



Full wwPDB EM Validation Report ⓘ

Nov 19, 2022 – 10:30 AM EST

PDB ID : 7LIV
EMDB ID : EMD-23386
Title : Structure of human transfer RNA visualized in the cytomegalovirus, a DNA virus
Authors : Liu, Y.T.; Strugatsky, D.; Liu, W.; Zhou, Z.H.
Deposited on : 2021-01-28
Resolution : 3.60 Å(reported)

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

We welcome your comments at 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>.

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

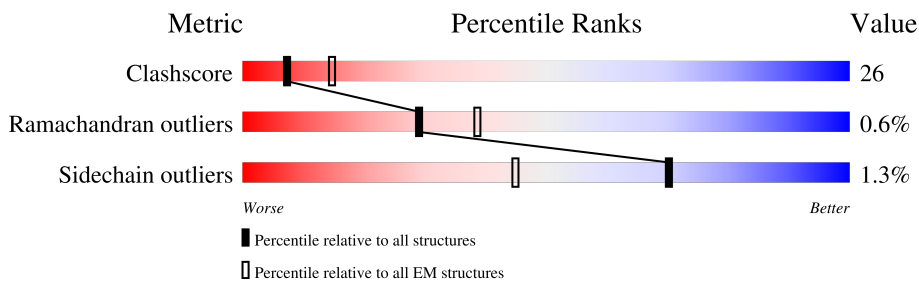
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 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.




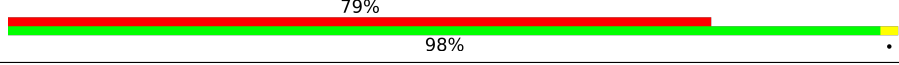

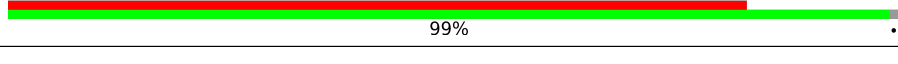
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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 ≥ 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	1370	
1	C	1370	
1	J	1370	
2	4	285	
2	5	285	
2	6	285	
3	D	75	
3	E	75	

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Mol	Chain	Length	Quality of chain
3	Z	75	 <p>64% 56% 28% 16%</p>
4	p	290	 <p>79% 98%</p>
5	q	306	 <p>60% 78% 21%</p>
5	r	306	 <p>83% 99%</p>

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 47058 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 Major capsid protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	J	1348	Total	C	N	O	S	0	0
			10681	6802	1851	1967	61		
1	A	1328	Total	C	N	O	S	0	0
			10526	6706	1827	1934	59		
1	C	1348	Total	C	N	O	S	0	0
			10681	6802	1851	1967	61		

- Molecule 2 is a protein called Tegument protein pp150.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	5	285	Total	C	N	O	S	0	0
			2328	1468	426	421	13		
2	6	285	Total	C	N	O	S	0	0
			2328	1468	426	421	13		
2	4	285	Total	C	N	O	S	0	0
			2328	1468	426	421	13		

- Molecule 3 is a protein called Small capsomere-interacting protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	Z	63	Total	C	N	O	S	0	0
			513	321	97	91	4		
3	D	63	Total	C	N	O	S	0	0
			513	321	97	91	4		
3	E	63	Total	C	N	O	S	0	0
			513	321	97	91	4		

- Molecule 4 is a protein called Triplex capsid protein 1.

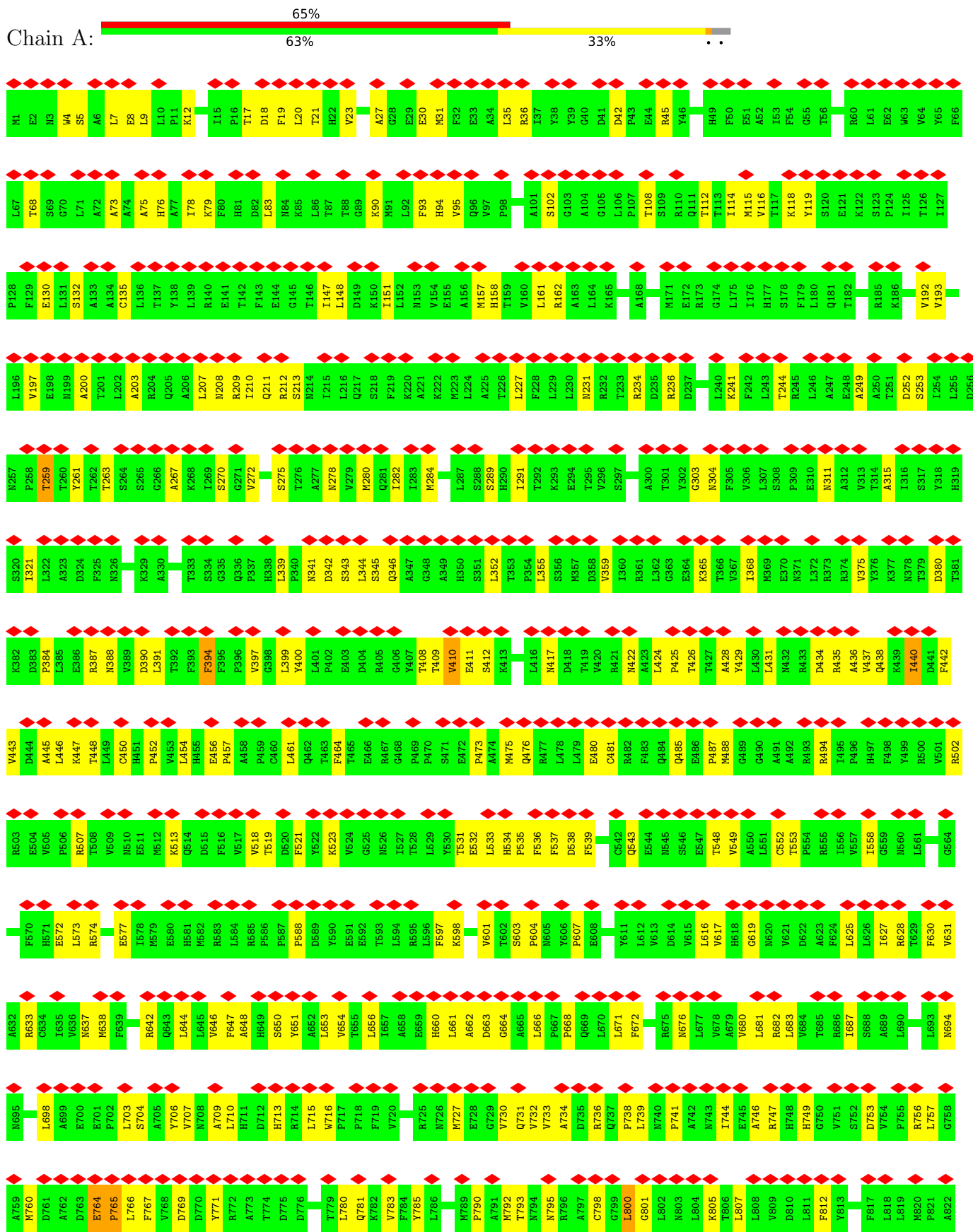
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	p	290	Total	C	N	O	S	0	0
			2325	1485	411	417	12		

