARG:HB2	2.04	0.40
4:X:32:PRO:HB2	4:X:34:ILE:CD1	2.51	0.40
1:A:237:THR:CG2	1:A:238:VAL:N	2.84	0.40
1:A:292:MET:CE	1:A:309:PRO:HD3	2.52	0.40
1:A:556:ASP:OD1	4:6:50:LYS:CG	2.69	0.40
2:B:137:TRP:CA	2:B:145:ALA:CB	2.82	0.40
1:D:89:GLU:HB3	1:D:153:PRO:HG3	2.03	0.40
1:D:400:ALA:CB	1:D:606:THR:CG2	3.00	0.40
2:E:163:ALA:O	2:K:20:ASP:OD2	2.39	0.40
1:G:193:ILE:HD13	1:G:252:ILE:HD11	2.04	0.40
2:H:63:GLU:O	2:H:67:MET:HG3	2.22	0.40
1:J:63:MLY:HD3	1:J:63:MLY:HH23	1.76	0.40
4:1:250:ILE:HG22	4:1:254:ARG:HB2	2.04	0.40
4:4:32:PRO:HB2	4:4:34:ILE:CD1	2.51	0.40
4:4:287:ILE:N	4:6:202:THR:CG2	2.77	0.40
4:8:88:HIS:HA	4:8:92:ASN:OD1	2.22	0.40
4:V:32:PRO:HB2	4:V:34:ILE:CD1	2.51	0.40
4:V:324:THR:N	4:X:245:GLY:CA	2.69	0.40
4:W:193:LEU:HD12	4:W:193:LEU:HA	1.96	0.40
4:W:288:ASP:OD1	4:Y:204:ALA:HA	2.21	0.40
4:X:227:MET:O	4:X:230:ALA:HB3	2.21	0.40
4:Y:120:THR:HG21	4:Y:370:VAL:CG1	2.52	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM

entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	789/840 (94%)	650 (82%)	113 (14%)	26 (3%)	4	26
1	D	789/840 (94%)	651 (82%)	112 (14%)	26 (3%)	4	26
1	G	789/840 (94%)	649 (82%)	113 (14%)	27 (3%)	3	26
1	J	791/840 (94%)	651 (82%)	112 (14%)	28 (4%)	3	25
2	B	143/145 (99%)	126 (88%)	9 (6%)	8 (6%)	2	19
2	E	143/145 (99%)	126 (88%)	9 (6%)	8 (6%)	2	19
2	H	143/145 (99%)	126 (88%)	9 (6%)	8 (6%)	2	19
2	K	143/145 (99%)	126 (88%)	9 (6%)	8 (6%)	2	19
3	C	143/147 (97%)	133 (93%)	10 (7%)	0	100	100
3	F	143/147 (97%)	133 (93%)	10 (7%)	0	100	100
3	I	143/147 (97%)	133 (93%)	10 (7%)	0	100	100
3	L	143/147 (97%)	133 (93%)	10 (7%)	0	100	100
4	0	370/375 (99%)	334 (90%)	30 (8%)	6 (2%)	9	44
4	1	370/375 (99%)	335 (90%)	29 (8%)	6 (2%)	9	44
4	2	370/375 (99%)	334 (90%)	30 (8%)	6 (2%)	9	44
4	3	370/375 (99%)	335 (90%)	29 (8%)	6 (2%)	9	44
4	4	370/375 (99%)	334 (90%)	30 (8%)	6 (2%)	9	44
4	5	370/375 (99%)	335 (90%)	29 (8%)	6 (2%)	9	44
4	6	370/375 (99%)	335 (90%)	29 (8%)	6 (2%)	9	44
4	7	370/375 (99%)	334 (90%)	30 (8%)	6 (2%)	9	44
4	8	370/375 (99%)	335 (90%)	29 (8%)	6 (2%)	9	44
4	V	370/375 (99%)	334 (90%)	30 (8%)	6 (2%)	9	44
4	W	370/375 (99%)	334 (90%)	30 (8%)	6 (2%)	9	44
4	X	370/375 (99%)	334 (90%)	30 (8%)	6 (2%)	9	44
4	Y	370/375 (99%)	334 (90%)	30 (8%)	6 (2%)	9	44
4	Z	370/375 (99%)	335 (90%)	29 (8%)	6 (2%)	9	44
All	All	9482/9778 (97%)	8319 (88%)	940 (10%)	223 (2%)	9	33

All (223) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	73	LYS
1	A	202	SER
1	A	572	LYS
1	A	712	PRO
1	A	729	ALA
1	A	757	GLN
1	A	762	HIS
2	B	131	GLU
2	B	141	PRO
1	D	73	LYS
1	D	202	SER
1	D	572	LYS
1	D	712	PRO
1	D	729	ALA
1	D	757	GLN
1	D	762	HIS
2	E	131	GLU
2	E	141	PRO
1	G	73	LYS
1	G	202	SER
1	G	572	LYS
1	G	712	PRO
1	G	729	ALA
1	G	757	GLN
1	G	762	HIS
2	H	131	GLU
2	H	141	PRO
1	J	73	LYS
1	J	202	SER
1	J	572	LYS
1	J	712	PRO
1	J	729	ALA
1	J	757	GLN
1	J	762	HIS
1	J	785	GLU
2	K	131	GLU
2	K	141	PRO
4	0	246	GLN
4	1	246	GLN
4	2	246	GLN
4	3	246	GLN
4	4	246	GLN
4	5	246	GLN

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
4	6	246	GLN
4	7	246	GLN
4	8	246	GLN
4	V	246	GLN
4	W	246	GLN
4	X	246	GLN
4	Y	246	GLN
4	Z	246	GLN
1	A	11	GLY
1	A	21	GLU
1	A	219	GLU
1	A	517	MET
1	A	532	ILE
1	A	637	LYS
2	B	130	PRO
2	B	147	ASN
2	B	151	LYS
2	B	161	GLU
1	D	11	GLY
1	D	21	GLU
1	D	219	GLU
1	D	517	MET
1	D	532	ILE
1	D	637	LYS
2	E	130	PRO
2	E	147	ASN
2	E	151	LYS
2	E	161	GLU
1	G	11	GLY
1	G	21	GLU
1	G	219	GLU
1	G	517	MET
1	G	532	ILE
1	G	637	LYS
1	G	785	GLU
2	H	130	PRO
2	H	147	ASN
2	H	151	LYS
1	J	11	GLY
1	J	21	GLU
1	J	219	GLU
1	J	517	MET

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	J	637	LYS
2	K	130	PRO
2	K	147	ASN
2	K	151	LYS
2	K	161	GLU
4	0	274	ILE
4	1	274	ILE
4	2	274	ILE
4	3	274	ILE
4	4	274	ILE
4	5	274	ILE
4	6	274	ILE
4	7	274	ILE
4	8	274	ILE
4	V	274	ILE
4	W	274	ILE
4	X	274	ILE
4	Y	274	ILE
4	Z	274	ILE
1	A	58	GLY
1	A	294	ASN
1	A	644	SER
1	D	58	GLY
1	D	294	ASN
1	D	644	SER
1	G	58	GLY
1	G	294	ASN
1	G	644	SER
2	H	161	GLU
1	J	58	GLY
1	J	294	ASN
1	J	532	ILE
1	J	644	SER
4	0	233	SER
4	1	233	SER
4	2	233	SER
4	3	233	SER
4	4	233	SER
4	5	233	SER
4	6	233	SER
4	7	233	SER
4	8	233	SER

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
4	V	233	SER
4	W	233	SER
4	X	233	SER
4	Y	233	SER
4	Z	233	SER
1	A	435	GLU
1	A	817	GLN
1	D	269	LEU
1	D	435	GLU
1	D	817	GLN
1	G	269	LEU
1	G	435	GLU
1	G	817	GLN
1	J	435	GLU
1	J	817	GLN
4	0	2	GLU
4	0	253	GLU
4	1	2	GLU
4	1	253	GLU
4	2	2	GLU
4	2	253	GLU
4	3	2	GLU
4	3	253	GLU
4	4	2	GLU
4	4	253	GLU
4	5	2	GLU
4	6	2	GLU
4	6	253	GLU
4	7	2	GLU
4	7	253	GLU
4	8	2	GLU
4	V	2	GLU
4	V	253	GLU
4	W	2	GLU
4	X	2	GLU
4	X	253	GLU
4	Y	2	GLU
4	Y	253	GLU
4	Z	2	GLU
1	A	8	ALA
1	A	269	LEU
1	A	578	HIS

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
2	B	140	PHE
1	D	8	ALA
1	D	578	HIS
2	E	140	PHE
1	G	8	ALA
1	G	79	SER
1	G	578	HIS
2	H	140	PHE
1	J	8	ALA
1	J	269	LEU
1	J	578	HIS
2	K	140	PHE
4	5	253	GLU
4	8	253	GLU
4	W	253	GLU
4	Z	253	GLU
1	A	79	SER
1	A	199	ILE
1	A	556	ASP
2	B	142	PRO
1	D	79	SER
1	D	199	ILE
1	D	556	ASP
2	E	142	PRO
1	G	199	ILE
1	G	556	ASP
2	H	142	PRO
1	J	79	SER
1	J	199	ILE
1	J	556	ASP
1	J	822	SER
2	K	142	PRO
1	A	840	PRO
1	D	287	ILE
1	D	840	PRO
1	G	840	PRO
1	J	287	ILE
1	J	840	PRO
4	0	242	LEU
4	1	242	LEU
4	2	242	LEU
4	3	242	LEU

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Mol	Chain	Res	Type
4	4	242	LEU
4	5	242	LEU
4	6	242	LEU
4	7	242	LEU
4	8	242	LEU
4	V	242	LEU
4	W	242	LEU
4	X	242	LEU
4	Y	242	LEU
4	Z	242	LEU
1	A	287	ILE
1	G	287	ILE

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	672/672 (100%)	512 (76%)	160 (24%)	0	4
1	D	672/672 (100%)	515 (77%)	157 (23%)	1	4
1	G	672/672 (100%)	514 (76%)	158 (24%)	1	4
1	J	672/672 (100%)	514 (76%)	158 (24%)	1	4
2	B	120/120 (100%)	119 (99%)	1 (1%)	81	89
2	E	120/120 (100%)	119 (99%)	1 (1%)	81	89
2	H	120/120 (100%)	119 (99%)	1 (1%)	81	89
2	K	120/120 (100%)	119 (99%)	1 (1%)	81	89
3	C	117/117 (100%)	112 (96%)	5 (4%)	29	53
3	F	117/117 (100%)	112 (96%)	5 (4%)	29	53
3	I	117/117 (100%)	112 (96%)	5 (4%)	29	53
3	L	117/117 (100%)	112 (96%)	5 (4%)	29	53
4	0	315/318 (99%)	269 (85%)	46 (15%)	3	15
4	1	315/318 (99%)	268 (85%)	47 (15%)	3	15

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	2	315/318 (99%)	268 (85%)	47 (15%)	3	15
4	3	315/318 (99%)	268 (85%)	47 (15%)	3	15
4	4	315/318 (99%)	268 (85%)	47 (15%)	3	15
4	5	315/318 (99%)	269 (85%)	46 (15%)	3	15
4	6	315/318 (99%)	268 (85%)	47 (15%)	3	15
4	7	315/318 (99%)	269 (85%)	46 (15%)	3	15
4	8	315/318 (99%)	268 (85%)	47 (15%)	3	15
4	V	315/318 (99%)	269 (85%)	46 (15%)	3	15
4	W	315/318 (99%)	269 (85%)	46 (15%)	3	15
4	X	315/318 (99%)	269 (85%)	46 (15%)	3	15
4	Y	315/318 (99%)	268 (85%)	47 (15%)	3	15
4	Z	315/318 (99%)	268 (85%)	47 (15%)	3	15
All	All	8046/8088 (100%)	6737 (84%)	1309 (16%)	5	13

All (1309) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	ASP
1	A	7	MET
1	A	12	GLU
1	A	15	PRO
1	A	17	LEU
1	A	20	SER
1	A	22	LYS
1	A	36	SER
1	A	37	SER
1	A	46	SER
1	A	61	THR
1	A	69	THR
1	A	70	LEU
1	A	72	VAL
1	A	73	LYS
1	A	75	ASP
1	A	76	GLN
1	A	97	LEU
1	A	106	LEU
1	A	109	ARG
1	A	114	MET

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	117	THR
1	A	121	LEU
1	A	126	VAL
1	A	127	ASN
1	A	135	TYR
1	A	136	ASN
1	A	146	LYS
1	A	149	GLN
1	A	155	ILE
1	A	157	SER
1	A	158	ILE
1	A	159	SER
1	A	165	PHE
1	A	167	LEU
1	A	169	ASP
1	A	173	GLN
1	A	178	THR
1	A	185	LYS
1	A	186	THR
1	A	187	VAL
1	A	189	THR
1	A	191	ARG
1	A	193	ILE
1	A	194	GLN
1	A	198	THR
1	A	199	ILE
1	A	218	LEU
1	A	219	GLU
1	A	221	GLN
1	A	223	ILE
1	A	227	PRO
1	A	229	LEU
1	A	244	SER
1	A	245	ARG
1	A	251	ARG
1	A	264	ASP
1	A	273	SER
1	A	274	ARG
1	A	278	GLN
1	A	282	GLU
1	A	287	ILE
1	A	290	GLN

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	294	ASN
1	A	298	GLU
1	A	300	ILE
1	A	325	ILE
1	A	331	LEU
1	A	336	SER
1	A	351	ILE
1	A	354	LEU
1	A	364	LEU
1	A	365	LYS
1	A	372	GLU
1	A	376	GLU
1	A	381	GLU
1	A	389	LEU
1	A	392	LEU
1	A	394	SER
1	A	399	LYS
1	A	405	ARG
1	A	410	ASN
1	A	439	LEU
1	A	447	GLN
1	A	448	GLN
1	A	449	LEU
1	A	453	GLN
1	A	455	ARG
1	A	457	TYR
1	A	462	LEU
1	A	471	ASP
1	A	474	SER
1	A	480	ILE
1	A	487	LEU
1	A	495	MET
1	A	499	GLU
1	A	506	GLU
1	A	513	ILE
1	A	518	ASP
1	A	524	GLU
1	A	532	ILE
1	A	534	SER
1	A	537	GLU
1	A	543	PRO
1	A	549	SER

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	561	LYS
1	A	562	SER
1	A	563	ASN
1	A	569	LYS
1	A	580	SER
1	A	593	SER
1	A	597	GLU
1	A	604	ASN
1	A	608	ILE
1	A	610	LEU
1	A	615	SER
1	A	621	LEU
1	A	625	THR
1	A	664	LEU
1	A	666	SER
1	A	673	ARG
1	A	675	ILE
1	A	676	ILE
1	A	686	MET
1	A	689	GLU
1	A	690	LEU
1	A	693	HIS
1	A	698	ASN
1	A	701	LEU
1	A	702	GLU
1	A	704	ILE
1	A	708	ARG
1	A	713	SER
1	A	714	ARG
1	A	716	LEU
1	A	719	ASP
1	A	722	GLN
1	A	723	ARG
1	A	727	LEU
1	A	728	ASN
1	A	745	GLU
1	A	752	ASP
1	A	753	VAL
1	A	754	ASP
1	A	762	HIS
1	A	774	LEU
1	A	785	GLU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	787	ILE
1	A	793	ARG
1	A	799	MET
1	A	802	GLU
1	A	804	ARG
1	A	810	ARG
1	A	816	ILE
1	A	822	SER
1	A	832	MET
1	A	834	LEU
1	A	838	ILE
1	A	842	LEU
1	A	843	LYS
2	B	142	PRO
3	C	48	LYS
3	C	68	PHE
3	C	83	THR
3	C	95	ASP
3	C	96	LYS
1	D	4	ASP
1	D	7	MET
1	D	12	GLU
1	D	15	PRO
1	D	17	LEU
1	D	20	SER
1	D	22	LYS
1	D	36	SER
1	D	37	SER
1	D	46	SER
1	D	61	THR
1	D	69	THR
1	D	70	LEU
1	D	72	VAL
1	D	73	LYS
1	D	75	ASP
1	D	76	GLN
1	D	97	LEU
1	D	106	LEU
1	D	109	ARG
1	D	114	MET
1	D	117	THR
1	D	121	LEU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	D	126	VAL
1	D	127	ASN
1	D	135	TYR
1	D	136	ASN
1	D	146	LYS
1	D	149	GLN
1	D	155	ILE
1	D	157	SER
1	D	158	ILE
1	D	159	SER
1	D	165	PHE
1	D	167	LEU
1	D	169	ASP
1	D	173	GLN
1	D	178	THR
1	D	185	LYS
1	D	186	THR
1	D	187	VAL
1	D	191	ARG
1	D	193	ILE
1	D	194	GLN
1	D	198	THR
1	D	199	ILE
1	D	218	LEU
1	D	219	GLU
1	D	221	GLN
1	D	223	ILE
1	D	229	LEU
1	D	244	SER
1	D	245	ARG
1	D	251	ARG
1	D	264	ASP
1	D	273	SER
1	D	274	ARG
1	D	278	GLN
1	D	282	GLU
1	D	287	ILE
1	D	290	GLN
1	D	294	ASN
1	D	298	GLU
1	D	300	ILE
1	D	325	ILE

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	D	331	LEU
1	D	336	SER
1	D	351	ILE
1	D	354	LEU
1	D	364	LEU
1	D	365	LYS
1	D	372	GLU
1	D	376	GLU
1	D	381	GLU
1	D	389	LEU
1	D	392	LEU
1	D	394	SER
1	D	399	LYS
1	D	405	ARG
1	D	410	ASN
1	D	439	LEU
1	D	447	GLN
1	D	448	GLN
1	D	449	LEU
1	D	453	GLN
1	D	455	ARG
1	D	457	TYR
1	D	462	LEU
1	D	471	ASP
1	D	474	SER
1	D	480	ILE
1	D	487	LEU
1	D	495	MET
1	D	499	GLU
1	D	506	GLU
1	D	513	ILE
1	D	518	ASP
1	D	524	GLU
1	D	532	ILE
1	D	534	SER
1	D	537	GLU
1	D	549	SER
1	D	561	LYS
1	D	562	SER
1	D	563	ASN
1	D	569	LYS
1	D	580	SER

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	D	593	SER
1	D	597	GLU
1	D	604	ASN
1	D	608	ILE
1	D	610	LEU
1	D	615	SER
1	D	621	LEU
1	D	625	THR
1	D	664	LEU
1	D	666	SER
1	D	673	ARG
1	D	675	ILE
1	D	676	ILE
1	D	686	MET
1	D	689	GLU
1	D	690	LEU
1	D	693	HIS
1	D	698	ASN
1	D	701	LEU
1	D	702	GLU
1	D	704	ILE
1	D	708	ARG
1	D	713	SER
1	D	714	ARG
1	D	716	LEU
1	D	719	ASP
1	D	722	GLN
1	D	723	ARG
1	D	727	LEU
1	D	728	ASN
1	D	745	GLU
1	D	752	ASP
1	D	753	VAL
1	D	754	ASP
1	D	762	HIS
1	D	774	LEU
1	D	785	GLU
1	D	787	ILE
1	D	793	ARG
1	D	799	MET
1	D	802	GLU
1	D	804	ARG

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	D	810	ARG
1	D	816	ILE
1	D	822	SER
1	D	832	MET
1	D	834	LEU
1	D	838	ILE
1	D	842	LEU
1	D	843	LYS
2	E	142	PRO
3	F	48	LYS
3	F	68	PHE
3	F	83	THR
3	F	95	ASP
3	F	96	LYS
1	G	4	ASP
1	G	7	MET
1	G	12	GLU
1	G	15	PRO
1	G	17	LEU
1	G	20	SER
1	G	22	LYS
1	G	36	SER
1	G	37	SER
1	G	46	SER
1	G	61	THR
1	G	69	THR
1	G	70	LEU
1	G	72	VAL
1	G	73	LYS
1	G	75	ASP
1	G	76	GLN
1	G	97	LEU
1	G	106	LEU
1	G	109	ARG
1	G	114	MET
1	G	117	THR
1	G	121	LEU
1	G	126	VAL
1	G	127	ASN
1	G	135	TYR
1	G	136	ASN
1	G	146	LYS

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	G	149	GLN
1	G	155	ILE
1	G	157	SER
1	G	158	ILE
1	G	159	SER
1	G	165	PHE
1	G	167	LEU
1	G	169	ASP
1	G	173	GLN
1	G	178	THR
1	G	185	LYS
1	G	186	THR
1	G	187	VAL
1	G	189	THR
1	G	191	ARG
1	G	193	ILE
1	G	194	GLN
1	G	198	THR
1	G	199	ILE
1	G	218	LEU
1	G	219	GLU
1	G	221	GLN
1	G	223	ILE
1	G	229	LEU
1	G	244	SER
1	G	245	ARG
1	G	251	ARG
1	G	264	ASP
1	G	273	SER
1	G	274	ARG
1	G	278	GLN
1	G	282	GLU
1	G	287	ILE
1	G	290	GLN
1	G	294	ASN
1	G	298	GLU
1	G	300	ILE
1	G	325	ILE
1	G	331	LEU
1	G	336	SER
1	G	351	ILE
1	G	354	LEU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	G	364	LEU
1	G	365	LYS
1	G	372	GLU
1	G	376	GLU
1	G	381	GLU
1	G	389	LEU
1	G	392	LEU
1	G	394	SER
1	G	399	LYS
1	G	405	ARG
1	G	410	ASN
1	G	439	LEU
1	G	447	GLN
1	G	448	GLN
1	G	449	LEU
1	G	453	GLN
1	G	455	ARG
1	G	457	TYR
1	G	462	LEU
1	G	471	ASP
1	G	474	SER
1	G	480	ILE
1	G	487	LEU
1	G	495	MET
1	G	499	GLU
1	G	506	GLU
1	G	513	ILE
1	G	518	ASP
1	G	524	GLU
1	G	532	ILE
1	G	534	SER
1	G	537	GLU
1	G	549	SER
1	G	561	LYS
1	G	562	SER
1	G	563	ASN
1	G	569	LYS
1	G	580	SER
1	G	593	SER
1	G	597	GLU
1	G	604	ASN
1	G	608	ILE

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	G	610	LEU
1	G	615	SER
1	G	621	LEU
1	G	625	THR
1	G	664	LEU
1	G	666	SER
1	G	673	ARG
1	G	675	ILE
1	G	676	ILE
1	G	686	MET
1	G	689	GLU
1	G	690	LEU
1	G	693	HIS
1	G	698	ASN
1	G	701	LEU
1	G	702	GLU
1	G	704	ILE
1	G	708	ARG
1	G	713	SER
1	G	714	ARG
1	G	716	LEU
1	G	719	ASP
1	G	722	GLN
1	G	723	ARG
1	G	727	LEU
1	G	728	ASN
1	G	745	GLU
1	G	752	ASP
1	G	753	VAL
1	G	754	ASP
1	G	762	HIS
1	G	774	LEU
1	G	785	GLU
1	G	787	ILE
1	G	793	ARG
1	G	799	MET
1	G	802	GLU
1	G	804	ARG
1	G	810	ARG
1	G	816	ILE
1	G	822	SER
1	G	832	MET