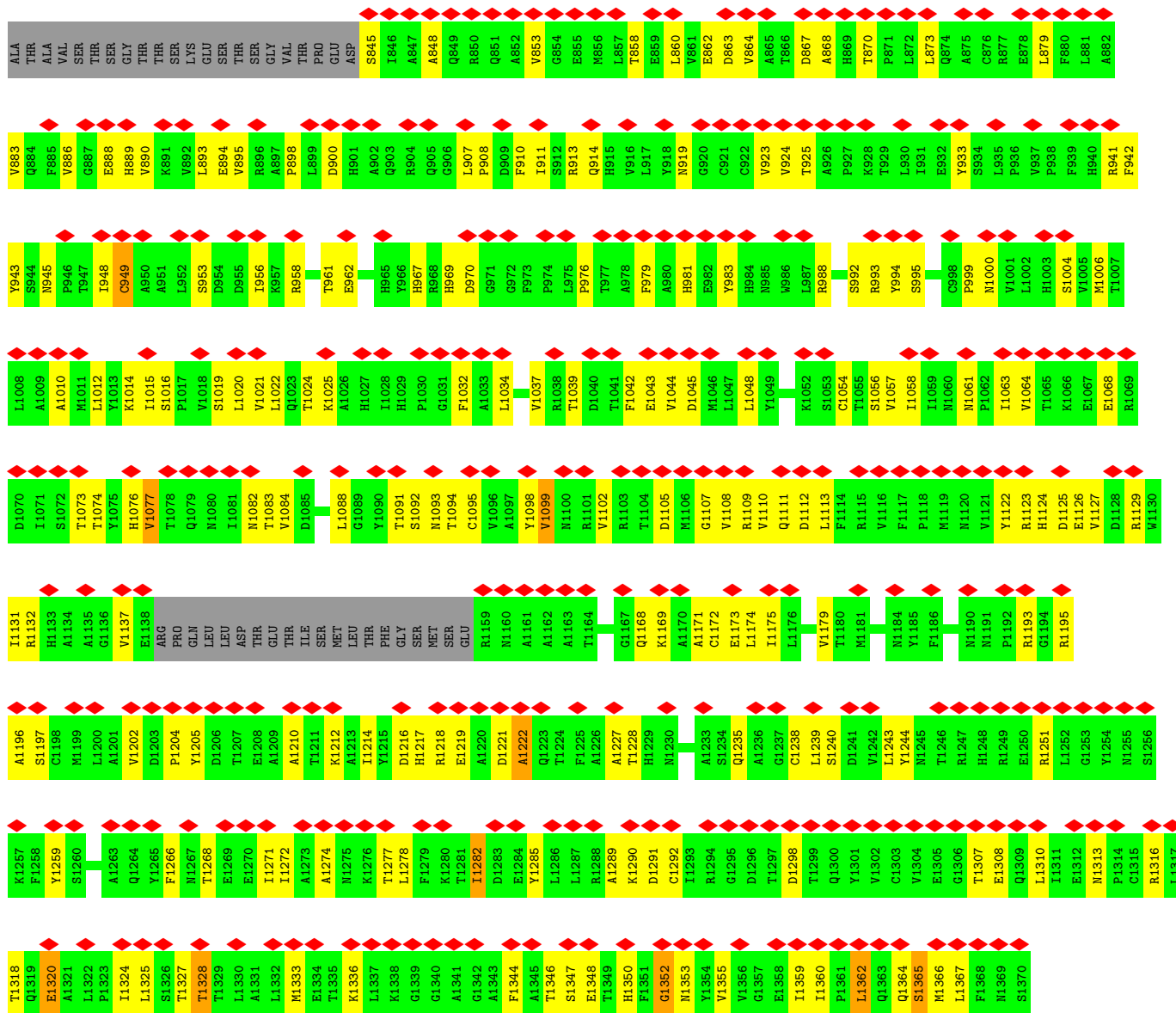
- Molecule 5 is a protein called Triplex capsid protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	q	241	Total	C	N	O	S	0	0
			1911	1236	328	331	16		
5	r	304	Total	C	N	O	S	0	0
			2411	1544	420	429	18		

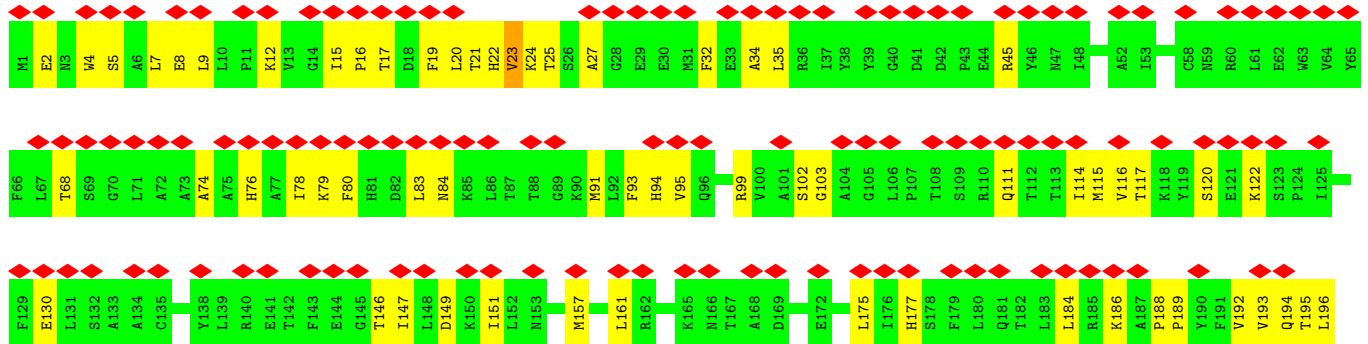


• Molecule 1: Major capsid protein

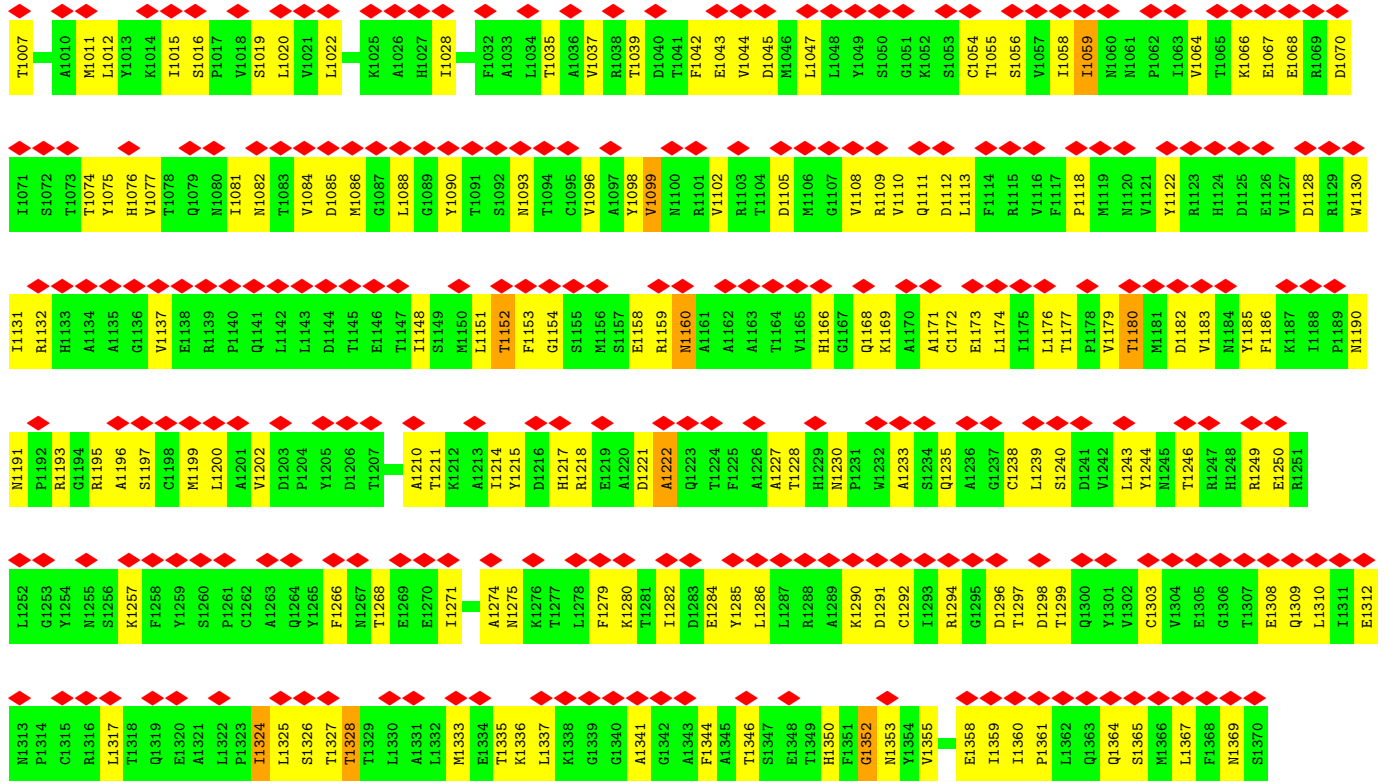




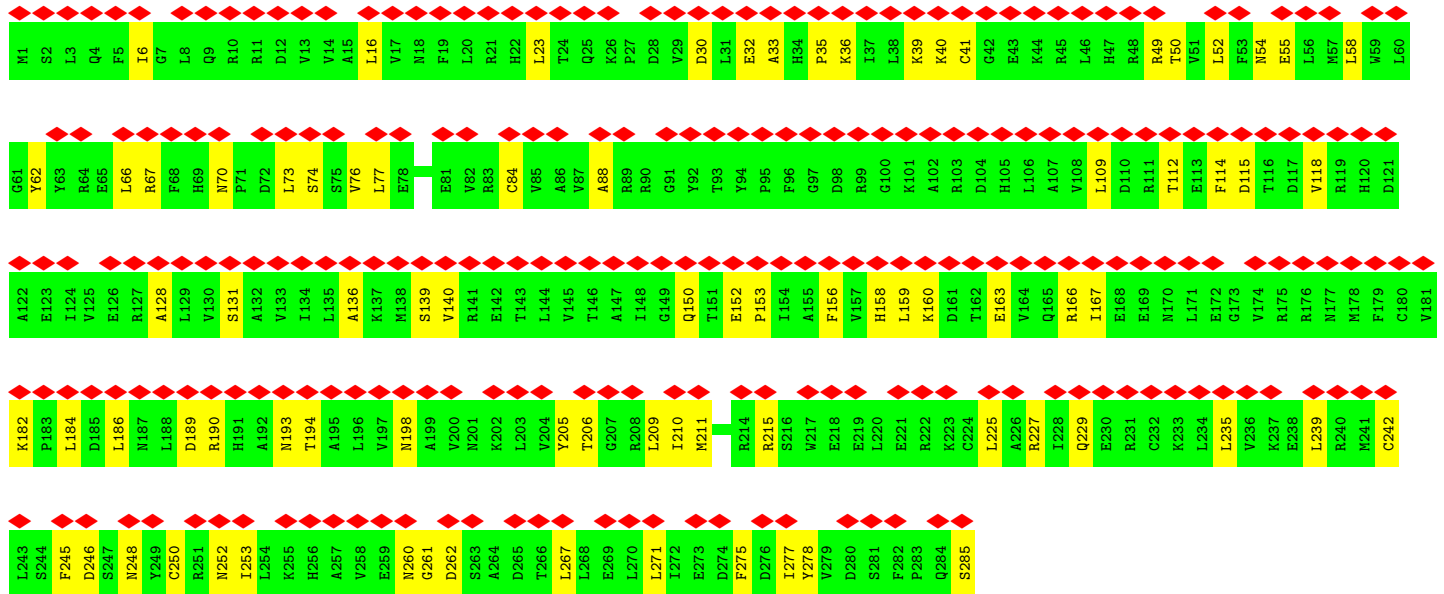
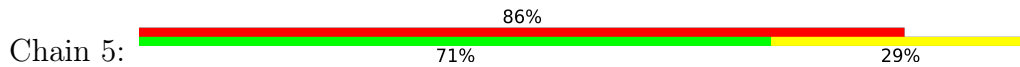
• Molecule 1: Major capsid protein



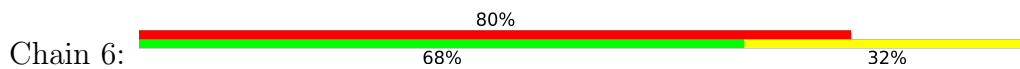
V197	P258	H319	T379	D441	R502	E572	A632	G696	D761	ALA	Q884	S844
E198	T259	I321	D380	F442	R503	L573	R633	D697	A762	THR	F885	N945
N199	T260	L322	T381	V443	E504	R574	G634	L698	D763	ALA	V886	P946
A200	Y261	A323	K382	D444	R507	E577	I635	A699	E764	SER	E887	T947
T201	T262	A324	D383	A445	F508	E578	V636	E700	F765	THR	R888	T948
L202	T263	D324	P384	L446	V509	L579	N637	E701	L766	SER	H889	C949
A203	S264	F325	L385	K447	N510	M579	N638	F702	F767	GLY	H890	A950
R204	S265	N326	E386	T448	K513	E580	F639	L703	V768	THR	K891	A951
Q205	G266	S327	R387	L449	K514	E581	H640	S704	D769	SER	V892	L952
A206	A267	Y328	N388	C450	Q515	H582	R642	T641	D770	LYS	L893	S953
L207	K268	K329	V389	H451	D515	H583	Q643	A706	Y771	GLU	E894	D954
N208	I269	A330	N390	L454	V518	L584	L644	L710	R772	SER	V895	D955
R209	S270	H331	L391	H455	T519	R585	L645	H711	D775	THR	R896	I956
I210	M273	L332	T392	E456	F520	P586	V646	D712	E776	GLY	A897	I957
Q211	V274	T333	F395	P457	F521	F587	F647	D713	E777	VAL	P898	R958
R212	S275	S334	P396	A458	F522	P588	F648	H714	L780	THR	D900	E962
L215	A277	G335	V397	P459	K523	D589	A648	R715	Q781	ASP	H901	F963
L216	A278	H338	G398	C460	K524	V590	V651	L716	K782	THR	A902	P964
Q217	V279	L339	L399	L461	V524	Y591	L652	W716	K783	GLU	Q903	H965
Q218	M280	L340	Y400	Q462	G525	E592	T653	F717	F784	PRO	R904	Y966
S218	M281	L341	L401	T463	N526	T593	L654	F718	F785	GLU	Q905	H967
F219	Q281	N341	P402	F464	L529	L594	L655	F719	C787	THR	P906	R968
K220	I282	Q342	E403	T465	E532	R595	L656	H722	L788	THR	P908	D970
A221	I283	D343	E404	E466	L533	L596	L657	R725	W789	THR	D909	G971
K222	M284	S344	D404	R467	H534	F597	E659	R726	K790	THR	F910	G972
M223	S285	S345	E405	G468	H535	K598	H660	W727	A791	THR	S911	F973
L224	L286	Q346	L410	P469	F536	T599	L661	E728	M792	THR	S912	P974
A225	L287	A347	V410	P470	F537	T600	A662	E729	T793	THR	R913	L975
L226	S288	G348	E411	E472	D538	V601	D663	W730	N794	THR	Q914	P976
L227	S289	G349	S412	F473	F539	T602	L666	V730	W795	THR	H915	A978
F228	H290	H350	S413	A474	F540	S603	P667	Q731	R796	THR	V916	A979
L229	I291	H351	K413	A475	H541	P604	P668	W732	A797	THR	L917	F979
L230	T292	S351	W414	M475	C542	M605	L670	W733	C798	THR	Y918	E982
N231	K293	L352	L415	Q476	Q543	Y606	L671	A734	G799	THR	M919	Y983
R232	E294	T353	L416	R477	Q544	P607	L672	R736	L800	THR	G920	H984
T233	T295	G354	M417	L478	E544	E608	L673	Q737	C801	THR	A865	N985
R234	V296	L355	D418	L479	N545	E609	H673	F738	L802	THR	A866	Y986
D235	S297	S356	T419	E480	S546	L609	H674	W739	M803	THR	T866	L987
R236	A298	M357	V420	C481	E547	L610	V674	L740	R804	THR	D867	R988
D237	P299	P358	R421	R482	T548	Y611	R675	N740	K805	THR	A868	S989
A300	A300	D359	M422	F483	V549	L612	M676	P741	T806	THR	H869	P990
Y238	A301	V359	N423	Q484	A550	V613	A679	A742	L807	THR	T870	P991
V239	T301	I360	A423	Q485	L551	D614	V680	N743	L808	THR	F871	S992
L240	Y302	R361	A424	E486	C552	V615	L681	L744	M808	THR	L872	S993
K241	N304	L362	P425	P487	T553	L616	L682	W745	M809	THR	L873	R993
F242	F305	G363	T426	P488	P554	H618	H682	A746	D810	THR	L874	Y994
L243	V306	E364	T427	M488	R555	G619	L683	L747	L811	THR	L875	S995
R244	L307	K365	T428	G489	R556	G619	L683	R747	F812	THR	C876	A996
R245	L308	T366	Y429	G490	V557	M620	R686	H748	Y813	THR	H877	C996
L246	S308	V367	L430	A491	L558	V621	L687	H749	R814	THR	F878	T997
A247	P309	I368	L431	A492	L561	D622	S688	G750	P815	THR	L879	C998
E248	E310	M369	M432	R493	G564	A623	A689	V751	A816	THR	F880	P999
A249	N311	E370	R433	R494	L562	F624	L690	S752	F817	THR	F881	V1001
A250	A312	N371	D434	T495	P562	F624	L690	D753	L818	THR	L881	L1002
T251	V313	L372	R435	P496	D563	L625	P691	R756	L819	THR	A882	L1003
D252	T314	L373	A436	H497	G564	L626	P691	A759	M820	THR	R821	S1004
S253	A315	R373	A436	H497	G564	L626	P691	A759	M820	THR	R821	S1005
I254	T316	R374	V437	F498	L565	L627	G692	R756	M820	THR	R821	L1006
L255	S317	R374	Q438	F499	A566	R628	L694	A759	M820	THR	R821	L1006
D256	Y318	V375	K439	R500	P567	F630	H695	A759	M820	THR	R821	L1006
N257	Y318	K377	T440	V501	V631	V631	H695	A759	M820	THR	R821	L1006