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	G	834	LEU
1	G	838	ILE
1	G	842	LEU
1	G	843	LYS
2	H	142	PRO
3	I	48	LYS
3	I	68	PHE
3	I	83	THR
3	I	95	ASP
3	I	96	LYS
1	J	4	ASP
1	J	7	MET
1	J	12	GLU
1	J	15	PRO
1	J	17	LEU
1	J	20	SER
1	J	22	LYS
1	J	36	SER
1	J	37	SER
1	J	46	SER
1	J	61	THR
1	J	69	THR
1	J	70	LEU
1	J	72	VAL
1	J	73	LYS
1	J	75	ASP
1	J	76	GLN
1	J	97	LEU
1	J	106	LEU
1	J	109	ARG
1	J	114	MET
1	J	117	THR
1	J	121	LEU
1	J	126	VAL
1	J	127	ASN
1	J	135	TYR
1	J	136	ASN
1	J	146	LYS
1	J	149	GLN
1	J	155	ILE
1	J	157	SER
1	J	158	ILE

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	J	159	SER
1	J	165	PHE
1	J	167	LEU
1	J	169	ASP
1	J	173	GLN
1	J	178	THR
1	J	185	LYS
1	J	186	THR
1	J	187	VAL
1	J	189	THR
1	J	191	ARG
1	J	193	ILE
1	J	194	GLN
1	J	198	THR
1	J	199	ILE
1	J	218	LEU
1	J	219	GLU
1	J	221	GLN
1	J	223	ILE
1	J	229	LEU
1	J	244	SER
1	J	245	ARG
1	J	251	ARG
1	J	264	ASP
1	J	273	SER
1	J	274	ARG
1	J	278	GLN
1	J	282	GLU
1	J	287	ILE
1	J	290	GLN
1	J	294	ASN
1	J	298	GLU
1	J	300	ILE
1	J	325	ILE
1	J	331	LEU
1	J	336	SER
1	J	351	ILE
1	J	354	LEU
1	J	364	LEU
1	J	365	LYS
1	J	372	GLU
1	J	376	GLU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	J	381	GLU
1	J	389	LEU
1	J	392	LEU
1	J	394	SER
1	J	399	LYS
1	J	405	ARG
1	J	410	ASN
1	J	439	LEU
1	J	447	GLN
1	J	448	GLN
1	J	449	LEU
1	J	453	GLN
1	J	455	ARG
1	J	457	TYR
1	J	462	LEU
1	J	471	ASP
1	J	474	SER
1	J	480	ILE
1	J	487	LEU
1	J	495	MET
1	J	499	GLU
1	J	506	GLU
1	J	513	ILE
1	J	518	ASP
1	J	524	GLU
1	J	532	ILE
1	J	534	SER
1	J	537	GLU
1	J	543	PRO
1	J	549	SER
1	J	561	LYS
1	J	562	SER
1	J	563	ASN
1	J	569	LYS
1	J	580	SER
1	J	593	SER
1	J	597	GLU
1	J	604	ASN
1	J	608	ILE
1	J	610	LEU
1	J	615	SER
1	J	621	LEU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	J	625	THR
1	J	664	LEU
1	J	666	SER
1	J	673	ARG
1	J	675	ILE
1	J	676	ILE
1	J	686	MET
1	J	689	GLU
1	J	690	LEU
1	J	693	HIS
1	J	698	ASN
1	J	701	LEU
1	J	702	GLU
1	J	708	ARG
1	J	713	SER
1	J	714	ARG
1	J	716	LEU
1	J	719	ASP
1	J	722	GLN
1	J	723	ARG
1	J	727	LEU
1	J	728	ASN
1	J	745	GLU
1	J	752	ASP
1	J	753	VAL
1	J	754	ASP
1	J	762	HIS
1	J	774	LEU
1	J	785	GLU
1	J	787	ILE
1	J	793	ARG
1	J	799	MET
1	J	802	GLU
1	J	804	ARG
1	J	810	ARG
1	J	816	ILE
1	J	822	SER
1	J	832	MET
1	J	834	LEU
1	J	838	ILE
1	J	842	LEU
1	J	843	LYS

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
2	K	142	PRO
3	L	48	LYS
3	L	68	PHE
3	L	83	THR
3	L	95	ASP
3	L	96	LYS
4	0	33	SER
4	0	34	ILE
4	0	37	ARG
4	0	66	THR
4	0	72	GLU
4	0	80	ASP
4	0	100	GLU
4	0	109	PRO
4	0	116	ARG
4	0	145	SER
4	0	153	LEU
4	0	159	VAL
4	0	180	LEU
4	0	191	LYS
4	0	196	ARG
4	0	199	SER
4	0	201	VAL
4	0	206	ARG
4	0	221	LEU
4	0	223	PHE
4	0	229	THR
4	0	239	SER
4	0	242	LEU
4	0	246	GLN
4	0	263	GLN
4	0	281	SER
4	0	283	MET
4	0	287	ILE
4	0	291	LYS
4	0	293	LEU
4	0	297	ASN
4	0	299	MET
4	0	312	ARG
4	0	315	LYS
4	0	318	THR
4	0	320	LEU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
4	0	327	ILE
4	0	334	GLU
4	0	349	LEU
4	0	350	SER
4	0	351	THR
4	0	354	GLN
4	0	359	LYS
4	0	360	GLN
4	0	361	GLU
4	0	368	SER
4	1	16	LEU
4	1	33	SER
4	1	34	ILE
4	1	37	ARG
4	1	66	THR
4	1	72	GLU
4	1	80	ASP
4	1	100	GLU
4	1	109	PRO
4	1	116	ARG
4	1	145	SER
4	1	153	LEU
4	1	159	VAL
4	1	180	LEU
4	1	191	LYS
4	1	196	ARG
4	1	199	SER
4	1	201	VAL
4	1	206	ARG
4	1	221	LEU
4	1	223	PHE
4	1	229	THR
4	1	239	SER
4	1	242	LEU
4	1	246	GLN
4	1	263	GLN
4	1	281	SER
4	1	283	MET
4	1	287	ILE
4	1	291	LYS
4	1	293	LEU
4	1	297	ASN

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
4	1	299	MET
4	1	312	ARG
4	1	315	LYS
4	1	318	THR
4	1	320	LEU
4	1	327	ILE
4	1	334	GLU
4	1	349	LEU
4	1	350	SER
4	1	351	THR
4	1	354	GLN
4	1	359	LYS
4	1	360	GLN
4	1	361	GLU
4	1	368	SER
4	2	16	LEU
4	2	33	SER
4	2	34	ILE
4	2	37	ARG
4	2	66	THR
4	2	72	GLU
4	2	80	ASP
4	2	100	GLU
4	2	109	PRO
4	2	116	ARG
4	2	145	SER
4	2	153	LEU
4	2	159	VAL
4	2	180	LEU
4	2	191	LYS
4	2	196	ARG
4	2	199	SER
4	2	201	VAL
4	2	206	ARG
4	2	221	LEU
4	2	223	PHE
4	2	229	THR
4	2	239	SER
4	2	242	LEU
4	2	246	GLN
4	2	263	GLN
4	2	281	SER

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
4	2	283	MET
4	2	287	ILE
4	2	291	LYS
4	2	293	LEU
4	2	297	ASN
4	2	299	MET
4	2	312	ARG
4	2	315	LYS
4	2	318	THR
4	2	320	LEU
4	2	327	ILE
4	2	334	GLU
4	2	349	LEU
4	2	350	SER
4	2	351	THR
4	2	354	GLN
4	2	359	LYS
4	2	360	GLN
4	2	361	GLU
4	2	368	SER
4	3	16	LEU
4	3	33	SER
4	3	34	ILE
4	3	37	ARG
4	3	66	THR
4	3	72	GLU
4	3	80	ASP
4	3	100	GLU
4	3	109	PRO
4	3	116	ARG
4	3	145	SER
4	3	153	LEU
4	3	159	VAL
4	3	180	LEU
4	3	191	LYS
4	3	196	ARG
4	3	199	SER
4	3	201	VAL
4	3	206	ARG
4	3	221	LEU
4	3	223	PHE
4	3	229	THR

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
4	3	239	SER
4	3	242	LEU
4	3	246	GLN
4	3	263	GLN
4	3	281	SER
4	3	283	MET
4	3	287	ILE
4	3	291	LYS
4	3	293	LEU
4	3	297	ASN
4	3	299	MET
4	3	312	ARG
4	3	315	LYS
4	3	318	THR
4	3	320	LEU
4	3	327	ILE
4	3	334	GLU
4	3	349	LEU
4	3	350	SER
4	3	351	THR
4	3	354	GLN
4	3	359	LYS
4	3	360	GLN
4	3	361	GLU
4	3	368	SER
4	4	16	LEU
4	4	33	SER
4	4	34	ILE
4	4	37	ARG
4	4	66	THR
4	4	72	GLU
4	4	80	ASP
4	4	100	GLU
4	4	109	PRO
4	4	116	ARG
4	4	145	SER
4	4	153	LEU
4	4	159	VAL
4	4	180	LEU
4	4	191	LYS
4	4	196	ARG
4	4	199	SER

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
4	4	201	VAL
4	4	206	ARG
4	4	221	LEU
4	4	223	PHE
4	4	229	THR
4	4	239	SER
4	4	242	LEU
4	4	246	GLN
4	4	263	GLN
4	4	281	SER
4	4	283	MET
4	4	287	ILE
4	4	291	LYS
4	4	293	LEU
4	4	297	ASN
4	4	299	MET
4	4	312	ARG
4	4	315	LYS
4	4	318	THR
4	4	320	LEU
4	4	327	ILE
4	4	334	GLU
4	4	349	LEU
4	4	350	SER
4	4	351	THR
4	4	354	GLN
4	4	359	LYS
4	4	360	GLN
4	4	361	GLU
4	4	368	SER
4	5	33	SER
4	5	34	ILE
4	5	37	ARG
4	5	66	THR
4	5	72	GLU
4	5	80	ASP
4	5	100	GLU
4	5	109	PRO
4	5	116	ARG
4	5	145	SER
4	5	153	LEU
4	5	159	VAL

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
4	5	180	LEU
4	5	191	LYS
4	5	196	ARG
4	5	199	SER
4	5	201	VAL
4	5	206	ARG
4	5	221	LEU
4	5	223	PHE
4	5	229	THR
4	5	239	SER
4	5	242	LEU
4	5	246	GLN
4	5	263	GLN
4	5	281	SER
4	5	283	MET
4	5	287	ILE
4	5	291	LYS
4	5	293	LEU
4	5	297	ASN
4	5	299	MET
4	5	312	ARG
4	5	315	LYS
4	5	318	THR
4	5	320	LEU
4	5	327	ILE
4	5	334	GLU
4	5	349	LEU
4	5	350	SER
4	5	351	THR
4	5	354	GLN
4	5	359	LYS
4	5	360	GLN
4	5	361	GLU
4	5	368	SER
4	6	16	LEU
4	6	33	SER
4	6	34	ILE
4	6	37	ARG
4	6	66	THR
4	6	72	GLU
4	6	80	ASP
4	6	100	GLU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
4	6	109	PRO
4	6	116	ARG
4	6	145	SER
4	6	153	LEU
4	6	159	VAL
4	6	180	LEU
4	6	191	LYS
4	6	196	ARG
4	6	199	SER
4	6	201	VAL
4	6	206	ARG
4	6	221	LEU
4	6	223	PHE
4	6	229	THR
4	6	239	SER
4	6	242	LEU
4	6	246	GLN
4	6	263	GLN
4	6	281	SER
4	6	283	MET
4	6	287	ILE
4	6	291	LYS
4	6	293	LEU
4	6	297	ASN
4	6	299	MET
4	6	312	ARG
4	6	315	LYS
4	6	318	THR
4	6	320	LEU
4	6	327	ILE
4	6	334	GLU
4	6	349	LEU
4	6	350	SER
4	6	351	THR
4	6	354	GLN
4	6	359	LYS
4	6	360	GLN
4	6	361	GLU
4	6	368	SER
4	7	33	SER
4	7	34	ILE
4	7	37	ARG

*Continued on next page...*

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
4	7	66	THR
4	7	72	GLU
4	7	80	ASP
4	7	100	GLU
4	7	109	PRO
4	7	116	ARG
4	7	145	SER
4	7	153	LEU
4	7	159	VAL
4	7	180	LEU
4	7	191	LYS
4	7	196	ARG
4	7	199	SER
4	7	201	VAL
4	7	206	ARG
4	7	221	LEU
4	7	223	PHE
4	7	229	THR
4	7	239	SER
4	7	242	LEU
4	7	246	GLN
4	7	263	GLN
4	7	281	SER
4	7	283	MET
4	7	287	ILE
4	7	291	LYS
4	7	293	LEU
4	7	297	ASN
4	7	299	MET
4	7	312	ARG
4	7	315	LYS
4	7	318	THR
4	7	320	LEU
4	7	327	ILE
4	7	334	GLU
4	7	349	LEU
4	7	350	SER
4	7	351	THR
4	7	354	GLN
4	7	359	LYS
4	7	360	GLN
4	7	361	GLU

*Continued on next page...*

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
4	7	368	SER
4	8	16	LEU
4	8	33	SER
4	8	34	ILE
4	8	37	ARG
4	8	66	THR
4	8	72	GLU
4	8	80	ASP
4	8	100	GLU
4	8	109	PRO
4	8	116	ARG
4	8	145	SER
4	8	153	LEU
4	8	159	VAL
4	8	180	LEU
4	8	191	LYS
4	8	196	ARG
4	8	199	SER
4	8	201	VAL
4	8	206	ARG
4	8	221	LEU
4	8	223	PHE
4	8	229	THR
4	8	239	SER
4	8	242	LEU
4	8	246	GLN
4	8	263	GLN
4	8	281	SER
4	8	283	MET
4	8	287	ILE
4	8	291	LYS
4	8	293	LEU
4	8	297	ASN
4	8	299	MET
4	8	312	ARG
4	8	315	LYS
4	8	318	THR
4	8	320	LEU
4	8	327	ILE
4	8	334	GLU
4	8	349	LEU
4	8	350	SER

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
4	8	351	THR
4	8	354	GLN
4	8	359	LYS
4	8	360	GLN
4	8	361	GLU
4	8	368	SER
4	V	33	SER
4	V	34	ILE
4	V	37	ARG
4	V	66	THR
4	V	72	GLU
4	V	80	ASP
4	V	100	GLU
4	V	109	PRO
4	V	116	ARG
4	V	145	SER
4	V	153	LEU
4	V	159	VAL
4	V	180	LEU
4	V	191	LYS
4	V	196	ARG
4	V	199	SER
4	V	201	VAL
4	V	206	ARG
4	V	221	LEU
4	V	223	PHE
4	V	229	THR
4	V	239	SER
4	V	242	LEU
4	V	246	GLN
4	V	263	GLN
4	V	281	SER
4	V	283	MET
4	V	287	ILE
4	V	291	LYS
4	V	293	LEU
4	V	297	ASN
4	V	299	MET
4	V	312	ARG
4	V	315	LYS
4	V	318	THR
4	V	320	LEU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
4	V	327	ILE
4	V	334	GLU
4	V	349	LEU
4	V	350	SER
4	V	351	THR
4	V	354	GLN
4	V	359	LYS
4	V	360	GLN
4	V	361	GLU
4	V	368	SER
4	W	33	SER
4	W	34	ILE
4	W	37	ARG
4	W	66	THR
4	W	72	GLU
4	W	80	ASP
4	W	100	GLU
4	W	109	PRO
4	W	116	ARG
4	W	145	SER
4	W	153	LEU
4	W	159	VAL
4	W	180	LEU
4	W	191	LYS
4	W	196	ARG
4	W	199	SER
4	W	201	VAL
4	W	206	ARG
4	W	221	LEU
4	W	223	PHE
4	W	229	THR
4	W	239	SER
4	W	242	LEU
4	W	246	GLN
4	W	263	GLN
4	W	281	SER
4	W	283	MET
4	W	287	ILE
4	W	291	LYS
4	W	293	LEU
4	W	297	ASN
4	W	299	MET

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
4	W	312	ARG
4	W	315	LYS
4	W	318	THR
4	W	320	LEU
4	W	327	ILE
4	W	334	GLU
4	W	349	LEU
4	W	350	SER
4	W	351	THR
4	W	354	GLN
4	W	359	LYS
4	W	360	GLN
4	W	361	GLU
4	W	368	SER
4	X	33	SER
4	X	34	ILE
4	X	37	ARG
4	X	66	THR
4	X	72	GLU
4	X	80	ASP
4	X	100	GLU
4	X	109	PRO
4	X	116	ARG
4	X	145	SER
4	X	153	LEU
4	X	159	VAL
4	X	180	LEU
4	X	191	LYS
4	X	196	ARG
4	X	199	SER
4	X	201	VAL
4	X	206	ARG
4	X	221	LEU
4	X	223	PHE
4	X	229	THR
4	X	239	SER
4	X	242	LEU
4	X	246	GLN
4	X	263	GLN
4	X	281	SER
4	X	283	MET
4	X	287	ILE

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
4	X	291	LYS
4	X	293	LEU
4	X	297	ASN
4	X	299	MET
4	X	312	ARG
4	X	315	LYS
4	X	318	THR
4	X	320	LEU
4	X	327	ILE
4	X	334	GLU
4	X	349	LEU
4	X	350	SER
4	X	351	THR
4	X	354	GLN
4	X	359	LYS
4	X	360	GLN
4	X	361	GLU
4	X	368	SER
4	Y	16	LEU
4	Y	33	SER
4	Y	34	ILE
4	Y	37	ARG
4	Y	66	THR
4	Y	72	GLU
4	Y	80	ASP
4	Y	100	GLU
4	Y	109	PRO
4	Y	116	ARG
4	Y	145	SER
4	Y	153	LEU
4	Y	159	VAL
4	Y	180	LEU
4	Y	191	LYS
4	Y	196	ARG
4	Y	199	SER
4	Y	201	VAL
4	Y	206	ARG
4	Y	221	LEU
4	Y	223	PHE
4	Y	229	THR
4	Y	239	SER
4	Y	242	LEU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
4	Y	246	GLN
4	Y	263	GLN
4	Y	281	SER
4	Y	283	MET
4	Y	287	ILE
4	Y	291	LYS
4	Y	293	LEU
4	Y	297	ASN
4	Y	299	MET
4	Y	312	ARG
4	Y	315	LYS
4	Y	318	THR
4	Y	320	LEU
4	Y	327	ILE
4	Y	334	GLU
4	Y	349	LEU
4	Y	350	SER
4	Y	351	THR
4	Y	354	GLN
4	Y	359	LYS
4	Y	360	GLN
4	Y	361	GLU
4	Y	368	SER
4	Z	16	LEU
4	Z	33	SER
4	Z	34	ILE
4	Z	37	ARG
4	Z	66	THR
4	Z	72	GLU
4	Z	80	ASP
4	Z	100	GLU
4	Z	109	PRO
4	Z	116	ARG
4	Z	145	SER
4	Z	153	LEU
4	Z	159	VAL
4	Z	180	LEU
4	Z	191	LYS
4	Z	196	ARG
4	Z	199	SER
4	Z	201	VAL
4	Z	206	ARG

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Mol	Chain	Res	Type
4	Z	221	LEU
4	Z	223	PHE
4	Z	229	THR
4	Z	239	SER
4	Z	242	LEU
4	Z	246	GLN
4	Z	263	GLN
4	Z	281	SER
4	Z	283	MET
4	Z	287	ILE
4	Z	291	LYS
4	Z	293	LEU
4	Z	297	ASN
4	Z	299	MET
4	Z	312	ARG
4	Z	315	LYS
4	Z	318	THR
4	Z	320	LEU
4	Z	327	ILE
4	Z	334	GLU
4	Z	349	LEU
4	Z	350	SER
4	Z	351	THR
4	Z	354	GLN
4	Z	359	LYS
4	Z	360	GLN
4	Z	361	GLU
4	Z	368	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (184) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	29	ASN
1	A	127	ASN
1	A	149	GLN
1	A	164	GLN
1	A	188	ASN
1	A	194	GLN
1	A	221	GLN
1	A	253	HIS
1	A	290	GLN
1	A	368	GLN

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	424	ASN
1	A	453	GLN
1	A	481	ASN
1	A	484	ASN
1	A	563	ASN
1	A	564	ASN
1	A	578	HIS
1	A	612	GLN
1	A	656	ASN
1	A	670	HIS
1	A	762	HIS
2	B	159	HIS
3	C	52	ASN
1	D	29	ASN
1	D	127	ASN
1	D	149	GLN
1	D	164	GLN
1	D	188	ASN
1	D	194	GLN
1	D	221	GLN
1	D	253	HIS
1	D	290	GLN
1	D	368	GLN
1	D	424	ASN
1	D	447	GLN
1	D	453	GLN
1	D	481	ASN
1	D	484	ASN
1	D	563	ASN
1	D	564	ASN
1	D	578	HIS
1	D	612	GLN
1	D	656	ASN
1	D	670	HIS
1	D	698	ASN
1	D	757	GLN
1	D	762	HIS
1	D	817	GLN
2	E	159	HIS
3	F	39	GLN
3	F	52	ASN
3	F	81	GLN

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	G	29	ASN
1	G	127	ASN
1	G	164	GLN
1	G	188	ASN
1	G	194	GLN
1	G	221	GLN
1	G	253	HIS
1	G	290	GLN
1	G	368	GLN
1	G	424	ASN
1	G	447	GLN
1	G	453	GLN
1	G	481	ASN
1	G	484	ASN
1	G	563	ASN
1	G	564	ASN
1	G	578	HIS
1	G	612	GLN
1	G	656	ASN
1	G	670	HIS
1	G	728	ASN
1	G	762	HIS
3	I	39	GLN
3	I	40	ASN
3	I	52	ASN
3	I	81	GLN
3	I	109	HIS
1	J	29	ASN
1	J	127	ASN
1	J	164	GLN
1	J	188	ASN
1	J	194	GLN
1	J	221	GLN
1	J	253	HIS
1	J	290	GLN
1	J	368	GLN
1	J	424	ASN
1	J	447	GLN
1	J	453	GLN
1	J	481	ASN
1	J	484	ASN
1	J	563	ASN

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	J	564	ASN
1	J	578	HIS
1	J	612	GLN
1	J	656	ASN
1	J	670	HIS
1	J	698	ASN
1	J	762	HIS
2	K	159	HIS
3	L	39	GLN
3	L	52	ASN
4	0	41	GLN
4	0	92	ASN
4	0	137	GLN
4	0	252	ASN
4	0	263	GLN
4	0	354	GLN
4	1	41	GLN
4	1	92	ASN
4	1	137	GLN
4	1	252	ASN
4	1	263	GLN
4	1	354	GLN
4	2	41	GLN
4	2	92	ASN
4	2	137	GLN
4	2	252	ASN
4	2	263	GLN
4	2	354	GLN
4	3	41	GLN
4	3	92	ASN
4	3	137	GLN
4	3	252	ASN
4	3	263	GLN
4	3	354	GLN
4	4	41	GLN
4	4	92	ASN
4	4	137	GLN
4	4	252	ASN
4	4	263	GLN
4	5	41	GLN
4	5	92	ASN
4	5	137	GLN