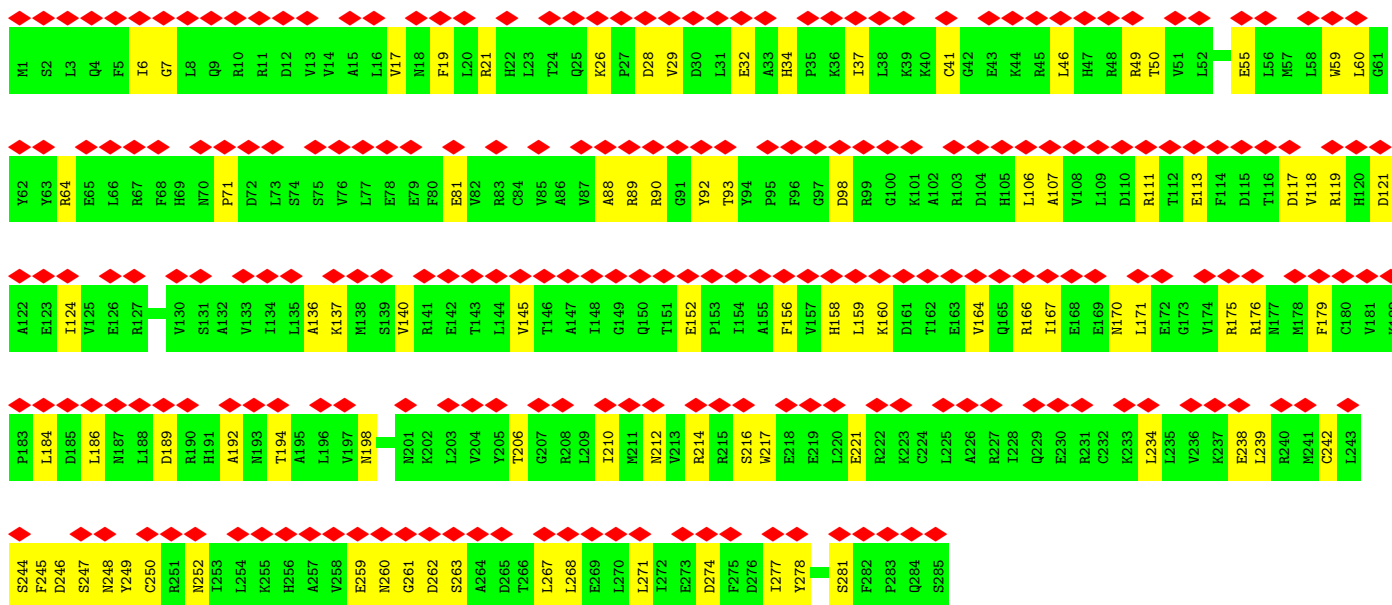


• Molecule 2: Tegument protein pp150

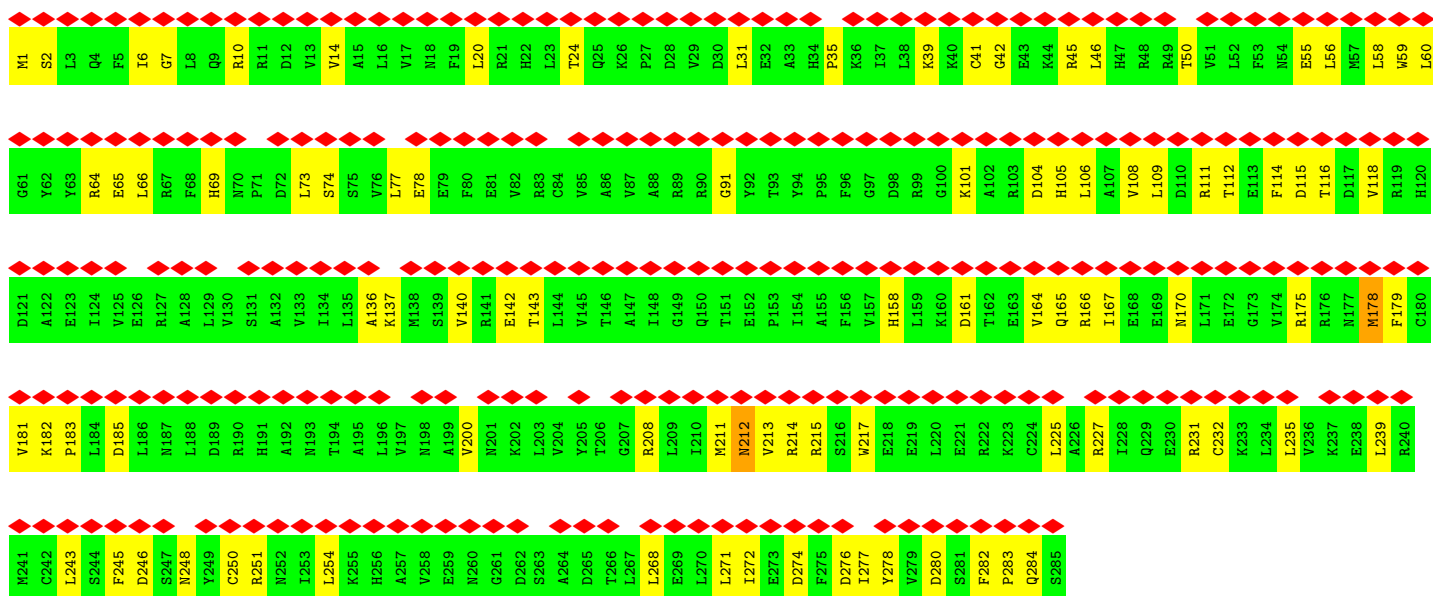


• Molecule 2: Tegument protein pp150

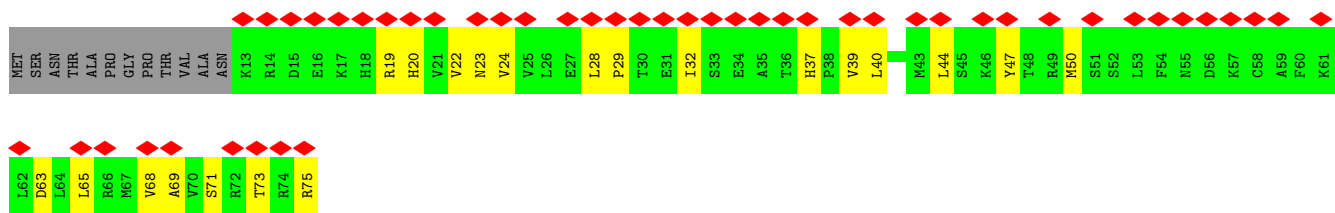




• Molecule 2: Tegument protein pp150



• Molecule 3: Small capsomere-interacting protein



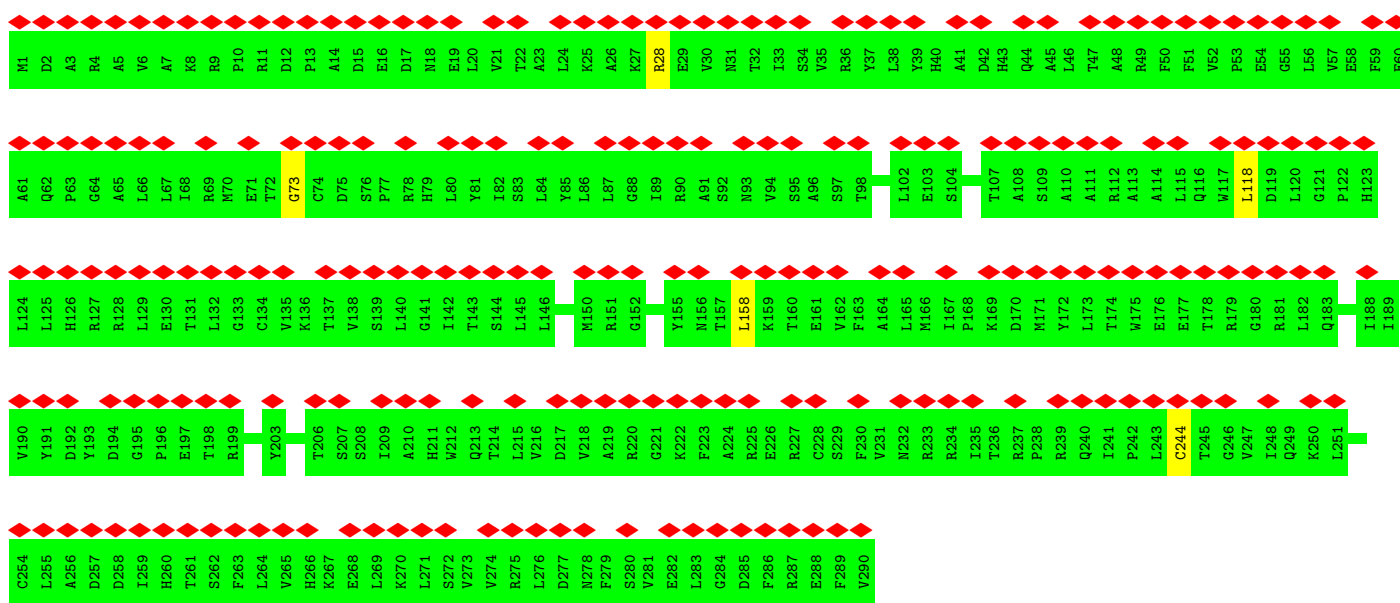
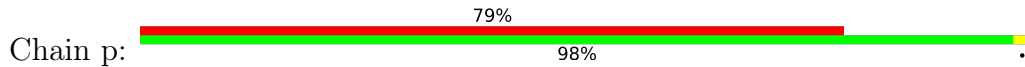
• Molecule 3: Small capsomere-interacting protein



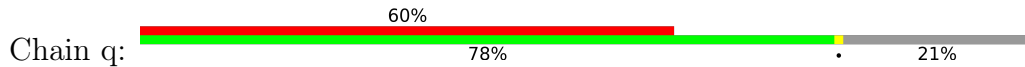
• Molecule 3: Small capsomere-interacting protein

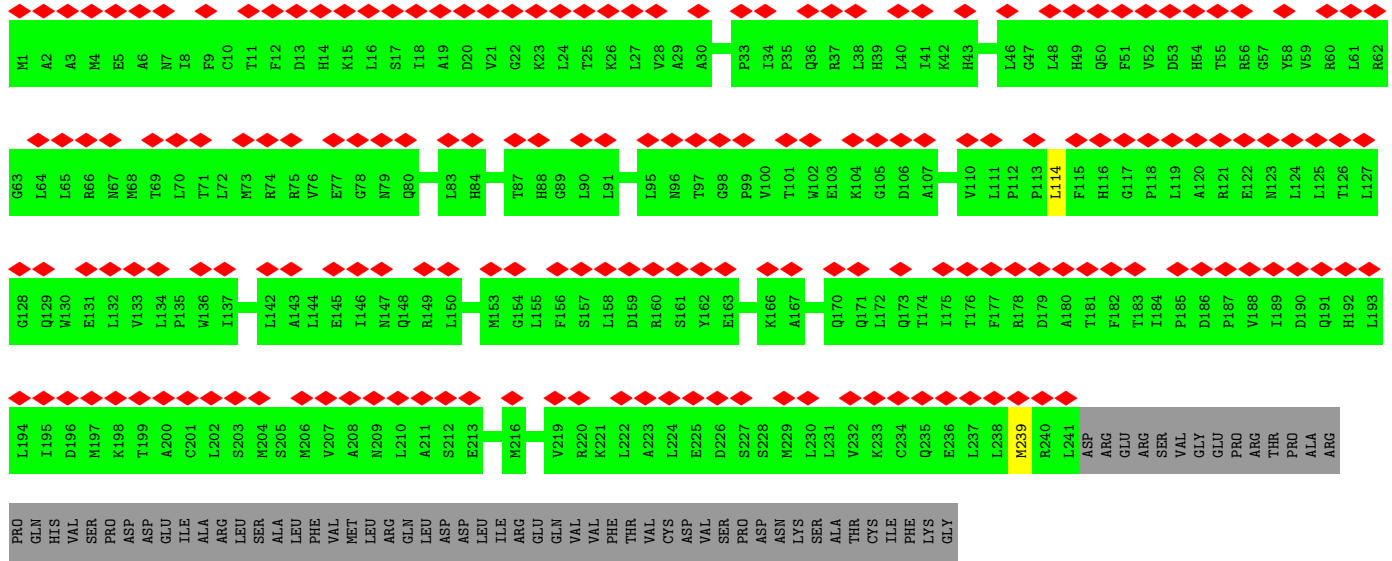


• Molecule 4: Triplex capsid protein 1

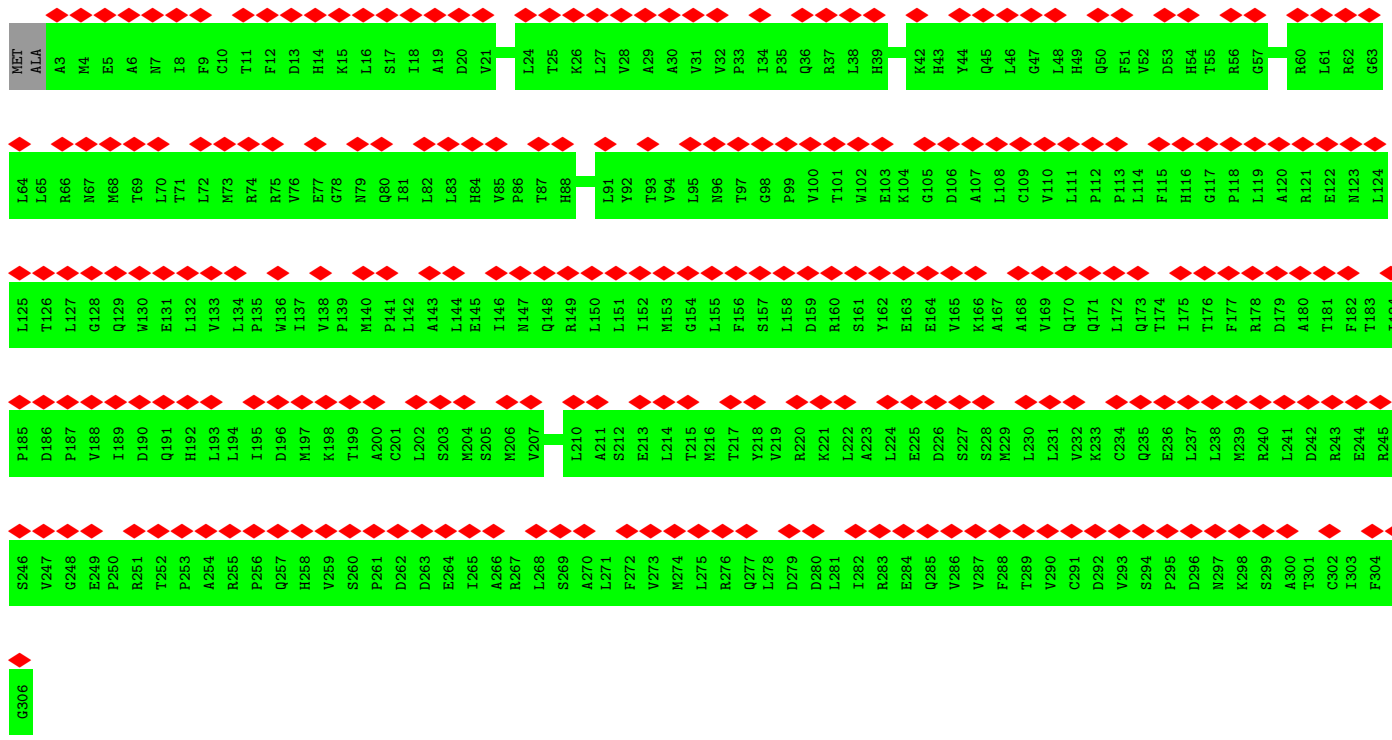
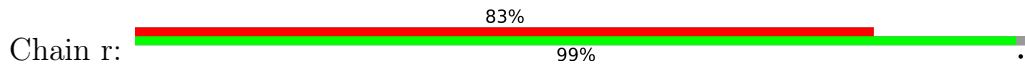


• Molecule 5: Triplex capsid protein 2





• Molecule 5: Triplex capsid protein 2



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	97166	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	18.9	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.083	Depositor
Minimum map value	-0.047	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.02	Depositor
Map size (\AA)	412.16, 412.16, 412.16	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.61, 1.61, 1.61	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.48	0/10779	0.56	0/14684
1	C	0.49	0/10937	0.56	0/14899
1	J	0.48	0/10937	0.56	0/14899
2	4	0.38	0/2366	0.51	0/3192
2	5	0.36	0/2366	0.49	0/3192
2	6	0.40	0/2366	0.51	0/3192
3	D	0.42	0/520	0.50	0/697
3	E	0.41	0/520	0.57	0/697
3	Z	0.41	0/520	0.53	0/697
4	p	0.42	0/2374	0.57	0/3221
5	q	0.39	0/1949	0.55	0/2649
5	r	0.40	0/2458	0.59	0/3339
All	All	0.46	0/48092	0.55	0/65358

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	10526	0	10468	605	0
1	C	10681	0	10620	681	0
1	J	10681	0	10618	630	0
2	4	2328	0	2363	81	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	5	2328	0	2363	70	0
2	6	2328	0	2363	81	0
3	D	513	0	539	56	0
3	E	513	0	539	26	0
3	Z	513	0	539	33	0
4	p	2325	0	2362	0	0
5	q	1911	0	2007	0	0
5	r	2411	0	2500	0	0
All	All	47058	0	47281	2125	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 26.