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
4	5	252	ASN
4	5	263	GLN
4	6	41	GLN
4	6	92	ASN
4	6	137	GLN
4	6	252	ASN
4	6	263	GLN
4	7	41	GLN
4	7	92	ASN
4	7	137	GLN
4	7	252	ASN
4	7	263	GLN
4	8	41	GLN
4	8	92	ASN
4	8	137	GLN
4	8	252	ASN
4	8	263	GLN
4	8	354	GLN
4	V	41	GLN
4	V	92	ASN
4	V	137	GLN
4	V	252	ASN
4	V	263	GLN
4	V	354	GLN
4	W	41	GLN
4	W	92	ASN
4	W	137	GLN
4	W	252	ASN
4	W	263	GLN
4	W	354	GLN
4	X	41	GLN
4	X	92	ASN
4	X	137	GLN
4	X	252	ASN
4	X	263	GLN
4	X	354	GLN
4	Y	41	GLN
4	Y	92	ASN
4	Y	137	GLN
4	Y	252	ASN
4	Y	263	GLN
4	Y	354	GLN

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Mol	Chain	Res	Type
4	Z	41	GLN
4	Z	92	ASN
4	Z	137	GLN
4	Z	252	ASN
4	Z	263	GLN
4	Z	354	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

180 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	MLY	A	436	1	9,10,11	1.04	1 (11%)	6,11,13	0.50	0
1	MLY	D	248	1	9,10,11	0.83	0	6,11,13	0.62	0
1	MLY	A	505	1	9,10,11	0.89	1 (11%)	6,11,13	0.34	0
1	MLY	J	55	1	9,10,11	0.72	0	6,11,13	0.78	0
1	MLY	G	839	1	9,10,11	0.70	0	6,11,13	0.80	0
1	MLY	J	436	1	9,10,11	1.06	1 (11%)	6,11,13	0.49	0
1	MLY	D	659	1	9,10,11	0.83	0	6,11,13	0.60	0
1	MLY	G	367	1	9,10,11	0.66	0	6,11,13	0.38	0
1	MLY	G	659	1	9,10,11	0.84	0	6,11,13	0.59	0
1	MLY	J	87	1	9,10,11	1.23	1 (11%)	6,11,13	0.43	0
1	MLY	J	839	1	9,10,11	0.71	0	6,11,13	0.76	0
1	MLY	D	236	1	9,10,11	0.79	1 (11%)	6,11,13	0.47	0
1	MLY	A	138	1	9,10,11	1.32	1 (11%)	6,11,13	0.84	0
1	MLY	J	617	1	9,10,11	0.96	1 (11%)	6,11,13	0.33	0
1	MLY	D	138	1	9,10,11	1.39	1 (11%)	6,11,13	0.85	0
1	MLY	A	764	1	9,10,11	0.86	0	6,11,13	0.36	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	MLY	D	385	1	9,10,11	0.99	1 (11%)	6,11,13	0.44	0
1	MLY	J	768	1	9,10,11	0.77	0	6,11,13	0.42	0
1	MLY	A	353	1	9,10,11	0.86	0	6,11,13	0.78	0
1	MLY	G	138	1	9,10,11	1.31	1 (11%)	6,11,13	0.84	0
1	MLY	D	272	1	9,10,11	0.99	1 (11%)	6,11,13	0.57	0
1	MLY	J	63	1	9,10,11	0.90	0	6,11,13	0.43	0
1	MLY	J	551	1	9,10,11	0.52	0	6,11,13	0.18	0
1	MLY	A	415	1	9,10,11	0.76	0	6,11,13	0.19	0
1	MLY	A	19	1	9,10,11	1.12	1 (11%)	6,11,13	0.57	0
1	MLY	A	30	1	9,10,11	0.89	0	6,11,13	0.32	0
1	MLY	G	30	1	9,10,11	0.89	0	6,11,13	0.30	0
1	MLY	G	827	1	9,10,11	0.69	0	6,11,13	0.49	0
1	MLY	A	190	1	9,10,11	1.26	1 (11%)	6,11,13	0.51	0
1	MLY	D	764	1	9,10,11	0.84	0	6,11,13	0.35	0
1	MLY	G	551	1	9,10,11	0.52	0	6,11,13	0.20	0
1	MLY	G	431	1	9,10,11	0.54	0	6,11,13	0.46	0
1	MLY	D	63	1	9,10,11	0.90	0	6,11,13	0.45	0
1	MLY	J	130	1	9,10,11	0.78	0	6,11,13	0.75	0
1	MLY	A	369	1	9,10,11	0.71	0	6,11,13	0.45	0
1	MLY	A	87	1	9,10,11	1.20	1 (11%)	6,11,13	0.43	0
1	MLY	J	296	1	9,10,11	0.67	0	6,11,13	0.36	0
1	MLY	G	768	1	9,10,11	0.74	0	6,11,13	0.42	0
1	MLY	G	107	1	9,10,11	0.47	0	6,11,13	0.34	0
1	MLY	G	248	1	9,10,11	0.81	0	6,11,13	0.63	0
1	MLY	G	837	1	9,10,11	0.59	0	6,11,13	0.53	0
1	MLY	G	84	1	9,10,11	0.49	0	6,11,13	0.80	0
1	MLY	A	295	1	9,10,11	0.84	0	6,11,13	0.33	0
1	MLY	G	190	1	9,10,11	1.26	1 (11%)	6,11,13	0.52	0
1	MLY	A	617	1	9,10,11	0.94	1 (11%)	6,11,13	0.34	0
1	MLY	J	486	1	9,10,11	0.63	0	6,11,13	0.39	0
1	MLY	D	551	1	9,10,11	0.53	0	6,11,13	0.20	0
1	MLY	D	84	1	9,10,11	0.51	0	6,11,13	0.80	0
1	MLY	D	827	1	9,10,11	0.69	0	6,11,13	0.48	0
1	MLY	J	49	1	9,10,11	1.08	1 (11%)	6,11,13	0.75	0
1	MLY	A	59	1	9,10,11	0.87	0	6,11,13	0.50	0
1	MLY	J	613	1	9,10,11	0.56	0	6,11,13	0.64	0
1	MLY	A	659	1	9,10,11	0.83	0	6,11,13	0.60	0
1	MLY	G	63	1	9,10,11	0.92	1 (11%)	6,11,13	0.43	0
1	MLY	J	248	1	9,10,11	0.82	0	6,11,13	0.62	0
1	MLY	J	84	1	9,10,11	0.49	0	6,11,13	0.80	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	MLY	A	236	1	9,10,11	0.80	1 (11%)	6,11,13	0.49	0
1	MLY	G	553	1,4	9,10,11	0.67	0	6,11,13	0.55	0
1	MLY	D	295	1	9,10,11	0.79	0	6,11,13	0.35	0
1	MLY	G	59	1	9,10,11	0.85	0	6,11,13	0.49	0
1	MLY	D	190	1	9,10,11	1.22	1 (11%)	6,11,13	0.54	0
1	MLY	J	295	1	9,10,11	0.78	0	6,11,13	0.35	0
1	MLY	D	768	1	9,10,11	0.74	0	6,11,13	0.41	0
1	MLY	G	505	1	9,10,11	0.87	1 (11%)	6,11,13	0.35	0
1	MLY	J	385	1	9,10,11	1.01	1 (11%)	6,11,13	0.44	0
1	MLY	A	486	1	9,10,11	0.65	0	6,11,13	0.39	0
1	MLY	A	528	1	9,10,11	0.89	0	6,11,13	0.66	0
1	MLY	A	348	1	9,10,11	0.85	0	6,11,13	0.48	0
1	MLY	A	600	1	9,10,11	0.51	0	6,11,13	0.38	0
1	MLY	A	837	1	9,10,11	0.61	0	6,11,13	0.54	0
1	MLY	G	35	1	9,10,11	0.72	0	6,11,13	0.39	0
1	MLY	A	782	1	9,10,11	0.78	0	6,11,13	0.35	0
1	MLY	D	598	1	9,10,11	0.93	1 (11%)	6,11,13	0.44	0
1	MLY	J	272	1	9,10,11	1.02	1 (11%)	6,11,13	0.55	0
1	MLY	J	598	1	9,10,11	0.90	1 (11%)	6,11,13	0.43	0
1	MLY	A	367	1	9,10,11	0.63	0	6,11,13	0.37	0
1	MLY	D	431	1	9,10,11	0.52	0	6,11,13	0.46	0
1	MLY	D	35	1	9,10,11	0.74	0	6,11,13	0.37	0
1	MLY	A	55	1	9,10,11	0.71	0	6,11,13	0.78	0
1	MLY	G	600	1	9,10,11	0.51	0	6,11,13	0.37	0
1	MLY	A	431	1	9,10,11	0.53	0	6,11,13	0.45	0
1	MLY	G	369	1	9,10,11	0.70	0	6,11,13	0.46	0
1	MLY	D	528	1	9,10,11	0.91	0	6,11,13	0.65	0
1	MLY	G	130	1	9,10,11	0.79	0	6,11,13	0.75	0
1	MLY	D	436	1	9,10,11	1.12	1 (11%)	6,11,13	0.49	0
1	MLY	D	30	1	9,10,11	0.91	0	6,11,13	0.32	0
1	MLY	D	59	1	9,10,11	0.87	0	6,11,13	0.49	0
1	MLY	D	369	1	9,10,11	0.70	0	6,11,13	0.44	0
1	MLY	D	130	1	9,10,11	0.80	0	6,11,13	0.74	0
1	MLY	D	55	1	9,10,11	0.72	0	6,11,13	0.79	0
1	MLY	A	839	1,2	9,10,11	0.70	0	6,11,13	0.80	0
1	MLY	A	107	1	9,10,11	0.45	0	6,11,13	0.34	0
1	MLY	J	837	1	9,10,11	0.58	0	6,11,13	0.55	0
1	MLY	A	63	1	9,10,11	0.91	0	6,11,13	0.43	0
1	MLY	A	130	1	9,10,11	0.81	0	6,11,13	0.75	0
1	MLY	J	138	1	9,10,11	1.34	1 (11%)	6,11,13	0.83	0
1	MLY	G	415	1	9,10,11	0.75	0	6,11,13	0.19	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	MLY	D	553	1,4	9,10,11	0.68	0	6,11,13	0.56	0
1	MLY	G	295	1	9,10,11	0.81	0	6,11,13	0.33	0
1	MLY	G	19	1	9,10,11	1.15	1 (11%)	6,11,13	0.59	0
1	MLY	G	49	1	9,10,11	1.08	1 (11%)	6,11,13	0.75	0
1	MLY	A	681	1	9,10,11	0.60	0	6,11,13	0.46	0
1	MLY	J	764	1	9,10,11	0.84	0	6,11,13	0.38	0
1	MLY	D	486	1	9,10,11	0.66	0	6,11,13	0.39	0
1	MLY	D	600	1	9,10,11	0.50	0	6,11,13	0.38	0
1	MLY	D	782	1	9,10,11	0.79	0	6,11,13	0.34	0
1	MLY	D	837	1	9,10,11	0.61	0	6,11,13	0.56	0
1	MLY	D	367	1	9,10,11	0.61	0	6,11,13	0.38	0
1	MLY	G	296	1	9,10,11	0.64	0	6,11,13	0.37	0
1	MLY	A	504	1	9,10,11	0.90	0	6,11,13	0.25	0
1	MLY	D	617	1	9,10,11	0.97	1 (11%)	6,11,13	0.34	0
1	MLY	J	415	1	9,10,11	0.79	0	6,11,13	0.19	0
1	MLY	J	30	1	9,10,11	0.89	0	6,11,13	0.32	0
1	MLY	J	190	1	9,10,11	1.25	1 (11%)	6,11,13	0.52	0
1	MLY	A	827	1	9,10,11	0.71	0	6,11,13	0.46	0
1	MLY	A	768	1	9,10,11	0.75	0	6,11,13	0.40	0
1	MLY	J	367	1	9,10,11	0.62	0	6,11,13	0.37	0
1	MLY	D	681	1	9,10,11	0.57	0	6,11,13	0.45	0
1	MLY	G	353	1	9,10,11	0.86	0	6,11,13	0.80	0
1	MLY	G	385	1	9,10,11	1.00	1 (11%)	6,11,13	0.43	0
1	MLY	A	551	1	9,10,11	0.51	0	6,11,13	0.19	0
1	MLY	J	659	1	9,10,11	0.80	0	6,11,13	0.57	0
1	MLY	G	598	1	9,10,11	0.87	1 (11%)	6,11,13	0.42	0
1	MLY	G	613	1	9,10,11	0.59	0	6,11,13	0.64	0
1	MLY	G	617	1	9,10,11	0.95	1 (11%)	6,11,13	0.34	0
1	MLY	D	19	1	9,10,11	1.20	1 (11%)	6,11,13	0.57	0
1	MLY	G	436	1	9,10,11	1.06	1 (11%)	6,11,13	0.48	0
1	MLY	A	35	1	9,10,11	0.71	0	6,11,13	0.38	0
1	MLY	J	236	1	9,10,11	0.79	1 (11%)	6,11,13	0.48	0
1	MLY	G	348	1	9,10,11	0.86	1 (11%)	6,11,13	0.48	0
1	MLY	G	833	1	9,10,11	1.17	2 (22%)	6,11,13	0.33	0
1	MLY	J	431	1	9,10,11	0.53	0	6,11,13	0.44	0
1	MLY	A	49	1	9,10,11	1.07	1 (11%)	6,11,13	0.75	0
1	MLY	D	839	1	9,10,11	0.70	0	6,11,13	0.79	0
1	MLY	D	107	1	9,10,11	0.51	0	6,11,13	0.34	0
1	MLY	D	505	1	9,10,11	0.85	1 (11%)	6,11,13	0.35	0
1	MLY	J	504	1	9,10,11	0.86	0	6,11,13	0.23	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	MLY	A	613	1	9,10,11	0.57	0	6,11,13	0.63	0
1	MLY	J	35	1	9,10,11	0.72	0	6,11,13	0.39	0
1	MLY	D	833	1	9,10,11	1.14	2 (22%)	6,11,13	0.31	0
1	MLY	J	19	1	9,10,11	1.18	1 (11%)	6,11,13	0.57	0
1	MLY	A	248	1	9,10,11	0.84	0	6,11,13	0.60	0
1	MLY	A	84	1	9,10,11	0.48	0	6,11,13	0.79	0
1	MLY	D	87	1	9,10,11	1.16	1 (11%)	6,11,13	0.44	0
1	MLY	G	236	1	9,10,11	0.78	1 (11%)	6,11,13	0.47	0
1	MLY	J	505	1	9,10,11	0.92	1 (11%)	6,11,13	0.34	0
1	MLY	A	296	1	9,10,11	0.60	0	6,11,13	0.36	0
1	MLY	J	107	1	9,10,11	0.47	0	6,11,13	0.34	0
1	MLY	J	833	1	9,10,11	1.19	1 (11%)	6,11,13	0.31	0
1	MLY	A	833	1	9,10,11	1.15	1 (11%)	6,11,13	0.32	0
1	MLY	J	59	1	9,10,11	0.88	0	6,11,13	0.49	0
1	MLY	G	87	1	9,10,11	1.21	1 (11%)	6,11,13	0.43	0
1	MLY	J	369	1	9,10,11	0.70	0	6,11,13	0.45	0
1	MLY	D	353	1	9,10,11	0.84	0	6,11,13	0.79	0
1	MLY	G	528	1	9,10,11	0.89	0	6,11,13	0.67	0
1	MLY	G	486	1	9,10,11	0.64	0	6,11,13	0.38	0
1	MLY	A	385	1	9,10,11	1.00	1 (11%)	6,11,13	0.43	0
1	MLY	A	553	1,4	9,10,11	0.68	0	6,11,13	0.54	0
1	MLY	G	782	1	9,10,11	0.76	0	6,11,13	0.35	0
1	MLY	D	613	1	9,10,11	0.56	0	6,11,13	0.64	0
1	MLY	A	272	1	9,10,11	1.01	1 (11%)	6,11,13	0.56	0
1	MLY	A	598	1	9,10,11	0.91	1 (11%)	6,11,13	0.44	0
1	MLY	J	353	1	9,10,11	0.84	0	6,11,13	0.79	0
1	MLY	D	49	1	9,10,11	1.08	1 (11%)	6,11,13	0.73	0
1	MLY	D	296	1	9,10,11	0.64	0	6,11,13	0.37	0
1	MLY	G	504	1	9,10,11	0.88	0	6,11,13	0.23	0
1	MLY	D	348	1	9,10,11	0.81	0	6,11,13	0.47	0
1	MLY	J	553	1,4	9,10,11	0.67	0	6,11,13	0.53	0
1	MLY	G	764	1	9,10,11	0.82	0	6,11,13	0.36	0
1	MLY	J	681	1	9,10,11	0.59	0	6,11,13	0.46	0
1	MLY	G	55	1	9,10,11	0.74	0	6,11,13	0.79	0
1	MLY	J	528	1	9,10,11	0.88	0	6,11,13	0.66	0
1	MLY	D	504	1	9,10,11	0.88	0	6,11,13	0.22	0
1	MLY	G	272	1	9,10,11	0.99	1 (11%)	6,11,13	0.55	0
1	MLY	J	348	1	9,10,11	0.82	0	6,11,13	0.47	0
1	MLY	J	600	1	9,10,11	0.53	0	6,11,13	0.36	0
1	MLY	J	827	1	9,10,11	0.74	0	6,11,13	0.48	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	MLY	D	415	1	9,10,11	0.77	0	6,11,13	0.19	0
1	MLY	J	782	1	9,10,11	0.79	0	6,11,13	0.36	0
1	MLY	G	681	1	9,10,11	0.64	0	6,11,13	0.44	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MLY	A	436	1	-	4/8/9/11	-
1	MLY	D	248	1	-	6/8/9/11	-
1	MLY	A	505	1	-	5/8/9/11	-
1	MLY	J	55	1	-	6/8/9/11	-
1	MLY	G	839	1	-	3/8/9/11	-
1	MLY	J	436	1	-	4/8/9/11	-
1	MLY	D	659	1	-	3/8/9/11	-
1	MLY	G	367	1	-	2/8/9/11	-
1	MLY	G	659	1	-	3/8/9/11	-
1	MLY	J	87	1	-	2/8/9/11	-
1	MLY	J	839	1	-	3/8/9/11	-
1	MLY	D	236	1	-	3/8/9/11	-
1	MLY	A	138	1	-	4/8/9/11	-
1	MLY	J	617	1	-	1/8/9/11	-
1	MLY	D	138	1	-	4/8/9/11	-
1	MLY	A	764	1	-	2/8/9/11	-
1	MLY	D	385	1	-	2/8/9/11	-
1	MLY	J	768	1	-	4/8/9/11	-
1	MLY	A	353	1	-	4/8/9/11	-
1	MLY	G	138	1	-	4/8/9/11	-
1	MLY	D	272	1	-	3/8/9/11	-
1	MLY	J	63	1	-	4/8/9/11	-
1	MLY	J	551	1	-	3/8/9/11	-
1	MLY	A	415	1	-	3/8/9/11	-
1	MLY	A	19	1	-	4/8/9/11	-
1	MLY	A	30	1	-	2/8/9/11	-
1	MLY	G	30	1	-	2/8/9/11	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MLY	G	827	1	-	0/8/9/11	-
1	MLY	A	190	1	-	5/8/9/11	-
1	MLY	D	764	1	-	2/8/9/11	-
1	MLY	G	551	1	-	3/8/9/11	-
1	MLY	G	431	1	-	4/8/9/11	-
1	MLY	D	63	1	-	4/8/9/11	-
1	MLY	J	130	1	-	5/8/9/11	-
1	MLY	A	369	1	-	2/8/9/11	-
1	MLY	A	87	1	-	2/8/9/11	-
1	MLY	J	296	1	-	4/8/9/11	-
1	MLY	G	768	1	-	4/8/9/11	-
1	MLY	G	107	1	-	2/8/9/11	-
1	MLY	G	248	1	-	6/8/9/11	-
1	MLY	G	837	1	-	5/8/9/11	-
1	MLY	G	84	1	-	4/8/9/11	-
1	MLY	A	295	1	-	2/8/9/11	-
1	MLY	G	190	1	-	5/8/9/11	-
1	MLY	A	617	1	-	1/8/9/11	-
1	MLY	J	486	1	-	2/8/9/11	-
1	MLY	D	551	1	-	3/8/9/11	-
1	MLY	D	84	1	-	4/8/9/11	-
1	MLY	D	827	1	-	0/8/9/11	-
1	MLY	J	49	1	-	3/8/9/11	-
1	MLY	A	59	1	-	3/8/9/11	-
1	MLY	J	613	1	-	4/8/9/11	-
1	MLY	A	659	1	-	3/8/9/11	-
1	MLY	G	63	1	-	4/8/9/11	-
1	MLY	J	248	1	-	6/8/9/11	-
1	MLY	J	84	1	-	4/8/9/11	-
1	MLY	A	236	1	-	3/8/9/11	-
1	MLY	G	553	1,4	-	4/8/9/11	-
1	MLY	D	295	1	-	2/8/9/11	-
1	MLY	G	59	1	-	3/8/9/11	-
1	MLY	D	190	1	-	5/8/9/11	-
1	MLY	J	295	1	-	2/8/9/11	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MLY	D	768	1	-	4/8/9/11	-
1	MLY	G	505	1	-	5/8/9/11	-
1	MLY	J	385	1	-	2/8/9/11	-
1	MLY	A	486	1	-	2/8/9/11	-
1	MLY	A	528	1	-	5/8/9/11	-
1	MLY	A	348	1	-	5/8/9/11	-
1	MLY	A	600	1	-	3/8/9/11	-
1	MLY	A	837	1	-	5/8/9/11	-
1	MLY	G	35	1	-	3/8/9/11	-
1	MLY	A	782	1	-	6/8/9/11	-
1	MLY	D	598	1	-	5/8/9/11	-
1	MLY	J	272	1	-	3/8/9/11	-
1	MLY	J	598	1	-	5/8/9/11	-
1	MLY	A	367	1	-	2/8/9/11	-
1	MLY	D	431	1	-	4/8/9/11	-
1	MLY	D	35	1	-	3/8/9/11	-
1	MLY	A	55	1	-	6/8/9/11	-
1	MLY	G	600	1	-	3/8/9/11	-
1	MLY	A	431	1	-	4/8/9/11	-
1	MLY	G	369	1	-	2/8/9/11	-
1	MLY	D	528	1	-	4/8/9/11	-
1	MLY	G	130	1	-	5/8/9/11	-
1	MLY	D	436	1	-	4/8/9/11	-
1	MLY	D	30	1	-	2/8/9/11	-
1	MLY	D	59	1	-	3/8/9/11	-
1	MLY	D	369	1	-	2/8/9/11	-
1	MLY	D	130	1	-	5/8/9/11	-
1	MLY	D	55	1	-	6/8/9/11	-
1	MLY	A	839	1,2	-	3/8/9/11	-
1	MLY	A	107	1	-	2/8/9/11	-
1	MLY	J	837	1	-	5/8/9/11	-
1	MLY	A	63	1	-	4/8/9/11	-
1	MLY	A	130	1	-	5/8/9/11	-
1	MLY	J	138	1	-	4/8/9/11	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MLY	G	415	1	-	3/8/9/11	-
1	MLY	D	553	1,4	-	4/8/9/11	-
1	MLY	G	295	1	-	2/8/9/11	-
1	MLY	G	19	1	-	4/8/9/11	-
1	MLY	G	49	1	-	3/8/9/11	-
1	MLY	A	681	1	-	4/8/9/11	-
1	MLY	J	764	1	-	2/8/9/11	-
1	MLY	D	486	1	-	2/8/9/11	-
1	MLY	D	600	1	-	3/8/9/11	-
1	MLY	D	782	1	-	6/8/9/11	-
1	MLY	D	837	1	-	5/8/9/11	-
1	MLY	D	367	1	-	2/8/9/11	-
1	MLY	G	296	1	-	4/8/9/11	-
1	MLY	A	504	1	-	4/8/9/11	-
1	MLY	D	617	1	-	1/8/9/11	-
1	MLY	J	415	1	-	3/8/9/11	-
1	MLY	J	30	1	-	2/8/9/11	-
1	MLY	J	190	1	-	5/8/9/11	-
1	MLY	A	827	1	-	0/8/9/11	-
1	MLY	A	768	1	-	4/8/9/11	-
1	MLY	J	367	1	-	2/8/9/11	-
1	MLY	D	681	1	-	4/8/9/11	-
1	MLY	G	353	1	-	4/8/9/11	-
1	MLY	G	385	1	-	2/8/9/11	-
1	MLY	A	551	1	-	3/8/9/11	-
1	MLY	J	659	1	-	3/8/9/11	-
1	MLY	G	598	1	-	5/8/9/11	-
1	MLY	G	613	1	-	4/8/9/11	-
1	MLY	G	617	1	-	1/8/9/11	-
1	MLY	D	19	1	-	4/8/9/11	-
1	MLY	G	436	1	-	4/8/9/11	-
1	MLY	A	35	1	-	3/8/9/11	-
1	MLY	J	236	1	-	3/8/9/11	-
1	MLY	G	348	1	-	5/8/9/11	-
1	MLY	G	833	1	-	6/8/9/11	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MLY	J	431	1	-	4/8/9/11	-
1	MLY	A	49	1	-	3/8/9/11	-
1	MLY	D	839	1	-	3/8/9/11	-
1	MLY	D	107	1	-	2/8/9/11	-
1	MLY	D	505	1	-	5/8/9/11	-
1	MLY	J	504	1	-	4/8/9/11	-
1	MLY	A	613	1	-	4/8/9/11	-
1	MLY	J	35	1	-	3/8/9/11	-
1	MLY	D	833	1	-	6/8/9/11	-
1	MLY	J	19	1	-	4/8/9/11	-
1	MLY	A	248	1	-	6/8/9/11	-
1	MLY	A	84	1	-	4/8/9/11	-
1	MLY	D	87	1	-	2/8/9/11	-
1	MLY	G	236	1	-	3/8/9/11	-
1	MLY	J	505	1	-	5/8/9/11	-
1	MLY	A	296	1	-	4/8/9/11	-
1	MLY	J	107	1	-	2/8/9/11	-
1	MLY	J	833	1	-	6/8/9/11	-
1	MLY	A	833	1	-	6/8/9/11	-
1	MLY	J	59	1	-	3/8/9/11	-
1	MLY	G	87	1	-	2/8/9/11	-
1	MLY	J	369	1	-	2/8/9/11	-
1	MLY	D	353	1	-	4/8/9/11	-
1	MLY	G	528	1	-	4/8/9/11	-
1	MLY	G	486	1	-	2/8/9/11	-
1	MLY	A	385	1	-	2/8/9/11	-
1	MLY	A	553	1,4	-	4/8/9/11	-
1	MLY	G	782	1	-	6/8/9/11	-
1	MLY	D	613	1	-	4/8/9/11	-
1	MLY	A	272	1	-	3/8/9/11	-
1	MLY	A	598	1	-	5/8/9/11	-
1	MLY	J	353	1	-	4/8/9/11	-
1	MLY	D	49	1	-	3/8/9/11	-
1	MLY	D	296	1	-	4/8/9/11	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MLY	G	504	1	-	4/8/9/11	-
1	MLY	D	348	1	-	5/8/9/11	-
1	MLY	J	553	1,4	-	4/8/9/11	-
1	MLY	G	764	1	-	2/8/9/11	-
1	MLY	J	681	1	-	4/8/9/11	-
1	MLY	G	55	1	-	6/8/9/11	-
1	MLY	J	528	1	-	4/8/9/11	-
1	MLY	D	504	1	-	4/8/9/11	-
1	MLY	G	272	1	-	3/8/9/11	-
1	MLY	J	348	1	-	5/8/9/11	-
1	MLY	J	600	1	-	3/8/9/11	-
1	MLY	J	827	1	-	0/8/9/11	-
1	MLY	D	415	1	-	3/8/9/11	-
1	MLY	J	782	1	-	6/8/9/11	-
1	MLY	G	681	1	-	4/8/9/11	-