All (2125) 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:C:203:ALA:CB	1:C:207:LEU:HD21	1.30	1.60
1:A:207:LEU:CD1	1:A:212:ARG:HG3	1.38	1.53
1:C:19:PHE:CE1	1:C:23:VAL:N	1.78	1.51
1:J:440:ILE:CD1	1:J:1108:VAL:HG11	1.38	1.50
1:A:207:LEU:HD11	1:A:212:ARG:CG	1.39	1.49
1:C:360:ILE:HD11	1:C:369:MET:SD	1.50	1.49
3:E:37:HIS:HD2	3:E:40:LEU:CB	1.24	1.48
1:J:440:ILE:HD11	1:J:1108:VAL:CG2	1.45	1.47
1:A:21:THR:HG22	1:C:200:ALA:CA	1.44	1.46
1:C:633:ARG:NH2	1:C:870:THR:HG21	1.19	1.44
1:C:186:LYS:NZ	1:C:1055:THR:HG21	1.21	1.43
1:A:521:PHE:CZ	1:A:532:GLU:OE2	1.68	1.43
1:C:764:GLU:HB3	1:C:765:PRO:CD	1.48	1.42
3:Z:37:HIS:HD2	3:Z:40:LEU:CB	1.32	1.42
1:C:687:ILE:HD12	1:C:1006:MET:SD	1.58	1.42
1:A:212:ARG:NH2	1:A:1204:PRO:HD3	1.25	1.41
1:C:1035:THR:CG2	1:C:1176:LEU:CD1	1.96	1.41
1:A:212:ARG:HH22	1:A:1204:PRO:CD	1.34	1.41
3:E:37:HIS:CD2	3:E:40:LEU:HB3	1.57	1.39
1:J:764:GLU:HB3	1:J:765:PRO:CD	1.47	1.38
1:C:489:GLY:CA	1:C:763:ASP:OD2	1.70	1.38
1:C:1285:TYR:CD1	1:C:1317:LEU:HD21	1.58	1.38
1:C:790:PRO:HB3	1:C:942:PHE:CD2	1.56	1.37
1:J:115:MET:O	1:C:35:LEU:CD1	1.71	1.37
2:4:77:LEU:HD11	2:4:114:PHE:CE1	1.59	1.35

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:1172:CYS:SG	1:J:1261:PRO:HG2	1.65	1.35
1:A:668:PRO:O	1:A:672:PHE:CD2	1.77	1.34
1:A:764:GLU:HB3	1:A:765:PRO:CD	1.55	1.34
1:C:514:GLN:HB2	1:C:993:ARG:NH2	1.37	1.34
1:C:1035:THR:CG2	1:C:1176:LEU:HD12	1.52	1.33
1:C:1285:TYR:CZ	1:C:1317:LEU:HD11	1.61	1.33
2:4:77:LEU:HD11	2:4:114:PHE:CD1	1.63	1.32
1:A:21:THR:CG2	1:C:200:ALA:HA	1.59	1.32
1:C:19:PHE:CZ	1:C:23:VAL:N	1.98	1.32
1:J:35:LEU:CD1	1:A:115:MET:O	1.79	1.31
1:A:790:PRO:HB3	1:A:942:PHE:CD2	1.66	1.31
1:J:440:ILE:CD1	1:J:1108:VAL:CG1	2.06	1.30
1:J:764:GLU:CG	1:J:765:PRO:HD3	1.62	1.30
1:A:630:PHE:CZ	1:A:879:LEU:HD21	1.67	1.30
1:C:203:ALA:CB	1:C:207:LEU:CD2	2.07	1.30
1:C:764:GLU:CG	1:C:765:PRO:HD3	1.61	1.30
2:4:77:LEU:CD1	2:4:114:PHE:CE1	2.15	1.29
1:C:186:LYS:NZ	1:C:1055:THR:CG2	1.95	1.28
1:J:83:LEU:HD22	1:J:1080:ASN:ND2	1.49	1.28
1:J:790:PRO:HB3	1:J:942:PHE:CD2	1.67	1.28
1:C:1035:THR:HG21	1:C:1176:LEU:CD1	1.57	1.27
1:A:1328:THR:HG21	1:A:1353:ASN:OD1	1.35	1.26
1:C:360:ILE:CD1	1:C:369:MET:SD	2.24	1.25
1:J:193:VAL:HG11	1:J:1093:ASN:ND2	1.48	1.25
1:C:203:ALA:HB1	1:C:207:LEU:CD2	1.63	1.25
2:4:248:ASN:OD1	2:4:251:ARG:NH2	1.71	1.24
1:C:1285:TYR:CE1	1:C:1317:LEU:HD11	1.70	1.24
1:C:1285:TYR:CE2	1:C:1317:LEU:HD11	1.71	1.24
1:C:764:GLU:CB	1:C:765:PRO:CD	2.15	1.24
1:C:687:ILE:CD1	1:C:1006:MET:SD	2.25	1.23
1:A:21:THR:HG22	1:C:200:ALA:CB	1.67	1.23
1:J:7:LEU:CD1	1:J:12:LYS:HD3	1.67	1.23
1:C:275:SER:OG	1:C:1047:LEU:HD13	1.32	1.22
1:C:275:SER:OG	1:C:1047:LEU:CD1	1.87	1.21
1:A:795:ASN:OD1	1:A:942:PHE:CE1	1.93	1.21
1:C:733:VAL:CG1	1:C:735:ASP:O	1.87	1.21
1:C:633:ARG:CZ	1:C:870:THR:HG21	1.67	1.21
3:Z:37:HIS:CD2	3:Z:40:LEU:CB	2.23	1.21
1:J:764:GLU:CB	1:J:765:PRO:CD	2.16	1.20
1:A:521:PHE:HZ	1:A:532:GLU:OE2	0.94	1.20
3:E:37:HIS:CD2	3:E:40:LEU:CB	2.15	1.20

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:6:113:GLU:O	2:6:124:ILE:HD13	1.41	1.20
3:Z:37:HIS:CE1	3:Z:39:VAL:CG1	2.25	1.19
1:J:790:PRO:HB2	1:J:942:PHE:CE2	1.76	1.19
1:C:27:ALA:HB1	1:C:35:LEU:HD21	1.21	1.19
1:J:687:ILE:HG21	1:J:1006:MET:HE3	1.21	1.18
1:A:475:MET:SD	1:A:1218:ARG:NH1	2.17	1.18
1:C:7:LEU:CD1	1:C:12:LYS:HD3	1.72	1.18
3:D:47:TYR:CE2	3:D:64:LEU:HD21	1.79	1.17
1:J:1172:CYS:SG	1:J:1261:PRO:CG	2.32	1.17
1:C:19:PHE:CE1	1:C:23:VAL:CA	2.20	1.17
1:C:472:GLU:OE1	1:C:1218:ARG:NH1	1.77	1.16
1:A:19:PHE:CZ	1:C:1088:LEU:HD13	1.54	1.16
1:C:489:GLY:C	1:C:763:ASP:OD2	1.84	1.16
1:C:633:ARG:NH2	1:C:870:THR:CG2	2.08	1.16
3:D:26:LEU:CD1	3:D:64:LEU:CD1	2.24	1.15
1:J:440:ILE:HD13	1:J:1108:VAL:CG1	1.70	1.15
1:J:21:THR:HG22	1:A:200:ALA:CA	1.75	1.15
1:J:35:LEU:HD12	1:A:115:MET:O	0.97	1.15
1:A:90:LYS:HD3	1:A:119:TYR:CE1	1.81	1.15
1:A:800:LEU:CD2	1:A:923:VAL:HG21	1.77	1.15
3:D:47:TYR:HE2	3:D:64:LEU:HD21	0.99	1.15
1:A:800:LEU:HD23	1:A:923:VAL:CG2	1.76	1.15
1:C:1035:THR:HG23	1:C:1176:LEU:CD1	1.66	1.15
1:J:41:ASP:OD1	1:J:45:ARG:NH1	1.80	1.14
1:A:284:MET:SD	1:A:291:ILE:HD13	1.88	1.14
1:C:514:GLN:CB	1:C:993:ARG:NH2	2.10	1.14
1:J:790:PRO:CB	1:J:942:PHE:CE2	2.31	1.14
1:C:790:PRO:CB	1:C:942:PHE:CD2	2.30	1.14
1:J:7:LEU:HD12	1:J:12:LYS:HD3	1.15	1.14
1:C:1285:TYR:CG	1:C:1317:LEU:HD21	1.83	1.14
1:C:203:ALA:HB2	1:C:207:LEU:HD21	1.14	1.13
1:J:440:ILE:CD1	1:J:1108:VAL:HG21	1.77	1.13
1:J:440:ILE:HD11	1:J:1108:VAL:CG1	1.73	1.13
1:J:718:PRO:HD3	1:J:786:LEU:HD21	1.25	1.13
1:C:9:LEU:HD11	1:C:45:ARG:HG2	1.23	1.13
3:Z:37:HIS:CD2	3:Z:40:LEU:HB2	1.81	1.12
3:D:26:LEU:HD11	3:D:64:LEU:CD1	1.77	1.13
1:C:790:PRO:HB2	1:C:942:PHE:CE2	1.83	1.12
2:5:253:ILE:HG21	2:5:271:LEU:HD23	1.28	1.12
1:A:913:ARG:NH1	1:A:981:HIS:CD2	2.17	1.12
1:A:424:LEU:HD23	1:A:577:GLU:OE2	1.46	1.12