All (56) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	138	MLY	CB-CA	-3.80	1.48	1.53
1	J	138	MLY	CB-CA	-3.66	1.48	1.53
1	A	138	MLY	CB-CA	-3.60	1.48	1.53
1	G	138	MLY	CB-CA	-3.55	1.48	1.53
1	D	19	MLY	CB-CA	-3.23	1.49	1.53
1	J	19	MLY	CB-CA	-3.15	1.49	1.53
1	G	87	MLY	CB-CA	-3.14	1.49	1.53
1	J	87	MLY	CB-CA	-3.13	1.49	1.53
1	D	436	MLY	CB-CA	-3.09	1.49	1.53
1	G	19	MLY	CB-CA	-3.06	1.49	1.53
1	A	87	MLY	CB-CA	-3.06	1.49	1.53
1	A	19	MLY	CB-CA	-2.98	1.49	1.53
1	D	87	MLY	CB-CA	-2.98	1.49	1.53
1	G	436	MLY	CB-CA	-2.92	1.49	1.53
1	J	436	MLY	CB-CA	-2.90	1.49	1.53
1	A	436	MLY	CB-CA	-2.85	1.49	1.53
1	D	49	MLY	CB-CA	-2.83	1.49	1.53
1	J	49	MLY	CB-CA	-2.82	1.49	1.53
1	J	272	MLY	CB-CA	-2.82	1.49	1.53
1	G	49	MLY	CB-CA	-2.81	1.49	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	49	MLY	CB-CA	-2.78	1.49	1.53
1	A	272	MLY	CB-CA	-2.77	1.49	1.53
1	G	272	MLY	CB-CA	-2.70	1.50	1.53
1	D	272	MLY	CB-CA	-2.70	1.50	1.53
1	G	190	MLY	CB-CA	-2.59	1.50	1.53
1	J	190	MLY	CB-CA	-2.56	1.50	1.53
1	A	190	MLY	CB-CA	-2.55	1.50	1.53
1	J	833	MLY	CB-CA	-2.50	1.50	1.53
1	J	385	MLY	CB-CA	-2.48	1.50	1.53
1	D	190	MLY	CB-CA	-2.47	1.50	1.53
1	A	385	MLY	CB-CA	-2.45	1.50	1.53
1	G	385	MLY	CB-CA	-2.43	1.50	1.53
1	D	385	MLY	CB-CA	-2.38	1.50	1.53
1	D	598	MLY	CB-CA	-2.35	1.50	1.53
1	A	833	MLY	CB-CA	-2.30	1.50	1.53
1	J	505	MLY	CB-CA	-2.30	1.50	1.53
1	A	598	MLY	CB-CA	-2.28	1.50	1.53
1	D	617	MLY	CB-CA	-2.28	1.50	1.53
1	J	598	MLY	CB-CA	-2.25	1.50	1.53
1	G	833	MLY	CB-CA	-2.24	1.50	1.53
1	J	617	MLY	CB-CA	-2.24	1.50	1.53
1	A	505	MLY	CB-CA	-2.21	1.50	1.53
1	G	598	MLY	CB-CA	-2.18	1.50	1.53
1	D	833	MLY	CB-CA	-2.18	1.50	1.53
1	G	505	MLY	CB-CA	-2.17	1.50	1.53
1	A	617	MLY	CB-CA	-2.16	1.50	1.53
1	A	236	MLY	CA-N	-2.14	1.41	1.48
1	G	617	MLY	CB-CA	-2.14	1.50	1.53
1	D	236	MLY	CA-N	-2.13	1.41	1.48
1	J	236	MLY	CA-N	-2.10	1.41	1.48
1	G	236	MLY	CA-N	-2.09	1.41	1.48
1	D	505	MLY	CB-CA	-2.08	1.50	1.53
1	G	833	MLY	CA-N	-2.04	1.42	1.48
1	G	348	MLY	CB-CA	-2.04	1.50	1.53
1	G	63	MLY	CB-CA	-2.04	1.50	1.53
1	D	833	MLY	CA-N	-2.03	1.42	1.48

There are no bond angle outliers.

There are no chirality outliers.

All (637) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	19	MLY	C-CA-CB-CG
1	A	49	MLY	N-CA-CB-CG
1	A	49	MLY	C-CA-CB-CG
1	A	55	MLY	N-CA-CB-CG
1	A	55	MLY	C-CA-CB-CG
1	A	84	MLY	C-CA-CB-CG
1	A	130	MLY	C-CA-CB-CG
1	A	248	MLY	N-CA-CB-CG
1	A	248	MLY	C-CA-CB-CG
1	A	348	MLY	N-CA-CB-CG
1	A	436	MLY	C-CA-CB-CG
1	A	486	MLY	C-CA-CB-CG
1	A	505	MLY	N-CA-CB-CG
1	A	505	MLY	C-CA-CB-CG
1	A	528	MLY	C-CA-CB-CG
1	A	551	MLY	C-CA-CB-CG
1	A	553	MLY	C-CA-CB-CG
1	A	598	MLY	N-CA-CB-CG
1	A	598	MLY	C-CA-CB-CG
1	A	613	MLY	N-CA-CB-CG
1	A	613	MLY	C-CA-CB-CG
1	A	681	MLY	C-CA-CB-CG
1	A	782	MLY	C-CA-CB-CG
1	A	782	MLY	O-C-CA-CB
1	D	19	MLY	C-CA-CB-CG
1	D	49	MLY	N-CA-CB-CG
1	D	49	MLY	C-CA-CB-CG
1	D	55	MLY	N-CA-CB-CG
1	D	55	MLY	C-CA-CB-CG
1	D	84	MLY	C-CA-CB-CG
1	D	130	MLY	C-CA-CB-CG
1	D	248	MLY	N-CA-CB-CG
1	D	248	MLY	C-CA-CB-CG
1	D	436	MLY	C-CA-CB-CG
1	D	486	MLY	C-CA-CB-CG
1	D	505	MLY	N-CA-CB-CG
1	D	505	MLY	C-CA-CB-CG
1	D	528	MLY	C-CA-CB-CG
1	D	551	MLY	C-CA-CB-CG
1	D	553	MLY	C-CA-CB-CG
1	D	598	MLY	N-CA-CB-CG
1	D	598	MLY	C-CA-CB-CG
1	D	613	MLY	N-CA-CB-CG

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Mol	Chain	Res	Type	Atoms
1	D	613	MLY	C-CA-CB-CG
1	D	681	MLY	C-CA-CB-CG
1	D	782	MLY	C-CA-CB-CG
1	D	782	MLY	O-C-CA-CB
1	G	19	MLY	C-CA-CB-CG
1	G	49	MLY	N-CA-CB-CG
1	G	49	MLY	C-CA-CB-CG
1	G	55	MLY	N-CA-CB-CG
1	G	55	MLY	C-CA-CB-CG
1	G	84	MLY	C-CA-CB-CG
1	G	130	MLY	C-CA-CB-CG
1	G	248	MLY	N-CA-CB-CG
1	G	248	MLY	C-CA-CB-CG
1	G	348	MLY	N-CA-CB-CG
1	G	436	MLY	C-CA-CB-CG
1	G	486	MLY	C-CA-CB-CG
1	G	505	MLY	N-CA-CB-CG
1	G	505	MLY	C-CA-CB-CG
1	G	528	MLY	C-CA-CB-CG
1	G	551	MLY	C-CA-CB-CG
1	G	553	MLY	C-CA-CB-CG
1	G	598	MLY	N-CA-CB-CG
1	G	598	MLY	C-CA-CB-CG
1	G	613	MLY	N-CA-CB-CG
1	G	613	MLY	C-CA-CB-CG
1	G	681	MLY	C-CA-CB-CG
1	G	782	MLY	C-CA-CB-CG
1	G	782	MLY	O-C-CA-CB
1	J	19	MLY	C-CA-CB-CG
1	J	49	MLY	N-CA-CB-CG
1	J	49	MLY	C-CA-CB-CG
1	J	55	MLY	N-CA-CB-CG
1	J	55	MLY	C-CA-CB-CG
1	J	84	MLY	C-CA-CB-CG
1	J	130	MLY	C-CA-CB-CG
1	J	248	MLY	N-CA-CB-CG
1	J	248	MLY	C-CA-CB-CG
1	J	348	MLY	N-CA-CB-CG
1	J	436	MLY	C-CA-CB-CG
1	J	486	MLY	C-CA-CB-CG
1	J	505	MLY	N-CA-CB-CG
1	J	505	MLY	C-CA-CB-CG

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Mol	Chain	Res	Type	Atoms
1	J	528	MLY	C-CA-CB-CG
1	J	551	MLY	C-CA-CB-CG
1	J	553	MLY	C-CA-CB-CG
1	J	598	MLY	N-CA-CB-CG
1	J	598	MLY	C-CA-CB-CG
1	J	613	MLY	N-CA-CB-CG
1	J	613	MLY	C-CA-CB-CG
1	J	681	MLY	C-CA-CB-CG
1	J	782	MLY	C-CA-CB-CG
1	J	782	MLY	O-C-CA-CB
1	A	84	MLY	CD-CE-NZ-CH1
1	D	84	MLY	CD-CE-NZ-CH1
1	G	84	MLY	CD-CE-NZ-CH1
1	J	84	MLY	CD-CE-NZ-CH1
1	A	59	MLY	CD-CE-NZ-CH1
1	A	59	MLY	CD-CE-NZ-CH2
1	A	63	MLY	CD-CE-NZ-CH1
1	A	84	MLY	CD-CE-NZ-CH2
1	A	130	MLY	CD-CE-NZ-CH1
1	A	130	MLY	CD-CE-NZ-CH2
1	A	138	MLY	CD-CE-NZ-CH1
1	A	138	MLY	CD-CE-NZ-CH2
1	A	190	MLY	CD-CE-NZ-CH1
1	A	190	MLY	CD-CE-NZ-CH2
1	A	248	MLY	CD-CE-NZ-CH1
1	A	272	MLY	CD-CE-NZ-CH1
1	A	296	MLY	CD-CE-NZ-CH1
1	A	296	MLY	CD-CE-NZ-CH2
1	A	353	MLY	CD-CE-NZ-CH1
1	A	353	MLY	CD-CE-NZ-CH2
1	A	367	MLY	CD-CE-NZ-CH2
1	A	385	MLY	CD-CE-NZ-CH1
1	A	385	MLY	CD-CE-NZ-CH2
1	A	431	MLY	CD-CE-NZ-CH2
1	A	504	MLY	CD-CE-NZ-CH2
1	A	505	MLY	CD-CE-NZ-CH2
1	A	528	MLY	CD-CE-NZ-CH1
1	A	528	MLY	CD-CE-NZ-CH2
1	A	553	MLY	CD-CE-NZ-CH2
1	A	600	MLY	CD-CE-NZ-CH2
1	A	764	MLY	CD-CE-NZ-CH1
1	A	764	MLY	CD-CE-NZ-CH2

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Mol	Chain	Res	Type	Atoms
1	A	768	MLY	CD-CE-NZ-CH1
1	A	782	MLY	CD-CE-NZ-CH1
1	A	782	MLY	CD-CE-NZ-CH2
1	A	833	MLY	CD-CE-NZ-CH1
1	A	833	MLY	CD-CE-NZ-CH2
1	A	837	MLY	CD-CE-NZ-CH1
1	A	837	MLY	CD-CE-NZ-CH2
1	A	839	MLY	CD-CE-NZ-CH2
1	D	55	MLY	CD-CE-NZ-CH2
1	D	59	MLY	CD-CE-NZ-CH1
1	D	59	MLY	CD-CE-NZ-CH2
1	D	63	MLY	CD-CE-NZ-CH1
1	D	84	MLY	CD-CE-NZ-CH2
1	D	130	MLY	CD-CE-NZ-CH1
1	D	130	MLY	CD-CE-NZ-CH2
1	D	138	MLY	CD-CE-NZ-CH1
1	D	138	MLY	CD-CE-NZ-CH2
1	D	190	MLY	CD-CE-NZ-CH2
1	D	248	MLY	CD-CE-NZ-CH1
1	D	272	MLY	CD-CE-NZ-CH1
1	D	296	MLY	CD-CE-NZ-CH1
1	D	296	MLY	CD-CE-NZ-CH2
1	D	353	MLY	CD-CE-NZ-CH1
1	D	353	MLY	CD-CE-NZ-CH2
1	D	367	MLY	CD-CE-NZ-CH2
1	D	385	MLY	CD-CE-NZ-CH1
1	D	385	MLY	CD-CE-NZ-CH2
1	D	431	MLY	CD-CE-NZ-CH2
1	D	505	MLY	CD-CE-NZ-CH2
1	D	528	MLY	CD-CE-NZ-CH1
1	D	528	MLY	CD-CE-NZ-CH2
1	D	553	MLY	CD-CE-NZ-CH2
1	D	600	MLY	CD-CE-NZ-CH2
1	D	764	MLY	CD-CE-NZ-CH1
1	D	764	MLY	CD-CE-NZ-CH2
1	D	768	MLY	CD-CE-NZ-CH1
1	D	782	MLY	CD-CE-NZ-CH1
1	D	782	MLY	CD-CE-NZ-CH2
1	D	833	MLY	CD-CE-NZ-CH1
1	D	833	MLY	CD-CE-NZ-CH2
1	D	837	MLY	CD-CE-NZ-CH1
1	D	837	MLY	CD-CE-NZ-CH2

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Mol	Chain	Res	Type	Atoms
1	D	839	MLY	CD-CE-NZ-CH2
1	G	59	MLY	CD-CE-NZ-CH1
1	G	59	MLY	CD-CE-NZ-CH2
1	G	63	MLY	CD-CE-NZ-CH1
1	G	84	MLY	CD-CE-NZ-CH2
1	G	130	MLY	CD-CE-NZ-CH1
1	G	130	MLY	CD-CE-NZ-CH2
1	G	138	MLY	CD-CE-NZ-CH1
1	G	138	MLY	CD-CE-NZ-CH2
1	G	190	MLY	CD-CE-NZ-CH2
1	G	248	MLY	CD-CE-NZ-CH1
1	G	272	MLY	CD-CE-NZ-CH1
1	G	296	MLY	CD-CE-NZ-CH1
1	G	296	MLY	CD-CE-NZ-CH2
1	G	353	MLY	CD-CE-NZ-CH1
1	G	353	MLY	CD-CE-NZ-CH2
1	G	385	MLY	CD-CE-NZ-CH1
1	G	385	MLY	CD-CE-NZ-CH2
1	G	431	MLY	CD-CE-NZ-CH2
1	G	505	MLY	CD-CE-NZ-CH2
1	G	528	MLY	CD-CE-NZ-CH1
1	G	528	MLY	CD-CE-NZ-CH2
1	G	553	MLY	CD-CE-NZ-CH2
1	G	600	MLY	CD-CE-NZ-CH2
1	G	764	MLY	CD-CE-NZ-CH1
1	G	764	MLY	CD-CE-NZ-CH2
1	G	768	MLY	CD-CE-NZ-CH1
1	G	782	MLY	CD-CE-NZ-CH1
1	G	782	MLY	CD-CE-NZ-CH2
1	G	833	MLY	CD-CE-NZ-CH1
1	G	833	MLY	CD-CE-NZ-CH2
1	G	837	MLY	CD-CE-NZ-CH1
1	G	837	MLY	CD-CE-NZ-CH2
1	G	839	MLY	CD-CE-NZ-CH2
1	J	59	MLY	CD-CE-NZ-CH1
1	J	59	MLY	CD-CE-NZ-CH2
1	J	63	MLY	CD-CE-NZ-CH1
1	J	84	MLY	CD-CE-NZ-CH2
1	J	130	MLY	CD-CE-NZ-CH1
1	J	130	MLY	CD-CE-NZ-CH2
1	J	138	MLY	CD-CE-NZ-CH1
1	J	138	MLY	CD-CE-NZ-CH2

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Mol	Chain	Res	Type	Atoms
1	J	190	MLY	CD-CE-NZ-CH2
1	J	248	MLY	CD-CE-NZ-CH1
1	J	272	MLY	CD-CE-NZ-CH1
1	J	296	MLY	CD-CE-NZ-CH1
1	J	296	MLY	CD-CE-NZ-CH2
1	J	353	MLY	CD-CE-NZ-CH1
1	J	353	MLY	CD-CE-NZ-CH2
1	J	367	MLY	CD-CE-NZ-CH2
1	J	385	MLY	CD-CE-NZ-CH1
1	J	385	MLY	CD-CE-NZ-CH2
1	J	431	MLY	CD-CE-NZ-CH2
1	J	505	MLY	CD-CE-NZ-CH2
1	J	528	MLY	CD-CE-NZ-CH1
1	J	528	MLY	CD-CE-NZ-CH2
1	J	553	MLY	CD-CE-NZ-CH2
1	J	600	MLY	CD-CE-NZ-CH2
1	J	764	MLY	CD-CE-NZ-CH1
1	J	764	MLY	CD-CE-NZ-CH2
1	J	768	MLY	CD-CE-NZ-CH1
1	J	782	MLY	CD-CE-NZ-CH1
1	J	782	MLY	CD-CE-NZ-CH2
1	J	833	MLY	CD-CE-NZ-CH1
1	J	833	MLY	CD-CE-NZ-CH2
1	J	837	MLY	CD-CE-NZ-CH1
1	J	837	MLY	CD-CE-NZ-CH2
1	J	839	MLY	CD-CE-NZ-CH2
1	A	659	MLY	CG-CD-CE-NZ
1	D	659	MLY	CG-CD-CE-NZ
1	G	659	MLY	CG-CD-CE-NZ
1	J	659	MLY	CG-CD-CE-NZ
1	A	87	MLY	CG-CD-CE-NZ
1	G	87	MLY	CG-CD-CE-NZ
1	J	87	MLY	CG-CD-CE-NZ
1	A	35	MLY	CG-CD-CE-NZ
1	D	35	MLY	CG-CD-CE-NZ
1	D	87	MLY	CG-CD-CE-NZ
1	G	35	MLY	CG-CD-CE-NZ
1	J	35	MLY	CG-CD-CE-NZ
1	A	295	MLY	CG-CD-CE-NZ
1	D	295	MLY	CG-CD-CE-NZ
1	G	295	MLY	CG-CD-CE-NZ
1	J	295	MLY	CG-CD-CE-NZ

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>Atoms</b>
1	A	138	MLY	CG-CD-CE-NZ
1	A	782	MLY	CG-CD-CE-NZ
1	D	782	MLY	CG-CD-CE-NZ
1	G	782	MLY	CG-CD-CE-NZ
1	J	782	MLY	CG-CD-CE-NZ
1	D	138	MLY	CG-CD-CE-NZ
1	J	138	MLY	CG-CD-CE-NZ
1	G	138	MLY	CG-CD-CE-NZ
1	A	55	MLY	CD-CE-NZ-CH2
1	A	248	MLY	CD-CE-NZ-CH2
1	A	272	MLY	CD-CE-NZ-CH2
1	A	348	MLY	CD-CE-NZ-CH1
1	A	348	MLY	CD-CE-NZ-CH2
1	A	367	MLY	CD-CE-NZ-CH1
1	A	431	MLY	CD-CE-NZ-CH1
1	A	504	MLY	CD-CE-NZ-CH1
1	A	505	MLY	CD-CE-NZ-CH1
1	A	600	MLY	CD-CE-NZ-CH1
1	A	659	MLY	CD-CE-NZ-CH2
1	D	190	MLY	CD-CE-NZ-CH1
1	D	248	MLY	CD-CE-NZ-CH2
1	D	272	MLY	CD-CE-NZ-CH2
1	D	348	MLY	CD-CE-NZ-CH1
1	D	348	MLY	CD-CE-NZ-CH2
1	D	367	MLY	CD-CE-NZ-CH1
1	D	431	MLY	CD-CE-NZ-CH1
1	D	504	MLY	CD-CE-NZ-CH1
1	D	504	MLY	CD-CE-NZ-CH2
1	D	505	MLY	CD-CE-NZ-CH1
1	D	600	MLY	CD-CE-NZ-CH1
1	D	659	MLY	CD-CE-NZ-CH2
1	G	55	MLY	CD-CE-NZ-CH2
1	G	190	MLY	CD-CE-NZ-CH1
1	G	248	MLY	CD-CE-NZ-CH2
1	G	272	MLY	CD-CE-NZ-CH2
1	G	348	MLY	CD-CE-NZ-CH1
1	G	348	MLY	CD-CE-NZ-CH2
1	G	367	MLY	CD-CE-NZ-CH1
1	G	367	MLY	CD-CE-NZ-CH2
1	G	431	MLY	CD-CE-NZ-CH1
1	G	504	MLY	CD-CE-NZ-CH1
1	G	504	MLY	CD-CE-NZ-CH2

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Mol	Chain	Res	Type	Atoms
1	G	505	MLY	CD-CE-NZ-CH1
1	G	600	MLY	CD-CE-NZ-CH1
1	G	659	MLY	CD-CE-NZ-CH2
1	J	55	MLY	CD-CE-NZ-CH2
1	J	190	MLY	CD-CE-NZ-CH1
1	J	248	MLY	CD-CE-NZ-CH2
1	J	348	MLY	CD-CE-NZ-CH1
1	J	348	MLY	CD-CE-NZ-CH2
1	J	367	MLY	CD-CE-NZ-CH1
1	J	431	MLY	CD-CE-NZ-CH1
1	J	504	MLY	CD-CE-NZ-CH1
1	J	504	MLY	CD-CE-NZ-CH2
1	J	505	MLY	CD-CE-NZ-CH1
1	J	600	MLY	CD-CE-NZ-CH1
1	J	659	MLY	CD-CE-NZ-CH2
1	A	84	MLY	CG-CD-CE-NZ
1	A	130	MLY	CG-CD-CE-NZ
1	D	130	MLY	CG-CD-CE-NZ
1	G	84	MLY	CG-CD-CE-NZ
1	G	130	MLY	CG-CD-CE-NZ
1	J	84	MLY	CG-CD-CE-NZ
1	J	130	MLY	CG-CD-CE-NZ
1	G	504	MLY	CG-CD-CE-NZ
1	A	504	MLY	CG-CD-CE-NZ
1	A	681	MLY	CG-CD-CE-NZ
1	D	84	MLY	CG-CD-CE-NZ
1	D	681	MLY	CG-CD-CE-NZ
1	G	681	MLY	CG-CD-CE-NZ
1	J	504	MLY	CG-CD-CE-NZ
1	A	295	MLY	CA-CB-CG-CD
1	D	295	MLY	CA-CB-CG-CD
1	G	295	MLY	CA-CB-CG-CD
1	J	295	MLY	CA-CB-CG-CD
1	D	504	MLY	CG-CD-CE-NZ
1	J	681	MLY	CG-CD-CE-NZ
1	A	107	MLY	CD-CE-NZ-CH1
1	A	369	MLY	CD-CE-NZ-CH2
1	A	768	MLY	CD-CE-NZ-CH2
1	D	87	MLY	CD-CE-NZ-CH1
1	D	107	MLY	CD-CE-NZ-CH1
1	D	369	MLY	CD-CE-NZ-CH2
1	D	768	MLY	CD-CE-NZ-CH2

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Mol	Chain	Res	Type	Atoms
1	G	63	MLY	CD-CE-NZ-CH2
1	G	107	MLY	CD-CE-NZ-CH1
1	G	369	MLY	CD-CE-NZ-CH2
1	G	768	MLY	CD-CE-NZ-CH2
1	J	107	MLY	CD-CE-NZ-CH1
1	J	369	MLY	CD-CE-NZ-CH2
1	J	768	MLY	CD-CE-NZ-CH2
1	A	598	MLY	CG-CD-CE-NZ
1	G	598	MLY	CG-CD-CE-NZ
1	J	598	MLY	CG-CD-CE-NZ
1	D	598	MLY	CG-CD-CE-NZ
1	A	504	MLY	CA-CB-CG-CD
1	A	768	MLY	CA-CB-CG-CD
1	D	504	MLY	CA-CB-CG-CD
1	D	768	MLY	CA-CB-CG-CD
1	G	504	MLY	CA-CB-CG-CD
1	G	768	MLY	CA-CB-CG-CD
1	J	504	MLY	CA-CB-CG-CD
1	J	768	MLY	CA-CB-CG-CD
1	A	63	MLY	CD-CE-NZ-CH2
1	A	415	MLY	CD-CE-NZ-CH1
1	A	415	MLY	CD-CE-NZ-CH2
1	A	553	MLY	CD-CE-NZ-CH1
1	A	659	MLY	CD-CE-NZ-CH1
1	D	55	MLY	CD-CE-NZ-CH1
1	D	63	MLY	CD-CE-NZ-CH2
1	D	415	MLY	CD-CE-NZ-CH1
1	D	415	MLY	CD-CE-NZ-CH2
1	D	553	MLY	CD-CE-NZ-CH1
1	D	659	MLY	CD-CE-NZ-CH1
1	G	415	MLY	CD-CE-NZ-CH1
1	G	415	MLY	CD-CE-NZ-CH2
1	G	553	MLY	CD-CE-NZ-CH1
1	J	55	MLY	CD-CE-NZ-CH1
1	J	63	MLY	CD-CE-NZ-CH2
1	J	87	MLY	CD-CE-NZ-CH1
1	J	272	MLY	CD-CE-NZ-CH2
1	J	415	MLY	CD-CE-NZ-CH1
1	J	415	MLY	CD-CE-NZ-CH2
1	J	553	MLY	CD-CE-NZ-CH1
1	J	659	MLY	CD-CE-NZ-CH1
1	A	415	MLY	CA-CB-CG-CD

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Mol	Chain	Res	Type	Atoms
1	G	415	MLY	CA-CB-CG-CD
1	A	19	MLY	CD-CE-NZ-CH2
1	A	55	MLY	CD-CE-NZ-CH1
1	A	87	MLY	CD-CE-NZ-CH1
1	D	19	MLY	CD-CE-NZ-CH2
1	G	19	MLY	CD-CE-NZ-CH2
1	G	55	MLY	CD-CE-NZ-CH1
1	G	87	MLY	CD-CE-NZ-CH1
1	G	659	MLY	CD-CE-NZ-CH1
1	J	19	MLY	CD-CE-NZ-CH2
1	D	551	MLY	CG-CD-CE-NZ
1	G	551	MLY	CG-CD-CE-NZ
1	J	551	MLY	CG-CD-CE-NZ
1	A	551	MLY	CG-CD-CE-NZ
1	D	415	MLY	CA-CB-CG-CD
1	J	415	MLY	CA-CB-CG-CD
1	A	272	MLY	CE-CD-CG-CB
1	D	272	MLY	CE-CD-CG-CB
1	J	272	MLY	CE-CD-CG-CB
1	G	272	MLY	CE-CD-CG-CB
1	A	30	MLY	CE-CD-CG-CB
1	A	296	MLY	CE-CD-CG-CB
1	D	30	MLY	CE-CD-CG-CB
1	D	296	MLY	CE-CD-CG-CB
1	G	30	MLY	CE-CD-CG-CB
1	G	296	MLY	CE-CD-CG-CB
1	J	296	MLY	CE-CD-CG-CB
1	A	505	MLY	CE-CD-CG-CB
1	D	505	MLY	CE-CD-CG-CB
1	G	505	MLY	CE-CD-CG-CB
1	J	30	MLY	CE-CD-CG-CB
1	J	505	MLY	CE-CD-CG-CB
1	A	107	MLY	CD-CE-NZ-CH2
1	A	839	MLY	CD-CE-NZ-CH1
1	D	839	MLY	CD-CE-NZ-CH1
1	G	839	MLY	CD-CE-NZ-CH1
1	J	107	MLY	CD-CE-NZ-CH2
1	J	839	MLY	CD-CE-NZ-CH1
1	D	681	MLY	CE-CD-CG-CB
1	G	681	MLY	CE-CD-CG-CB
1	J	681	MLY	CE-CD-CG-CB
1	A	681	MLY	CE-CD-CG-CB

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Mol	Chain	Res	Type	Atoms
1	D	49	MLY	CE-CD-CG-CB
1	G	49	MLY	CE-CD-CG-CB
1	J	49	MLY	CE-CD-CG-CB
1	A	49	MLY	CE-CD-CG-CB
1	D	353	MLY	CE-CD-CG-CB
1	D	768	MLY	CE-CD-CG-CB
1	J	353	MLY	CE-CD-CG-CB
1	A	353	MLY	CE-CD-CG-CB
1	G	353	MLY	CE-CD-CG-CB
1	A	190	MLY	CE-CD-CG-CB
1	A	768	MLY	CE-CD-CG-CB
1	D	190	MLY	CE-CD-CG-CB
1	G	768	MLY	CE-CD-CG-CB
1	J	190	MLY	CE-CD-CG-CB
1	J	768	MLY	CE-CD-CG-CB
1	G	190	MLY	CE-CD-CG-CB
1	A	782	MLY	CE-CD-CG-CB
1	D	782	MLY	CE-CD-CG-CB
1	A	369	MLY	CE-CD-CG-CB
1	D	369	MLY	CE-CD-CG-CB
1	G	369	MLY	CE-CD-CG-CB
1	G	782	MLY	CE-CD-CG-CB
1	J	369	MLY	CE-CD-CG-CB
1	J	782	MLY	CE-CD-CG-CB
1	A	236	MLY	CD-CE-NZ-CH1
1	D	107	MLY	CD-CE-NZ-CH2
1	D	236	MLY	CD-CE-NZ-CH1
1	G	107	MLY	CD-CE-NZ-CH2
1	G	236	MLY	CD-CE-NZ-CH1
1	J	236	MLY	CD-CE-NZ-CH1
1	D	190	MLY	CG-CD-CE-NZ
1	A	436	MLY	CA-CB-CG-CD
1	A	837	MLY	CA-CB-CG-CD
1	D	436	MLY	CA-CB-CG-CD
1	D	837	MLY	CA-CB-CG-CD
1	G	436	MLY	CA-CB-CG-CD
1	G	837	MLY	CA-CB-CG-CD
1	J	436	MLY	CA-CB-CG-CD
1	J	837	MLY	CA-CB-CG-CD
1	G	190	MLY	CG-CD-CE-NZ
1	J	190	MLY	CG-CD-CE-NZ
1	A	190	MLY	CG-CD-CE-NZ

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Mol	Chain	Res	Type	Atoms
1	D	833	MLY	CE-CD-CG-CB
1	A	833	MLY	CE-CD-CG-CB
1	G	833	MLY	CE-CD-CG-CB
1	J	833	MLY	CE-CD-CG-CB
1	A	431	MLY	CA-CB-CG-CD
1	D	236	MLY	CA-CB-CG-CD
1	D	431	MLY	CA-CB-CG-CD
1	G	431	MLY	CA-CB-CG-CD
1	J	236	MLY	CA-CB-CG-CD
1	J	431	MLY	CA-CB-CG-CD
1	A	55	MLY	CG-CD-CE-NZ
1	G	55	MLY	CG-CD-CE-NZ
1	D	55	MLY	CG-CD-CE-NZ
1	D	551	MLY	CE-CD-CG-CB
1	J	55	MLY	CG-CD-CE-NZ
1	J	617	MLY	CE-CD-CG-CB
1	A	617	MLY	CE-CD-CG-CB
1	D	617	MLY	CE-CD-CG-CB
1	G	617	MLY	CE-CD-CG-CB
1	A	236	MLY	CA-CB-CG-CD
1	A	833	MLY	CA-CB-CG-CD
1	D	833	MLY	CA-CB-CG-CD
1	G	236	MLY	CA-CB-CG-CD
1	G	833	MLY	CA-CB-CG-CD
1	J	833	MLY	CA-CB-CG-CD
1	A	348	MLY	C-CA-CB-CG
1	D	348	MLY	C-CA-CB-CG
1	G	348	MLY	C-CA-CB-CG
1	J	348	MLY	C-CA-CB-CG
1	A	551	MLY	CE-CD-CG-CB
1	J	551	MLY	CE-CD-CG-CB
1	G	551	MLY	CE-CD-CG-CB
1	G	59	MLY	CE-CD-CG-CB
1	J	59	MLY	CE-CD-CG-CB
1	A	55	MLY	CE-CD-CG-CB
1	A	59	MLY	CE-CD-CG-CB
1	D	55	MLY	CE-CD-CG-CB
1	D	59	MLY	CE-CD-CG-CB
1	D	553	MLY	CE-CD-CG-CB
1	G	55	MLY	CE-CD-CG-CB
1	G	553	MLY	CE-CD-CG-CB
1	J	55	MLY	CE-CD-CG-CB

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Mol	Chain	Res	Type	Atoms
1	J	553	MLY	CE-CD-CG-CB
1	A	553	MLY	CE-CD-CG-CB
1	J	431	MLY	CE-CD-CG-CB
1	A	431	MLY	CE-CD-CG-CB
1	G	248	MLY	CE-CD-CG-CB
1	A	248	MLY	CE-CD-CG-CB
1	D	248	MLY	CE-CD-CG-CB
1	J	248	MLY	CE-CD-CG-CB
1	D	431	MLY	CE-CD-CG-CB
1	G	431	MLY	CE-CD-CG-CB
1	D	35	MLY	CE-CD-CG-CB
1	A	35	MLY	CE-CD-CG-CB
1	G	35	MLY	CE-CD-CG-CB
1	J	35	MLY	CE-CD-CG-CB
1	D	528	MLY	CG-CD-CE-NZ
1	G	528	MLY	CG-CD-CE-NZ
1	A	528	MLY	CG-CD-CE-NZ
1	J	528	MLY	CG-CD-CE-NZ
1	G	248	MLY	CG-CD-CE-NZ
1	A	138	MLY	CA-CB-CG-CD
1	A	296	MLY	CA-CB-CG-CD
1	D	138	MLY	CA-CB-CG-CD
1	G	138	MLY	CA-CB-CG-CD
1	J	138	MLY	CA-CB-CG-CD
1	J	296	MLY	CA-CB-CG-CD
1	A	248	MLY	CG-CD-CE-NZ
1	J	248	MLY	CG-CD-CE-NZ
1	D	248	MLY	CG-CD-CE-NZ
1	D	296	MLY	CA-CB-CG-CD
1	G	296	MLY	CA-CB-CG-CD
1	A	436	MLY	CE-CD-CG-CB
1	A	598	MLY	CE-CD-CG-CB
1	A	600	MLY	CE-CD-CG-CB
1	D	436	MLY	CE-CD-CG-CB
1	D	598	MLY	CE-CD-CG-CB
1	D	600	MLY	CE-CD-CG-CB
1	G	436	MLY	CE-CD-CG-CB
1	G	598	MLY	CE-CD-CG-CB
1	G	600	MLY	CE-CD-CG-CB
1	J	436	MLY	CE-CD-CG-CB
1	J	598	MLY	CE-CD-CG-CB
1	J	600	MLY	CE-CD-CG-CB

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Mol	Chain	Res	Type	Atoms
1	A	486	MLY	CE-CD-CG-CB
1	G	486	MLY	CE-CD-CG-CB
1	J	486	MLY	CE-CD-CG-CB
1	D	486	MLY	CE-CD-CG-CB
1	G	839	MLY	CE-CD-CG-CB
1	J	839	MLY	CE-CD-CG-CB
1	D	839	MLY	CE-CD-CG-CB
1	A	839	MLY	CE-CD-CG-CB
1	A	236	MLY	CD-CE-NZ-CH2
1	D	236	MLY	CD-CE-NZ-CH2
1	G	236	MLY	CD-CE-NZ-CH2
1	J	236	MLY	CD-CE-NZ-CH2
1	A	35	MLY	N-CA-CB-CG
1	A	63	MLY	N-CA-CB-CG
1	A	130	MLY	N-CA-CB-CG
1	A	436	MLY	N-CA-CB-CG
1	A	681	MLY	N-CA-CB-CG
1	A	833	MLY	N-CA-CB-CG
1	A	837	MLY	N-CA-CB-CG
1	D	35	MLY	N-CA-CB-CG
1	D	63	MLY	N-CA-CB-CG
1	D	130	MLY	N-CA-CB-CG
1	D	348	MLY	N-CA-CB-CG
1	D	436	MLY	N-CA-CB-CG
1	D	681	MLY	N-CA-CB-CG
1	D	833	MLY	N-CA-CB-CG
1	D	837	MLY	N-CA-CB-CG
1	G	35	MLY	N-CA-CB-CG
1	G	63	MLY	N-CA-CB-CG
1	G	130	MLY	N-CA-CB-CG
1	G	436	MLY	N-CA-CB-CG
1	G	681	MLY	N-CA-CB-CG
1	G	833	MLY	N-CA-CB-CG
1	G	837	MLY	N-CA-CB-CG
1	J	35	MLY	N-CA-CB-CG
1	J	63	MLY	N-CA-CB-CG
1	J	130	MLY	N-CA-CB-CG
1	J	436	MLY	N-CA-CB-CG
1	J	681	MLY	N-CA-CB-CG
1	J	833	MLY	N-CA-CB-CG
1	J	837	MLY	N-CA-CB-CG
1	D	833	MLY	C-CA-CB-CG

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Mol	Chain	Res	Type	Atoms
1	J	833	MLY	C-CA-CB-CG
1	A	19	MLY	CA-CB-CG-CD
1	D	19	MLY	CA-CB-CG-CD
1	G	19	MLY	CA-CB-CG-CD
1	J	19	MLY	CA-CB-CG-CD
1	D	837	MLY	CE-CD-CG-CB
1	G	837	MLY	CE-CD-CG-CB
1	A	19	MLY	CE-CD-CG-CB
1	A	837	MLY	CE-CD-CG-CB
1	J	837	MLY	CE-CD-CG-CB
1	D	19	MLY	CE-CD-CG-CB
1	J	19	MLY	CE-CD-CG-CB
1	G	19	MLY	CE-CD-CG-CB
1	G	613	MLY	CE-CD-CG-CB
1	J	613	MLY	CE-CD-CG-CB
1	A	613	MLY	CE-CD-CG-CB
1	D	613	MLY	CE-CD-CG-CB
1	A	598	MLY	CD-CE-NZ-CH2
1	D	598	MLY	CD-CE-NZ-CH2
1	G	598	MLY	CD-CE-NZ-CH2
1	J	598	MLY	CD-CE-NZ-CH2
1	A	63	MLY	C-CA-CB-CG
1	A	353	MLY	C-CA-CB-CG
1	A	833	MLY	C-CA-CB-CG
1	D	63	MLY	C-CA-CB-CG
1	D	353	MLY	C-CA-CB-CG
1	G	63	MLY	C-CA-CB-CG
1	G	353	MLY	C-CA-CB-CG
1	G	833	MLY	C-CA-CB-CG
1	J	63	MLY	C-CA-CB-CG
1	J	353	MLY	C-CA-CB-CG
1	A	30	MLY	CA-CB-CG-CD
1	D	30	MLY	CA-CB-CG-CD
1	G	30	MLY	CA-CB-CG-CD
1	J	30	MLY	CA-CB-CG-CD
1	J	348	MLY	CE-CD-CG-CB
1	A	348	MLY	CE-CD-CG-CB
1	D	348	MLY	CE-CD-CG-CB
1	G	348	MLY	CE-CD-CG-CB
1	A	613	MLY	CA-CB-CG-CD
1	J	613	MLY	CA-CB-CG-CD
1	D	613	MLY	CA-CB-CG-CD

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Mol	Chain	Res	Type	Atoms
1	G	613	MLY	CA-CB-CG-CD
1	A	190	MLY	CA-CB-CG-CD
1	A	528	MLY	CA-CB-CG-CD
1	D	190	MLY	CA-CB-CG-CD
1	G	190	MLY	CA-CB-CG-CD
1	J	190	MLY	CA-CB-CG-CD

There are no ring outliers.

124 monomers are involved in 525 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	436	MLY	2	0
1	D	248	MLY	2	0
1	A	505	MLY	11	0
1	J	55	MLY	1	0
1	G	839	MLY	4	0
1	J	436	MLY	2	0
1	D	659	MLY	2	0
1	G	659	MLY	2	0
1	J	87	MLY	3	0
1	J	839	MLY	5	0
1	A	138	MLY	1	0
1	J	617	MLY	1	0
1	D	138	MLY	1	0
1	A	764	MLY	7	0
1	J	768	MLY	41	0
1	G	138	MLY	1	0
1	D	272	MLY	1	0
1	J	63	MLY	4	0
1	J	551	MLY	1	0
1	A	415	MLY	1	0
1	A	30	MLY	1	0
1	G	30	MLY	1	0
1	G	827	MLY	1	0
1	A	190	MLY	2	0
1	D	764	MLY	2	0
1	G	551	MLY	2	0
1	D	63	MLY	3	0
1	A	369	MLY	1	0
1	A	87	MLY	3	0
1	J	296	MLY	3	0
1	G	768	MLY	15	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	G	107	MLY	3	0
1	G	248	MLY	2	0
1	G	837	MLY	1	0
1	G	84	MLY	18	0
1	A	295	MLY	6	0
1	G	190	MLY	2	0
1	A	617	MLY	1	0
1	J	486	MLY	3	0
1	D	551	MLY	1	0
1	J	49	MLY	2	0
1	A	59	MLY	2	0
1	A	659	MLY	2	0
1	G	63	MLY	3	0
1	J	248	MLY	2	0
1	J	84	MLY	25	0
1	G	553	MLY	16	0
1	D	295	MLY	6	0
1	G	59	MLY	3	0
1	D	190	MLY	2	0
1	J	295	MLY	6	0
1	D	768	MLY	6	0
1	A	486	MLY	3	0
1	A	528	MLY	2	0
1	A	348	MLY	5	0
1	A	600	MLY	1	0
1	A	837	MLY	1	0
1	A	782	MLY	1	0
1	D	598	MLY	1	0
1	J	272	MLY	1	0
1	J	598	MLY	1	0
1	A	55	MLY	1	0
1	G	600	MLY	1	0
1	G	369	MLY	1	0
1	D	528	MLY	3	0
1	D	436	MLY	2	0
1	D	30	MLY	1	0
1	D	59	MLY	2	0
1	D	55	MLY	1	0
1	A	839	MLY	15	0
1	A	107	MLY	3	0
1	J	837	MLY	1	0
1	A	63	MLY	3	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	J	138	MLY	1	0
1	G	415	MLY	1	0
1	D	553	MLY	16	0
1	G	295	MLY	5	0
1	G	49	MLY	2	0
1	J	764	MLY	26	0
1	D	486	MLY	3	0
1	D	600	MLY	1	0
1	D	782	MLY	32	0
1	D	837	MLY	1	0
1	G	296	MLY	2	0
1	A	504	MLY	4	0
1	D	617	MLY	1	0
1	J	415	MLY	1	0
1	J	30	MLY	1	0
1	J	190	MLY	2	0
1	A	768	MLY	14	0
1	A	551	MLY	2	0
1	J	659	MLY	2	0
1	G	598	MLY	1	0
1	G	617	MLY	1	0
1	G	436	MLY	2	0
1	G	348	MLY	4	0
1	A	49	MLY	3	0
1	D	839	MLY	16	0
1	D	107	MLY	2	0
1	A	248	MLY	2	0
1	D	87	MLY	3	0
1	A	296	MLY	2	0
1	J	107	MLY	3	0
1	J	59	MLY	3	0
1	G	87	MLY	2	0
1	G	528	MLY	3	0
1	G	486	MLY	3	0
1	A	553	MLY	17	0
1	G	782	MLY	1	0
1	A	272	MLY	1	0
1	A	598	MLY	1	0
1	D	49	MLY	3	0
1	D	296	MLY	3	0
1	D	348	MLY	6	0
1	J	553	MLY	17	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	G	764	MLY	12	0
1	G	55	MLY	1	0
1	J	528	MLY	3	0
1	G	272	MLY	1	0
1	J	348	MLY	5	0
1	J	600	MLY	1	0
1	J	827	MLY	1	0
1	D	415	MLY	1	0
1	J	782	MLY	1	0

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	G	4
1	J	4
1	D	4
1	A	4
3	C	1
3	F	1
3	I	1
3	L	1
2	B	1
2	E	1
2	H	1
2	K	1



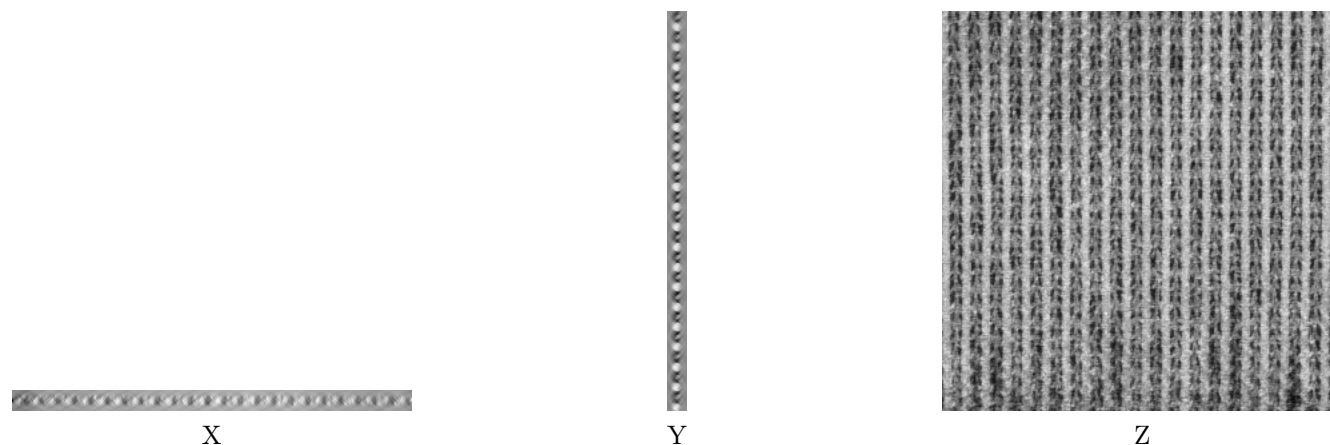
All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	G	769:ALA	C	770:GLY	N	4.89
1	J	769:ALA	C	770:GLY	N	4.67
1	D	769:ALA	C	770:GLY	N	4.54
1	D	709:LYS	C	710:GLY	N	3.32
1	A	709:LYS	C	710:GLY	N	3.28
1	A	769:ALA	C	770:GLY	N	2.79
1	C	4:LYS	C	5:ALA	N	2.61
1	F	4:LYS	C	5:ALA	N	2.61
1	I	4:LYS	C	5:ALA	N	2.61
1	L	4:LYS	C	5:ALA	N	2.61
1	G	709:LYS	C	710:GLY	N	2.16
1	B	140:PHE	C	141:PRO	N	1.09
1	E	140:PHE	C	141:PRO	N	1.09
1	H	140:PHE	C	141:PRO	N	1.09
1	K	140:PHE	C	141:PRO	N	1.09
1	A	637:LYS	C	638:GLY	N	1.06
1	G	637:LYS	C	638:GLY	N	1.06
1	J	637:LYS	C	638:GLY	N	1.06
1	D	637:LYS	C	638:GLY	N	1.05
1	A	649:VAL	C	650:SER	N	1.03
1	D	649:VAL	C	650:SER	N	1.03
1	G	649:VAL	C	650:SER	N	1.03
1	J	649:VAL	C	650:SER	N	1.03
1	J	709:LYS	C	710:GLY	N	0.33

## 6 Tomogram visualisation [i](#)

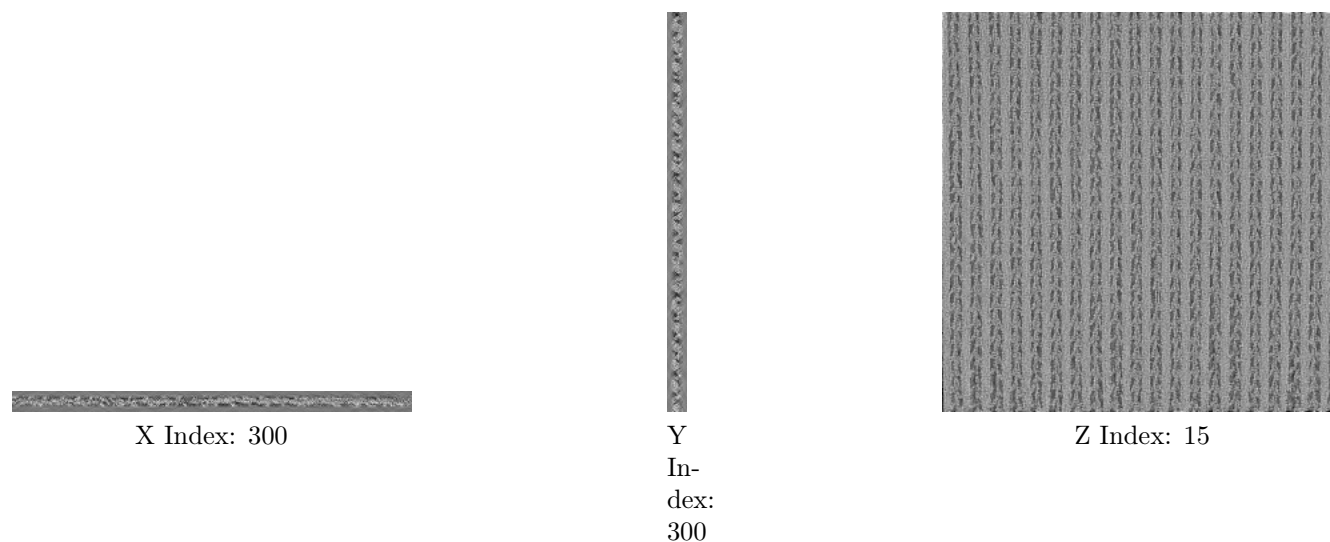
This section contains visualisations of the EMDB entry EMD-1001. These allow visual inspection of the internal detail of the tomogram and identification of artifacts.

### 6.1 Orthogonal projections [i](#)



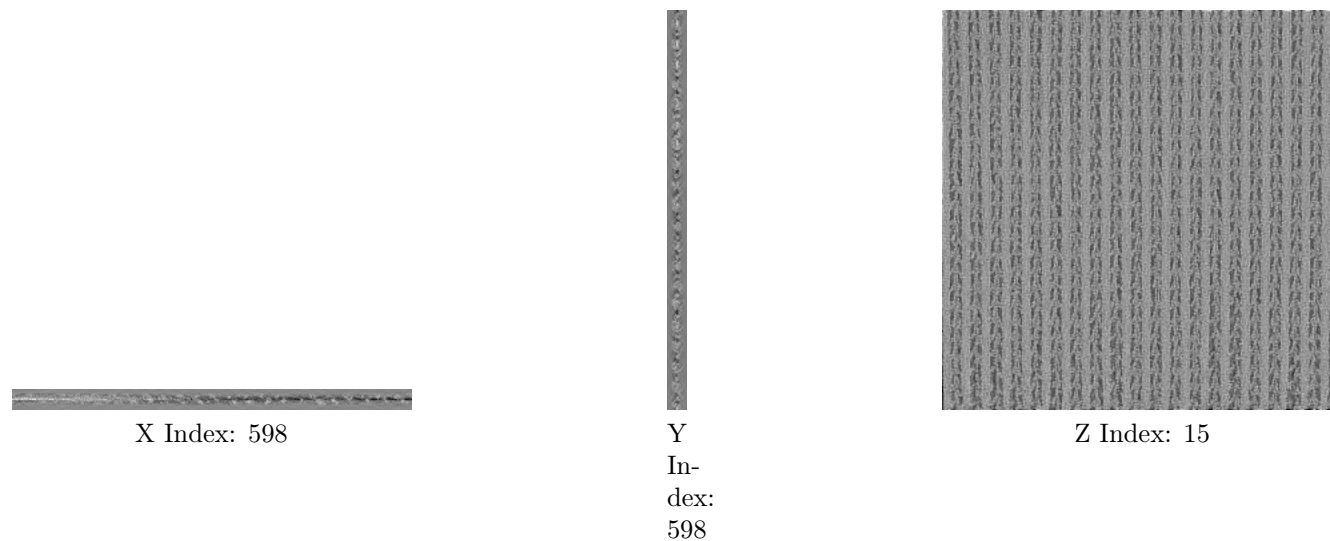
The images above show the tomogram projected in three orthogonal directions.

### 6.2 Central slices [i](#)



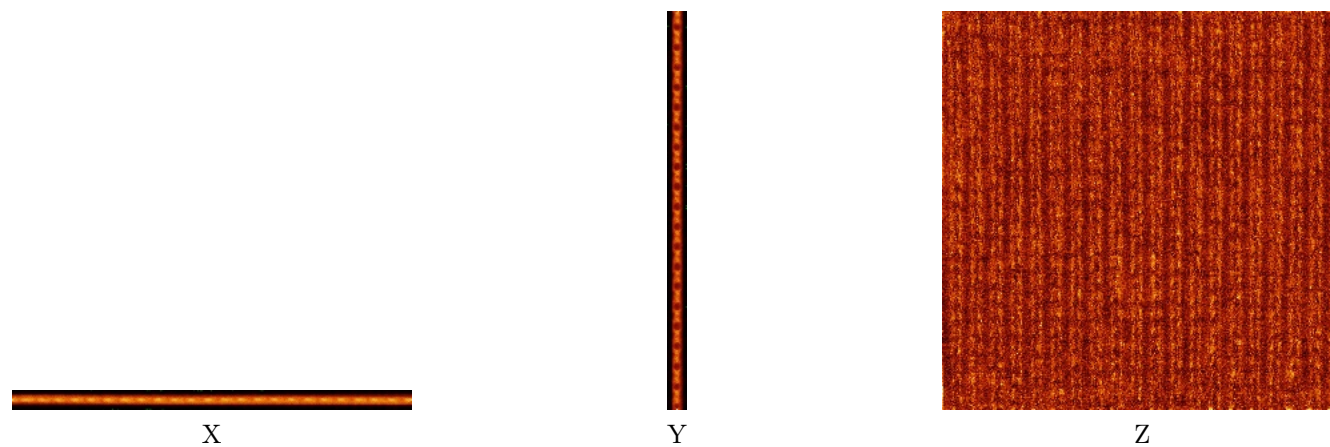
The images above show central slices of the tomogram in three orthogonal directions.

### 6.3 Largest variance slices [i](#)



The images above show the largest variance slices of the tomogram in three orthogonal directions.

### 6.4 Orthogonal standard-deviation projections (False-color) [i](#)



The images above show the tomogram projected in three orthogonal directions.

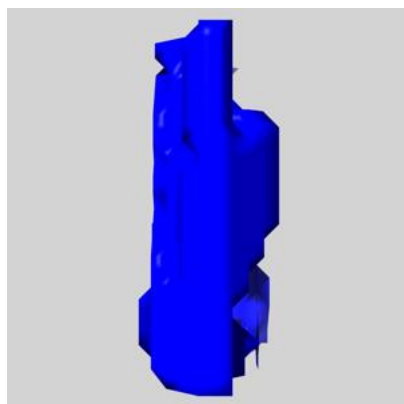
## 6.5 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

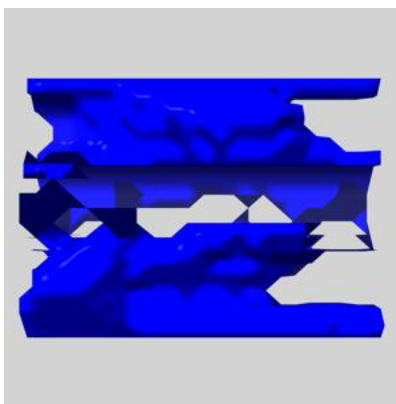
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

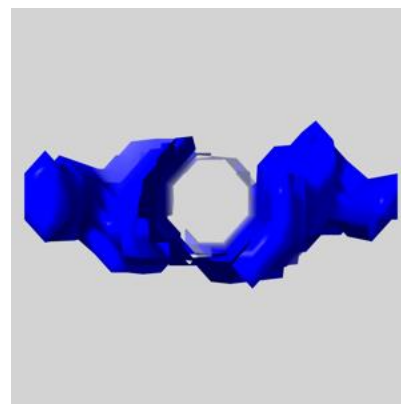
### 6.5.1 emd\_1001\_msk\_25.map [i](#)



X

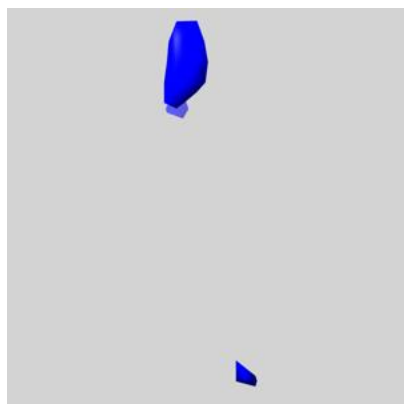


Y

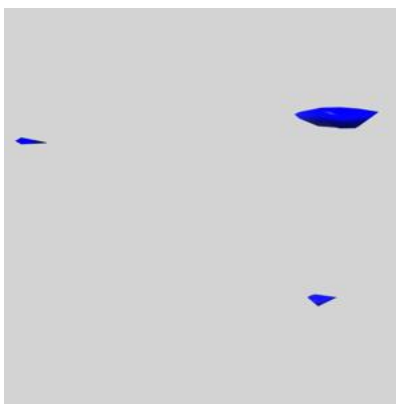


Z

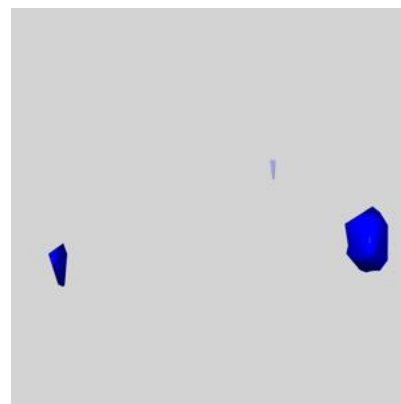
### 6.5.2 emd\_1001\_msk\_24.map [i](#)



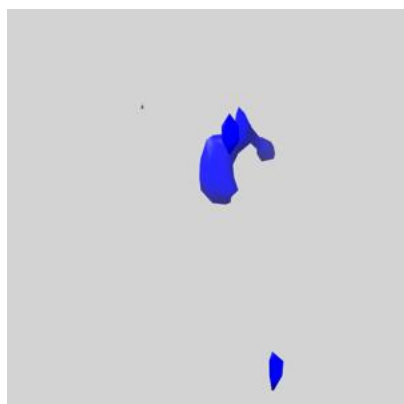
X



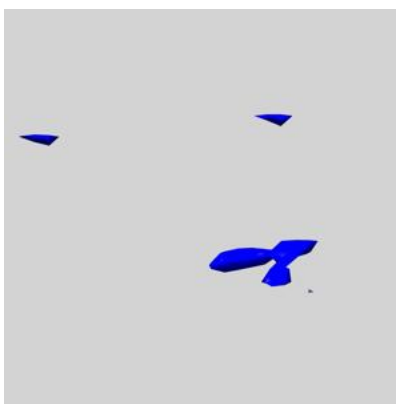
Y



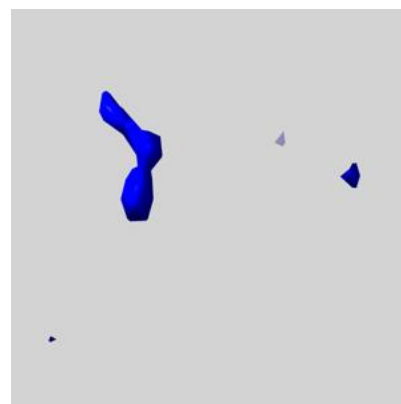
Z

6.5.3 emd\_1001\_msk\_23.map [i](#)

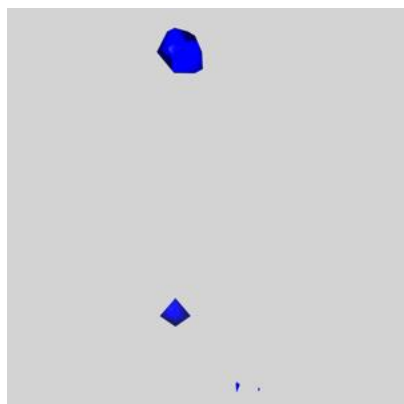
X



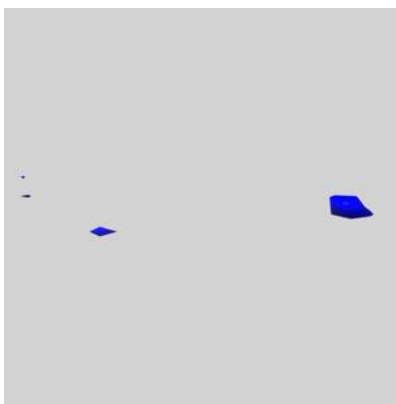
Y



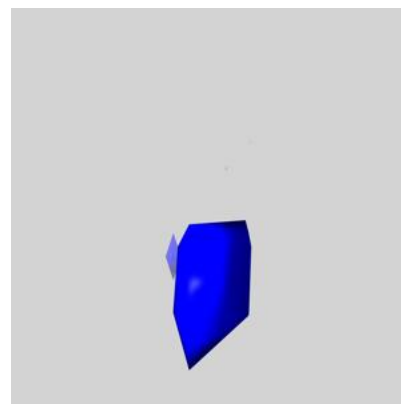
Z

6.5.4 emd\_1001\_msk\_22.map [i](#)

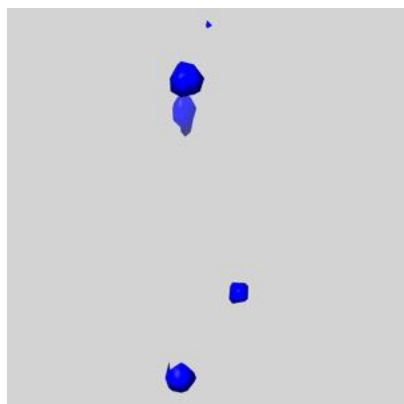
X



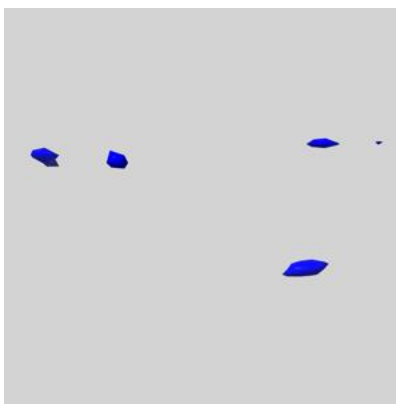
Y



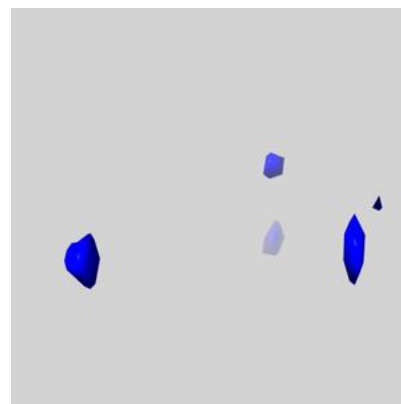
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6.5.5 emd\_1001\_msk\_21.map [i](#)

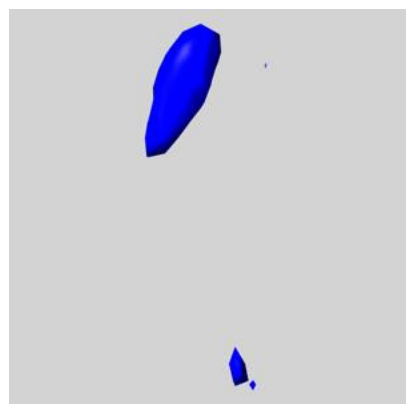
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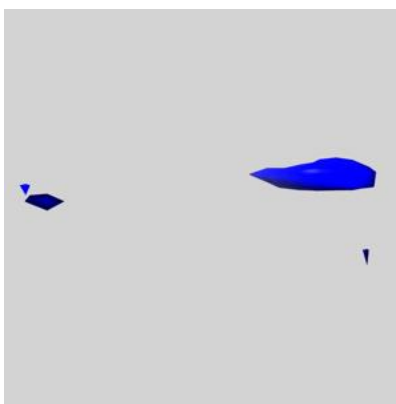
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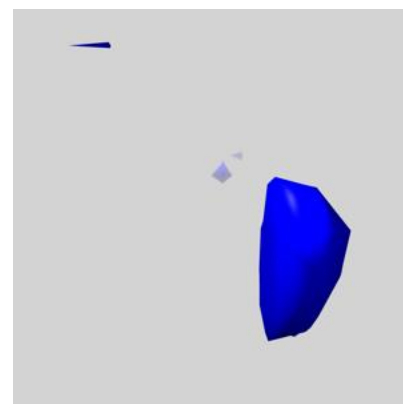
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6.5.6 emd\_1001\_msk\_20.map [i](#)

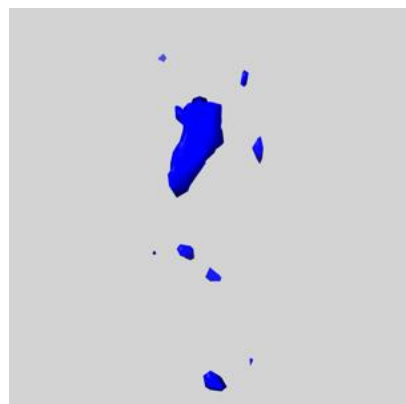
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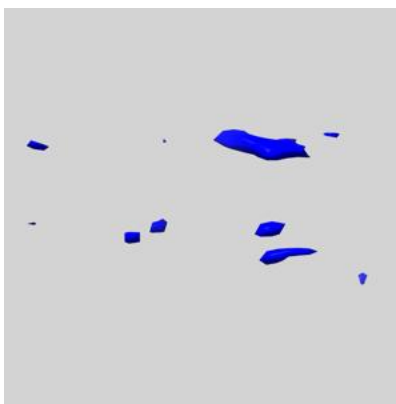
Y



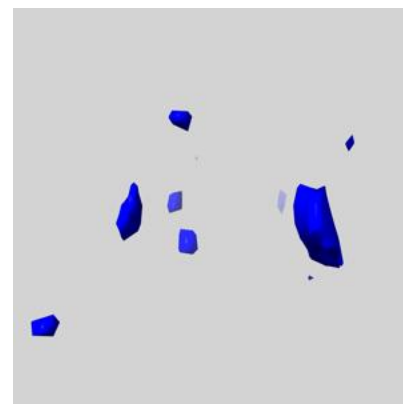
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6.5.7 emd\_1001\_msk\_19.map [i](#)

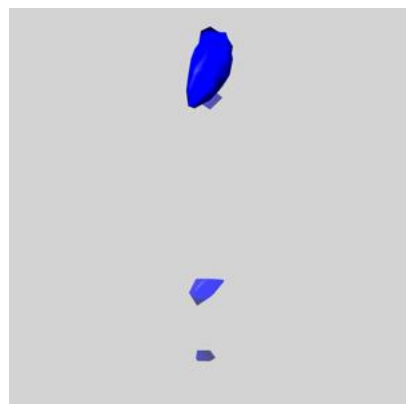
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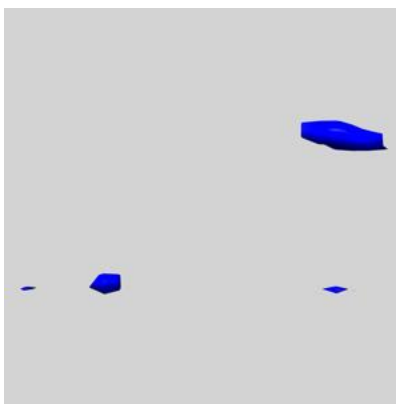
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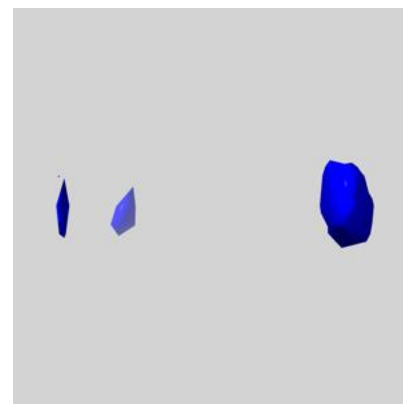
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6.5.8 emd\_1001\_msk\_18.map [i](#)

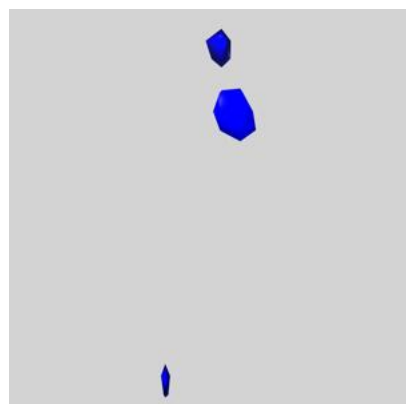
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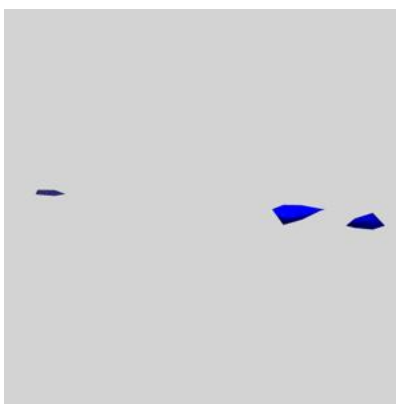
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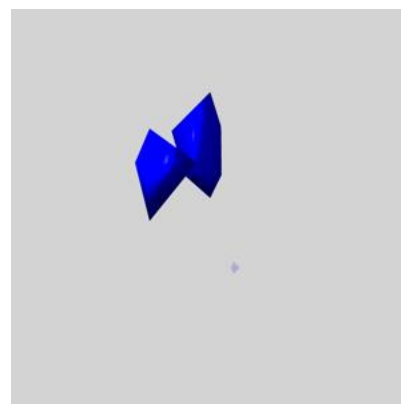
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6.5.9 emd\_1001\_msk\_17.map [i](#)

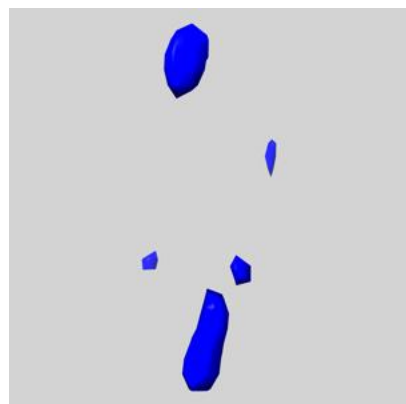
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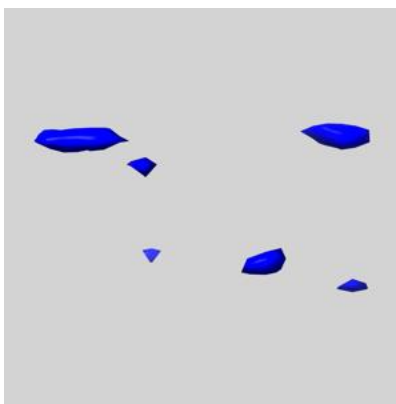
Y



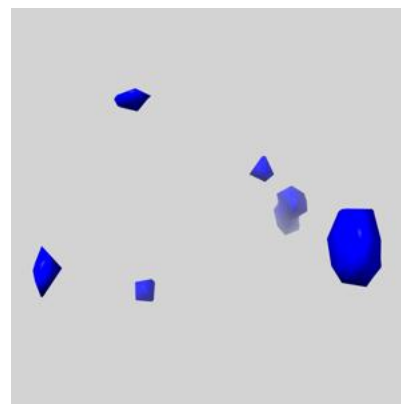
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6.5.10 emd\_1001\_msk\_16.map [i](#)

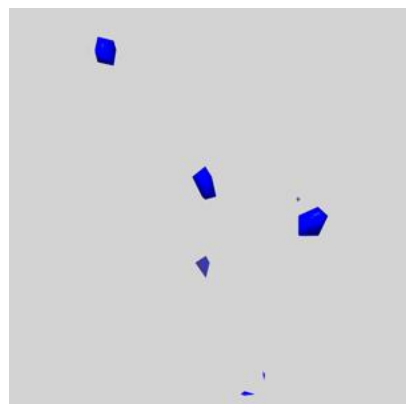
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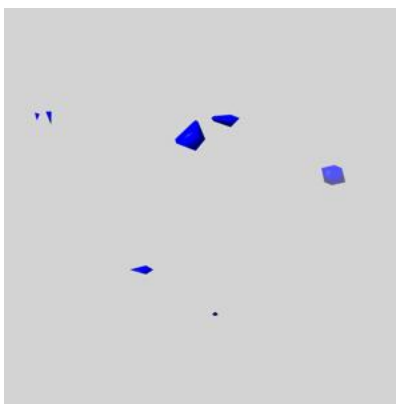
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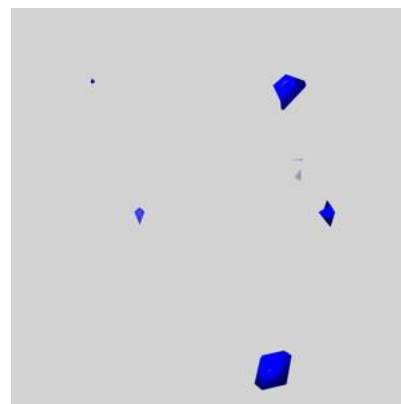
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6.5.11 emd\_1001\_msk\_15.map [i](#)

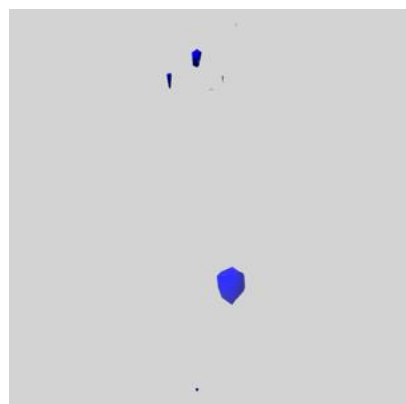
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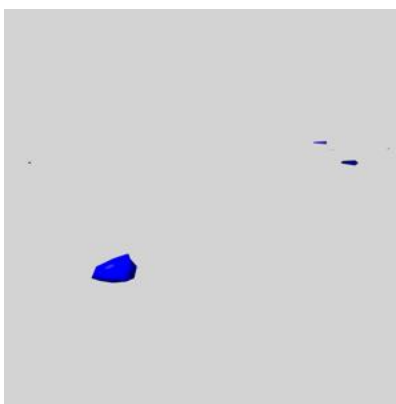
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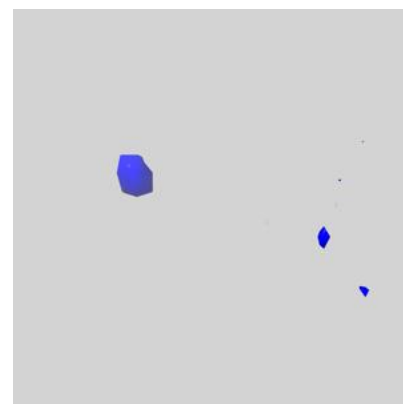
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6.5.12 emd\_1001\_msk\_14.map [i](#)

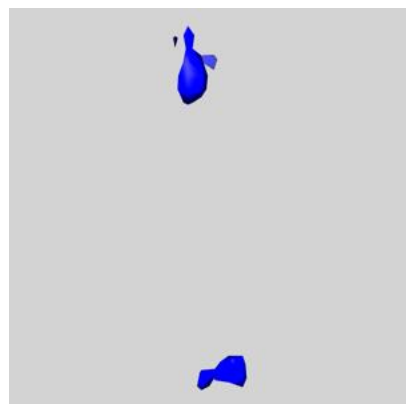
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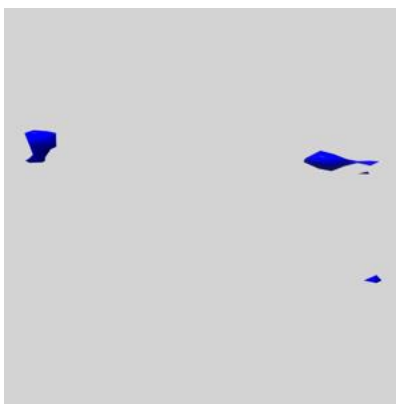
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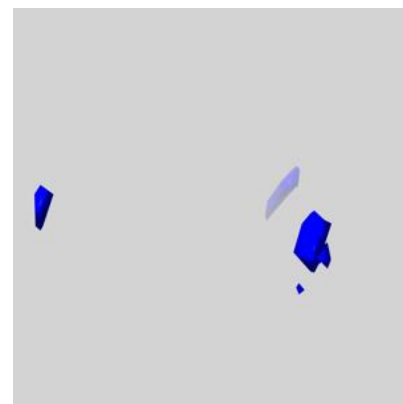
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6.5.13 emd\_1001\_msk\_13.map [i](#)

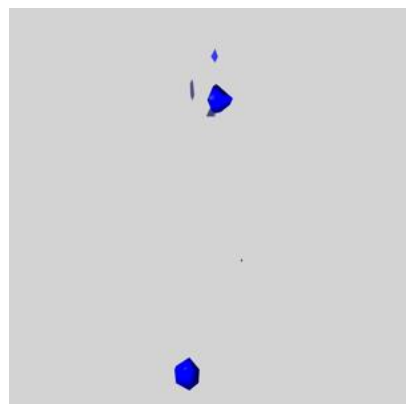
X



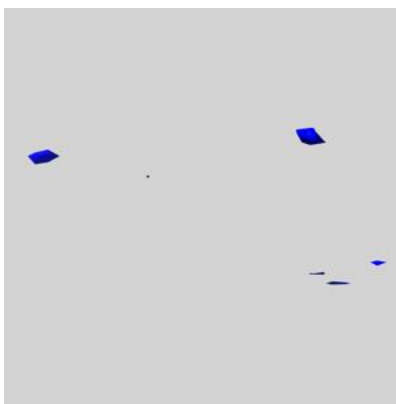
Y



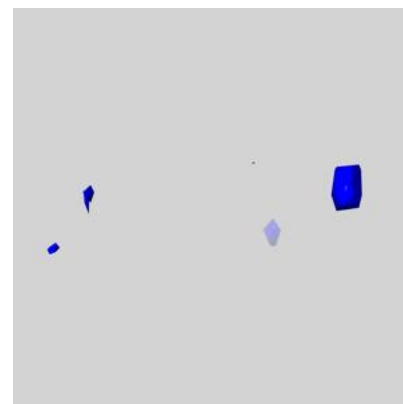
Z

6.5.14 emd\_1001\_msk\_12.map [i](#)

X

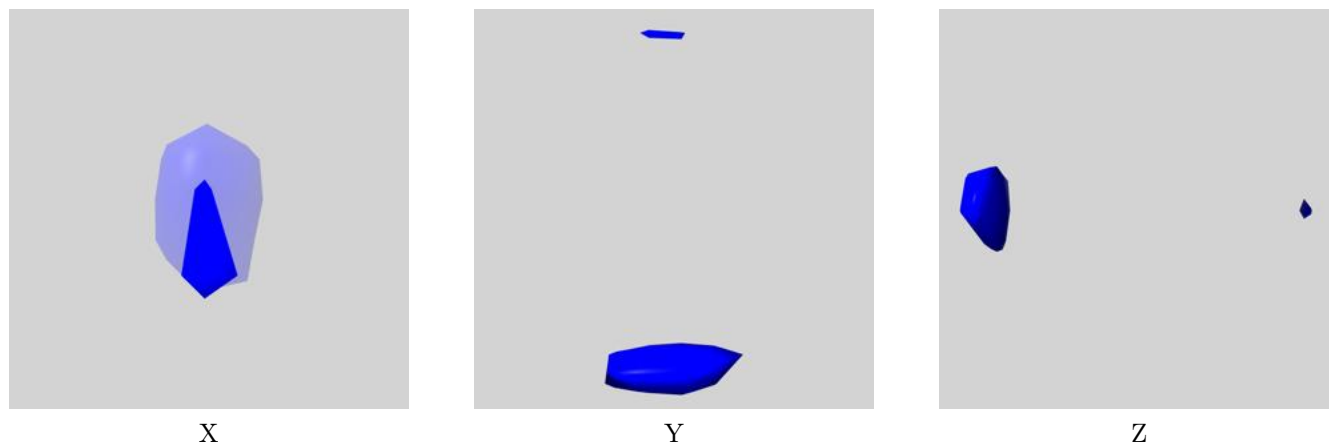
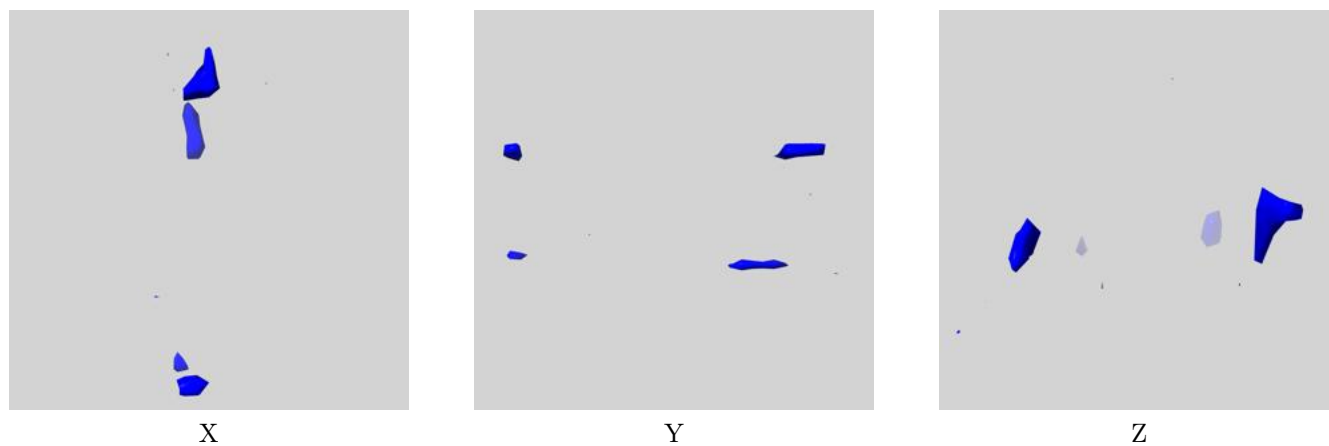
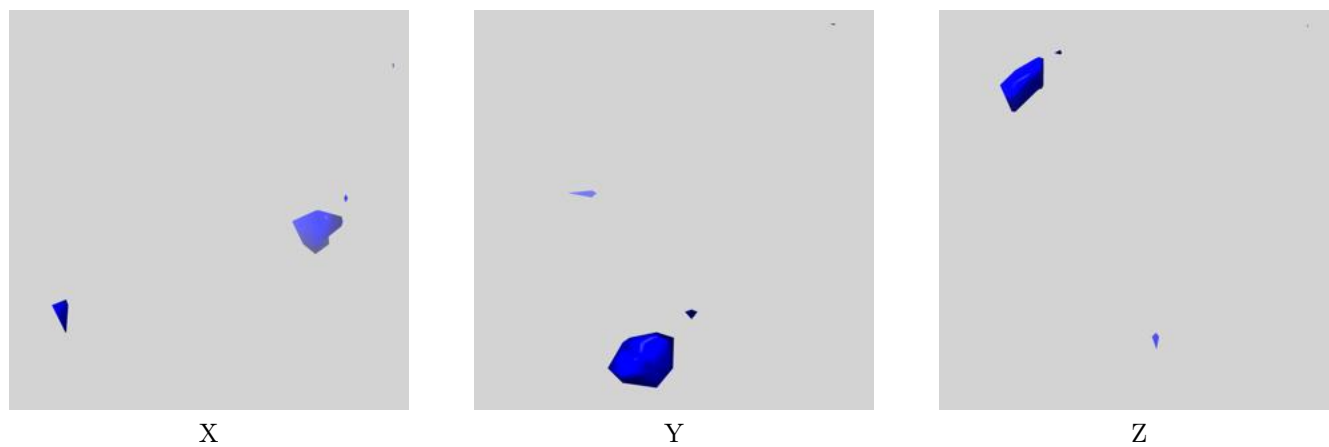


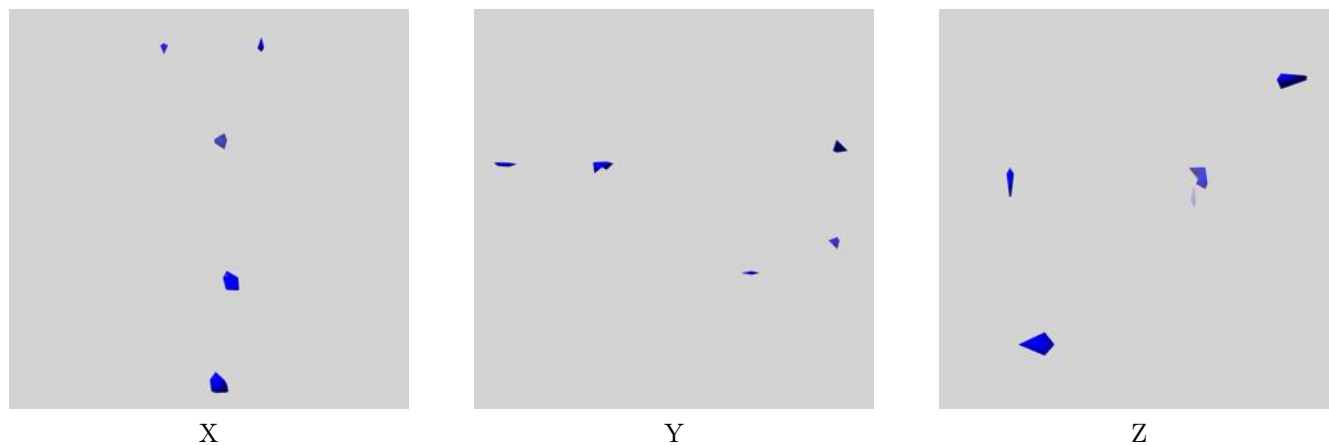
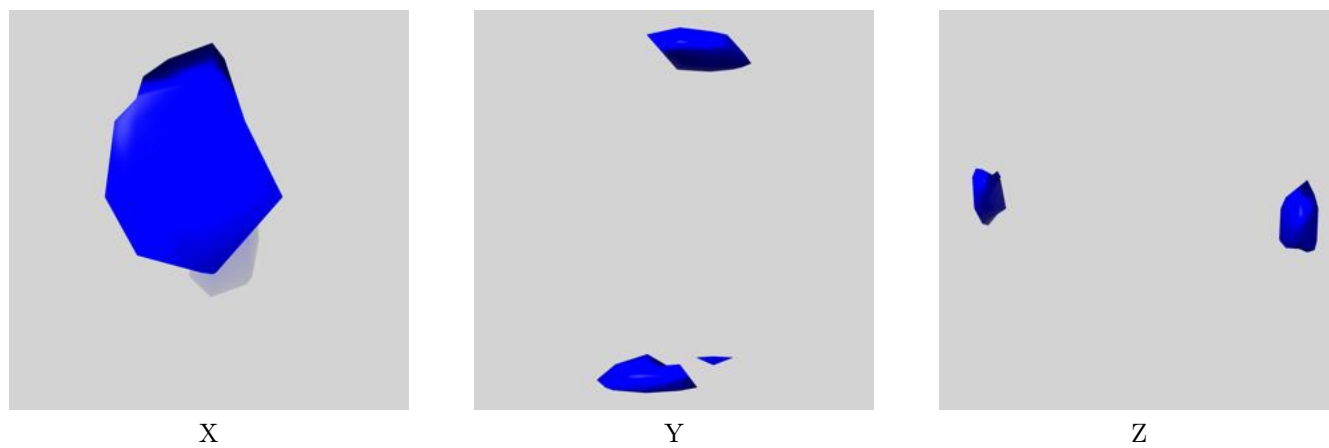
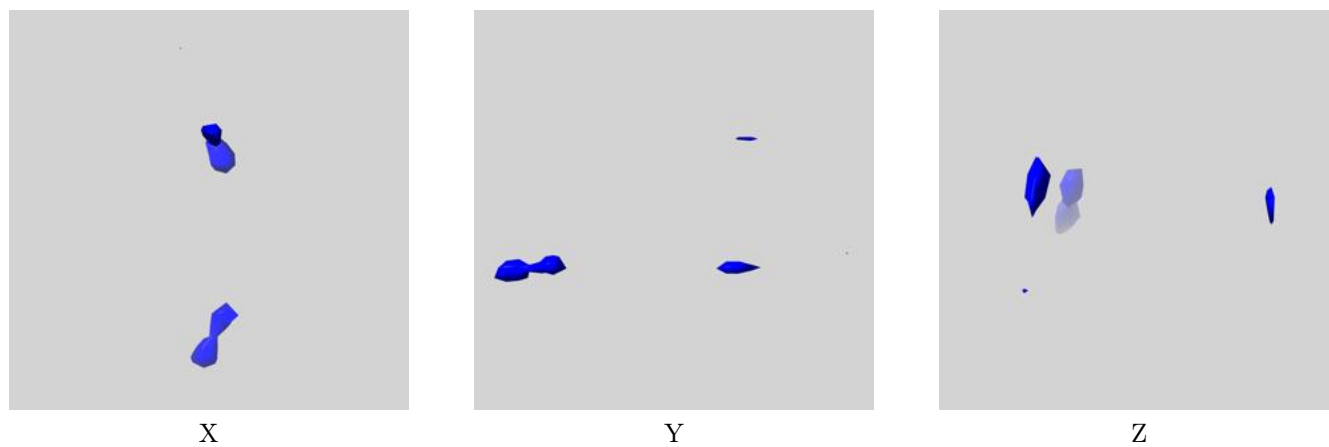
Y



Z

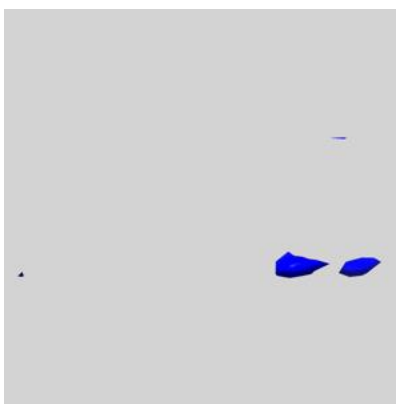


6.5.15 emd\_1001\_msk\_11.map [i](#)6.5.16 emd\_1001\_msk\_10.map [i](#)6.5.17 emd\_1001\_msk\_9.map [i](#)

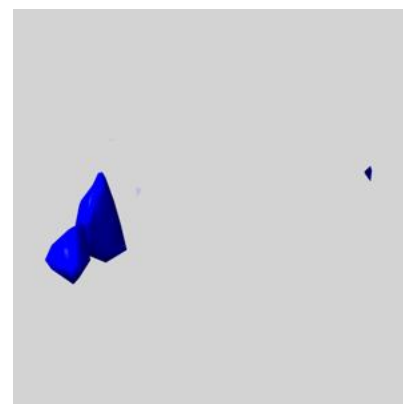
6.5.18 emd\_1001\_msk\_8.map [i](#)6.5.19 emd\_1001\_msk\_7.map [i](#)6.5.20 emd\_1001\_msk\_6.map [i](#)

6.5.21 emd\_1001\_msk\_5.map [i](#)

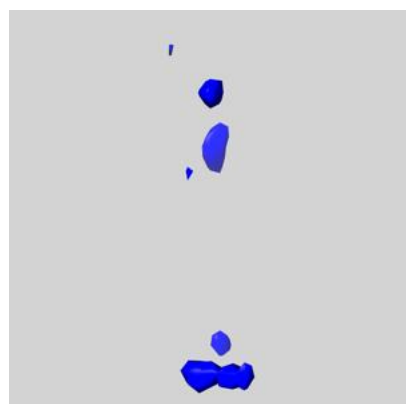
X



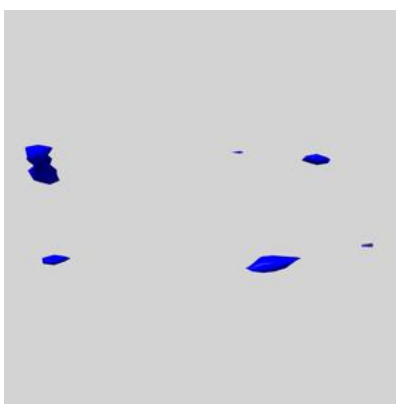
Y



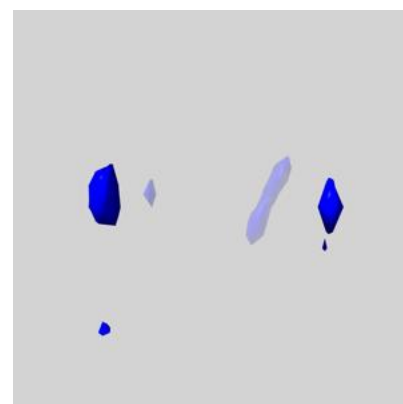
Z

6.5.22 emd\_1001\_msk\_4.map [i](#)

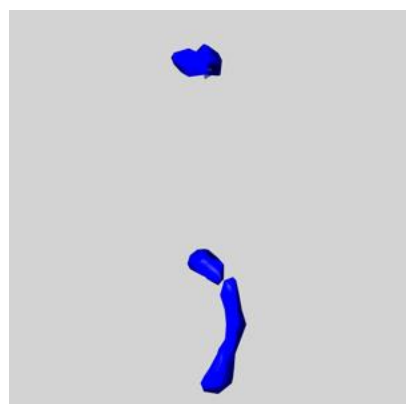
X



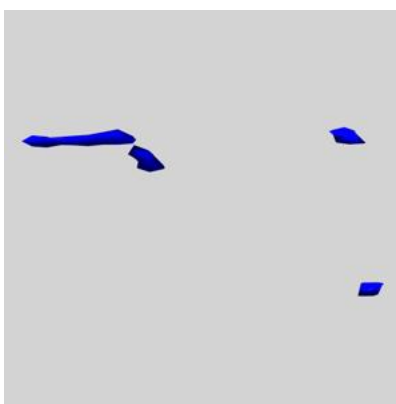
Y



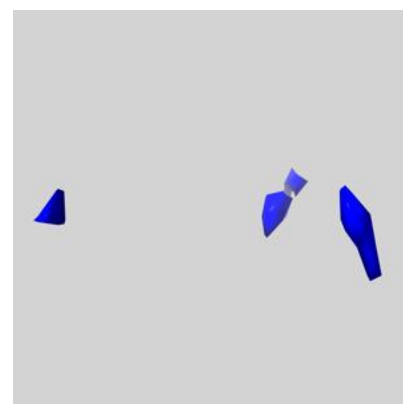
Z

6.5.23 emd\_1001\_msk\_3.map [i](#)

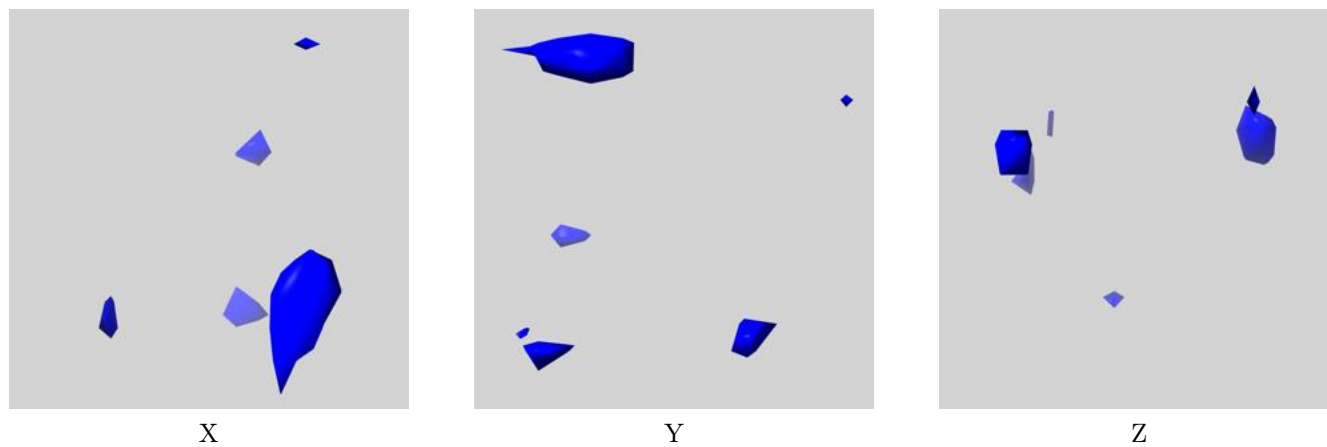
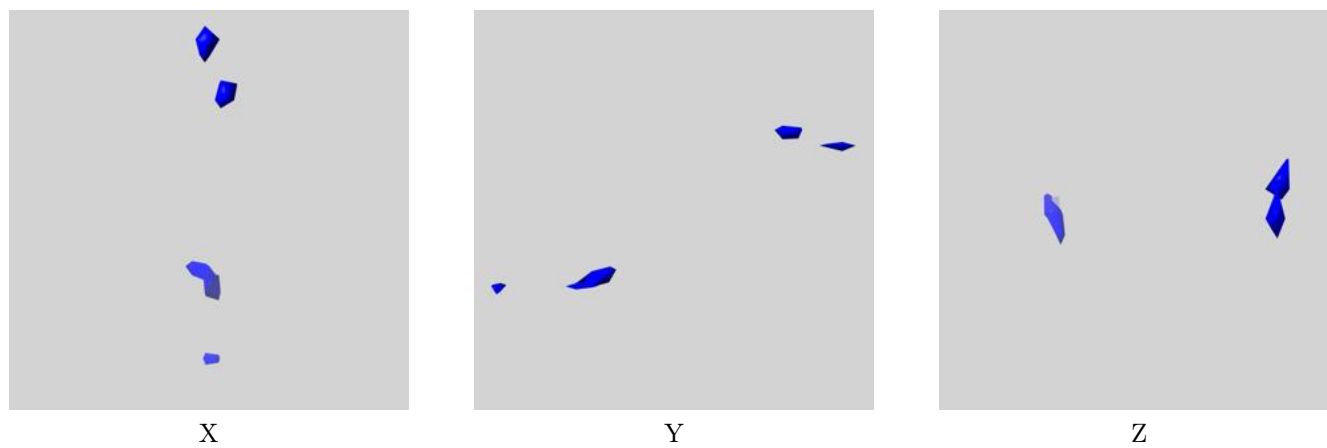
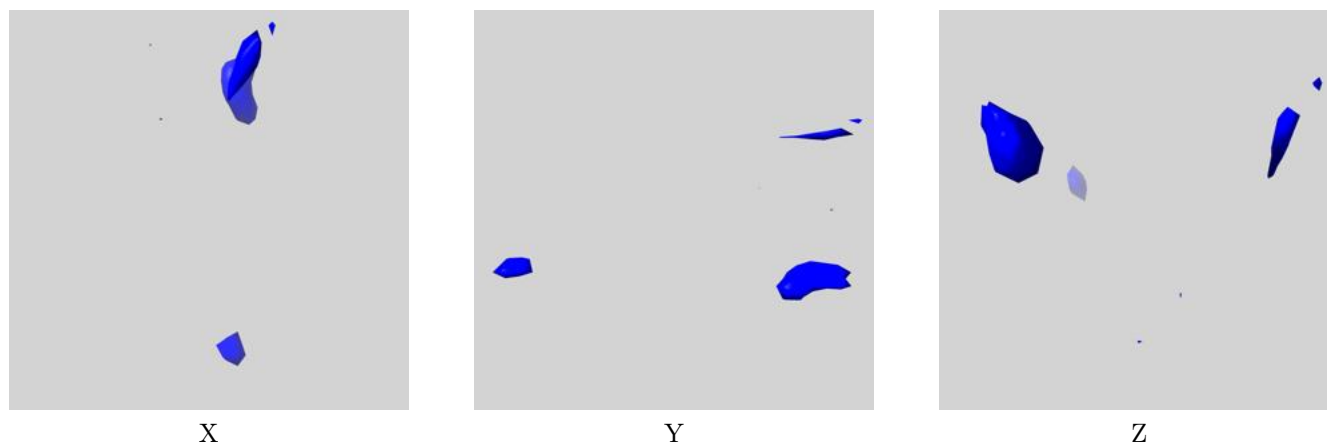
X



Y



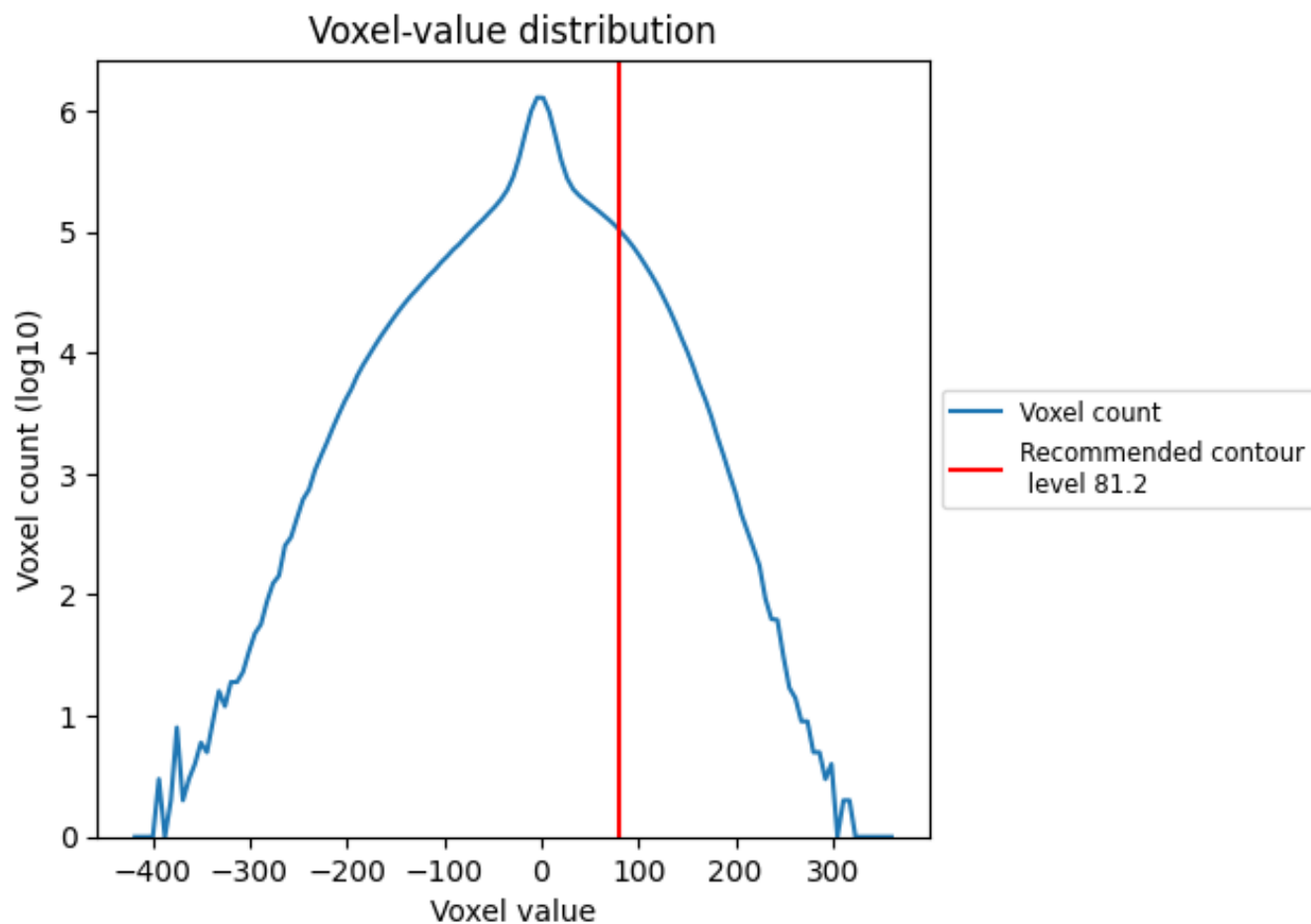
Z

6.5.24 emd\_1001\_msk\_2.map [i](#)6.5.25 emd\_1001\_msk\_1.map [i](#)6.5.26 emd\_1001\_msk\_26.map [i](#)

## 7 Tomogram analysis [i](#)

This section contains the results of statistical analysis of the tomogram.

### 7.1 Voxel-value distribution [i](#)



The voxel-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic.

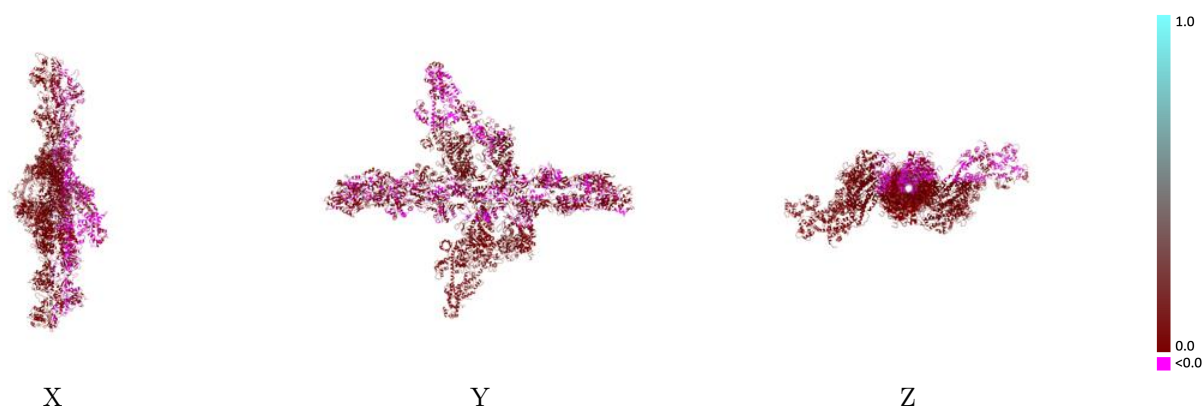
## 8 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-1001 and PDB model 1O1F. Per-residue inclusion information can be found in section 3 on page 7.

### 8.1 Map-model overlay [i](#)

This section was not generated.

### 8.2 Q-score mapped to coordinate model [i](#)

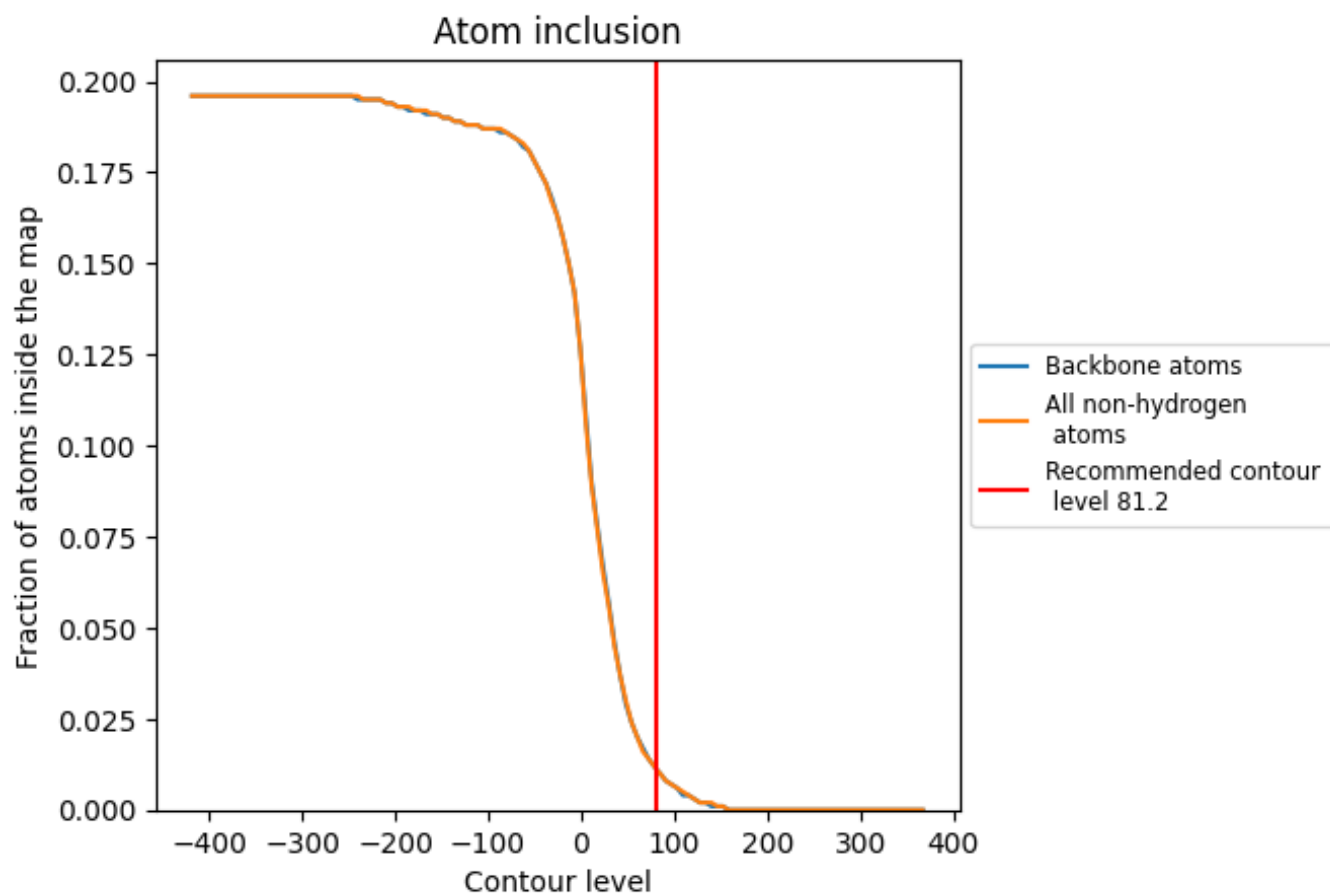


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

### 8.3 Atom inclusion mapped to coordinate model [i](#)

This section was not generated.























































## 8.4 Atom inclusion [i](#)



At the recommended contour level, 1% of all backbone atoms, 1% of all non-hydrogen atoms, are inside the map.

## 8.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (81.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.0110	 -0.0020
0	 0.0000	 -0.0030
1	 0.0000	 0.0070
2	 0.0000	 -0.0040
3	 0.0000	 0.0010
4	 0.0370	 -0.0030
5	 0.0000	 0.0010
6	 0.0080	 -0.0090
7	 0.0000	 -0.0010
8	 0.0640	 0.0030
A	 0.0000	 -0.0030
B	 0.0000	 0.0000
C	 0.0000	 0.0000
D	 0.0080	 -0.0060
E	 0.0000	 -0.0440
F	 0.0960	 0.0260
G	 0.0000	 0.0030
H	 0.0000	 0.0000
I	 0.0000	 0.0000
J	 0.0090	 -0.0000
K	 0.0000	 -0.0010
L	 0.2550	 -0.0210
V	 0.0000	 0.0010
W	 0.0000	 -0.0010
X	 0.0000	 -0.0020
Y	 0.0000	 -0.0080
Z	 0.0000	 0.0030