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:790:PRO:HB2	1:A:942:PHE:CE2	1.83	1.11
1:J:193:VAL:CG1	1:J:1093:ASN:HD21	1.64	1.11
1:J:207:LEU:HD11	1:J:212:ARG:HG3	1.15	1.11
1:C:1035:THR:CG2	1:C:1176:LEU:HD11	1.78	1.11
1:J:790:PRO:CB	1:J:942:PHE:CD2	2.34	1.11
1:A:431:LEU:HD22	1:A:436:ALA:C	1.71	1.11
1:C:9:LEU:CD1	1:C:45:ARG:CG	2.29	1.11
1:C:1285:TYR:CD1	1:C:1317:LEU:CD2	2.34	1.11
1:J:193:VAL:HG21	1:J:1093:ASN:CG	1.69	1.10
1:A:388:ASN:OD1	1:A:1043:GLU:HA	1.51	1.10
1:A:534:HIS:CE1	1:A:1239:LEU:HD22	1.85	1.10
1:C:489:GLY:HA2	1:C:763:ASP:OD2	1.41	1.10
1:J:115:MET:O	1:C:35:LEU:HD12	0.93	1.10
1:C:795:ASN:OD1	1:C:942:PHE:CD1	2.04	1.10
3:Z:37:HIS:NE2	3:Z:39:VAL:HG13	1.65	1.10
1:J:723:LEU:HB2	1:J:772:ARG:NH2	1.67	1.09
1:C:1285:TYR:CZ	1:C:1317:LEU:CD1	2.34	1.09
1:A:790:PRO:CB	1:A:942:PHE:CE2	2.36	1.09
1:J:35:LEU:HD13	1:A:116:VAL:HG12	1.19	1.09
1:J:440:ILE:HD11	1:J:1108:VAL:CB	1.83	1.08
1:J:534:HIS:CD2	1:J:537:PHE:HD1	1.70	1.08
1:C:1285:TYR:CD1	1:C:1317:LEU:HD11	1.87	1.08
1:J:440:ILE:HD11	1:J:1108:VAL:HG21	1.21	1.08
1:A:193:VAL:HG11	1:A:1093:ASN:HD21	1.15	1.08
1:A:426:THR:CG2	1:A:442:PHE:HE2	1.66	1.08
3:Z:37:HIS:HD2	3:Z:40:LEU:HB2	0.96	1.08
1:J:22:HIS:CG	1:J:23:VAL:H	1.68	1.08
1:A:12:LYS:HE3	1:C:94:HIS:HB3	1.33	1.08
1:A:19:PHE:CZ	1:C:1088:LEU:CD1	2.23	1.07
1:A:1034:LEU:HD22	1:A:1173:GLU:OE2	1.54	1.07
1:C:1160:ASN:ND2	1:C:1298:ASP:H	1.51	1.07
1:A:764:GLU:CB	1:A:765:PRO:CD	2.31	1.07
1:C:9:LEU:HD11	1:C:45:ARG:CG	1.84	1.07
1:C:19:PHE:HE1	1:C:22:HIS:C	1.55	1.07
1:J:764:GLU:HG3	1:J:765:PRO:HD3	1.07	1.07
1:A:942:PHE:CZ	1:A:995:SER:HB3	1.88	1.07
1:C:19:PHE:CE1	1:C:23:VAL:HA	1.80	1.07
1:C:1285:TYR:CE1	1:C:1317:LEU:CD1	2.37	1.07
1:J:80:PHE:CE2	1:J:86:LEU:HD23	1.90	1.06
1:J:117:THR:HG21	1:C:2:GLU:OE2	1.54	1.06
1:A:431:LEU:CD2	1:A:436:ALA:C	2.24	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1285:TYR:CD2	1:C:1317:LEU:HD11	1.88	1.06
2:4:101:LYS:O	2:4:104:ASP:OD1	1.73	1.06
1:J:231:ASN:OD1	1:J:1098:TYR:CD1	2.08	1.06
1:J:598:LYS:HD2	1:J:1000:ASN:CB	1.85	1.06
3:D:26:LEU:HD11	3:D:64:LEU:HD11	1.14	1.06
1:J:538:ASP:OD1	1:J:555:ARG:CZ	2.04	1.06
1:A:790:PRO:CB	1:A:942:PHE:CD2	2.39	1.06
1:A:598:LYS:CD	1:A:792:MET:O	2.04	1.05
1:C:231:ASN:OD1	1:C:1098:TYR:CD1	2.09	1.05
1:J:207:LEU:CD1	1:J:212:ARG:HG3	1.85	1.05
1:C:440:ILE:HD12	1:C:1108:VAL:CG1	1.85	1.05
1:A:521:PHE:HE1	1:A:532:GLU:OE1	1.39	1.05
1:J:687:ILE:HG21	1:J:1006:MET:CE	1.87	1.05
1:A:668:PRO:HB2	1:A:672:PHE:HE2	1.21	1.05
1:C:7:LEU:HD12	1:C:12:LYS:HD3	1.31	1.05
1:J:21:THR:HG22	1:A:200:ALA:HA	1.10	1.04
1:J:41:ASP:OD1	1:J:45:ARG:CZ	2.05	1.04
1:J:723:LEU:HB2	1:J:772:ARG:HH21	1.20	1.04
1:C:508:THR:OG1	1:C:982:GLU:OE1	1.73	1.04
1:C:1341:ALA:O	1:C:1364:GLN:NE2	1.90	1.04
1:C:790:PRO:CB	1:C:942:PHE:CE2	2.39	1.04
1:C:203:ALA:HB2	1:C:207:LEU:CD2	1.81	1.03
1:J:27:ALA:HB1	1:J:35:LEU:HD21	1.37	1.03
1:A:90:LYS:CD	1:A:119:TYR:HE1	1.70	1.03
1:J:440:ILE:CD1	1:J:1108:VAL:CG2	2.34	1.03
1:A:426:THR:CG2	1:A:442:PHE:CE2	2.43	1.02
1:J:83:LEU:CD2	1:J:1080:ASN:ND2	2.22	1.02
1:A:90:LYS:HD3	1:A:119:TYR:HE1	0.90	1.02
1:C:942:PHE:CZ	1:C:995:SER:HB3	1.95	1.02
3:E:37:HIS:CE1	3:E:39:VAL:HG13	1.95	1.02
1:A:1105:ASP:OD2	1:A:1169:LYS:CB	2.07	1.01
1:C:766:LEU:HD22	1:C:891:LYS:HD2	1.37	1.01
1:J:41:ASP:OD1	1:J:45:ARG:NH2	1.93	1.01
1:C:203:ALA:HB1	1:C:207:LEU:HD21	1.04	1.01
1:J:41:ASP:CG	1:J:45:ARG:HH22	1.64	1.01
1:A:668:PRO:HB2	1:A:672:PHE:CE2	1.94	1.01
1:A:942:PHE:HZ	1:A:995:SER:HB3	1.21	1.01
1:A:1034:LEU:CD2	1:A:1173:GLU:OE2	2.08	1.01
1:C:633:ARG:HH22	1:C:870:THR:HG21	1.20	1.01
1:C:795:ASN:OD1	1:C:942:PHE:CE1	2.14	1.01
3:D:25:VAL:O	3:D:57:LYS:CE	2.09	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:7:LEU:HD11	1:A:12:LYS:HD3	1.43	1.01
1:C:764:GLU:HG3	1:C:765:PRO:HD3	1.01	1.01
1:J:35:LEU:HD13	1:A:116:VAL:CG1	1.90	1.01
1:A:27:ALA:HB1	1:A:35:LEU:CD2	1.91	1.01
1:C:489:GLY:O	1:C:763:ASP:OD1	1.79	1.01
1:J:764:GLU:HB3	1:J:765:PRO:HD2	1.01	1.00
1:C:440:ILE:HD12	1:C:1108:VAL:HG11	1.40	1.00
1:J:718:PRO:HD3	1:J:786:LEU:CD2	1.89	1.00
1:C:19:PHE:HE1	1:C:23:VAL:N	1.28	1.00
1:J:116:VAL:HG12	1:C:35:LEU:HD13	1.43	1.00
1:C:764:GLU:CB	1:C:765:PRO:HD3	1.85	1.00
2:4:77:LEU:HD12	2:4:114:PHE:CE1	1.97	1.00
1:A:7:LEU:CD1	1:A:12:LYS:HD3	1.92	0.99
3:D:25:VAL:O	3:D:57:LYS:HE3	1.62	0.99
1:A:426:THR:HG23	1:A:442:PHE:HE2	1.25	0.99
1:J:119:TYR:OH	1:C:2:GLU:OE2	1.78	0.99
1:J:21:THR:CG2	1:A:200:ALA:HA	1.92	0.99
1:J:116:VAL:CG1	1:C:35:LEU:HD13	1.93	0.99
1:A:193:VAL:HG21	1:A:1093:ASN:CG	1.81	0.99
1:A:630:PHE:CZ	1:A:879:LEU:CD2	2.46	0.99
1:C:514:GLN:HB2	1:C:993:ARG:HH21	1.20	0.99
1:C:942:PHE:CZ	1:C:995:SER:CB	2.45	0.98
1:C:1035:THR:HG21	1:C:1176:LEU:HD11	1.33	0.98
1:J:430:LEU:CD2	1:J:1325:LEU:O	2.11	0.98
1:A:1344:PHE:HB2	1:A:1364:GLN:NE2	1.77	0.98
1:C:27:ALA:CB	1:C:35:LEU:HD21	1.93	0.98
1:J:764:GLU:CB	1:J:765:PRO:HD3	1.82	0.98
1:C:27:ALA:HB1	1:C:35:LEU:CD2	1.93	0.98
1:J:231:ASN:OD1	1:J:1098:TYR:CE1	2.17	0.98
1:A:1102:VAL:HG23	1:A:1366:MET:HE1	1.46	0.98
1:C:231:ASN:ND2	1:C:1099:VAL:H	1.61	0.98
3:Z:37:HIS:HD2	3:Z:40:LEU:HB3	1.27	0.98
1:A:924:VAL:HG12	1:A:925:THR:HG23	1.43	0.97
1:C:275:SER:HG	1:C:1047:LEU:CD1	1.78	0.97
1:A:1328:THR:CG2	1:A:1353:ASN:OD1	2.12	0.97
1:C:1285:TYR:CG	1:C:1317:LEU:HD11	1.99	0.97
1:J:228:PHE:CD1	1:J:1099:VAL:HG23	1.99	0.97
1:A:764:GLU:HB3	1:A:765:PRO:HD3	0.97	0.97
1:C:800:LEU:CD2	1:C:923:VAL:HG21	1.93	0.97
1:J:388:ASN:OD1	1:J:1311:ILE:HG13	1.63	0.97
1:A:795:ASN:OD1	1:A:942:PHE:CD1	2.18	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:6:113:GLU:O	2:6:124:ILE:CD1	2.12	0.96
1:J:7:LEU:HD12	1:J:12:LYS:CD	1.95	0.96
1:C:9:LEU:CD1	1:C:45:ARG:HG3	1.93	0.96
3:D:26:LEU:HD13	3:D:64:LEU:CD1	1.94	0.96
1:A:1102:VAL:HG23	1:A:1366:MET:CE	1.95	0.96
1:C:764:GLU:HB3	1:C:765:PRO:HD2	0.99	0.96
1:A:668:PRO:O	1:A:672:PHE:HD2	1.36	0.96
1:A:90:LYS:CD	1:A:119:TYR:CE1	2.47	0.96
1:A:888:GLU:O	1:A:919:ASN:ND2	1.98	0.96
1:C:1285:TYR:CE2	1:C:1317:LEU:CD1	2.49	0.96
1:C:231:ASN:HD21	1:C:1099:VAL:N	1.62	0.95
3:E:37:HIS:HD2	3:E:40:LEU:HB2	1.32	0.95
1:J:684:VAL:HG22	1:J:1006:MET:SD	2.07	0.95
1:C:424:LEU:HD23	1:C:577:GLU:OE2	1.67	0.95
1:A:207:LEU:HD11	1:A:212:ARG:HG2	1.45	0.95
1:A:598:LYS:NZ	1:A:792:MET:O	2.00	0.95
1:A:790:PRO:HB3	1:A:942:PHE:HD2	1.25	0.95
1:A:598:LYS:HD3	1:A:792:MET:O	1.65	0.94
1:C:186:LYS:HZ1	1:C:1055:THR:CG2	1.65	0.94
1:J:22:HIS:CD2	1:J:23:VAL:H	1.85	0.94
1:J:604:PRO:HA	1:J:925:THR:HG21	1.50	0.94
1:A:193:VAL:HG21	1:A:1093:ASN:ND2	1.83	0.94
1:C:514:GLN:HB2	1:C:993:ARG:HH22	1.24	0.94
1:J:7:LEU:CD1	1:J:12:LYS:CD	2.46	0.94
1:J:440:ILE:CG1	1:J:1108:VAL:HG21	1.97	0.94
1:A:913:ARG:HH11	1:A:981:HIS:CD2	1.86	0.94
1:A:35:LEU:HD13	1:C:116:VAL:HG13	1.50	0.94
2:5:253:ILE:HG21	2:5:271:LEU:CD2	1.97	0.94
3:Z:37:HIS:CD2	3:Z:40:LEU:HB3	1.95	0.94
3:E:37:HIS:CD2	3:E:40:LEU:HB2	2.02	0.94
1:C:426:THR:O	1:C:442:PHE:CE2	2.21	0.93
1:J:193:VAL:HG11	1:J:1093:ASN:HD21	0.79	0.93
1:C:1160:ASN:OD1	1:C:1298:ASP:HB3	1.68	0.93
1:C:646:VAL:HG12	1:C:647:PHE:CD1	2.04	0.93
1:A:193:VAL:HG11	1:A:1093:ASN:ND2	1.81	0.93
1:J:231:ASN:HD21	1:J:1099:VAL:H	1.05	0.93
1:A:426:THR:HG23	1:A:442:PHE:CE2	2.02	0.93
1:J:1069:ARG:HH11	1:J:1069:ARG:HG3	1.34	0.93
1:A:193:VAL:HG21	1:A:1093:ASN:OD1	1.66	0.93
1:A:766:LEU:HD21	1:A:893:LEU:HD21	1.48	0.93
1:C:489:GLY:O	1:C:763:ASP:CG	2.06	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:481:CYS:SG	1:A:507:ARG:O	2.25	0.93
1:C:766:LEU:HD22	1:C:891:LYS:CD	1.99	0.93
3:Z:37:HIS:CE1	3:Z:39:VAL:HG12	2.00	0.92
1:A:1056:SER:OG	1:A:1084:VAL:HG22	1.69	0.92
1:A:21:THR:HG22	1:C:200:ALA:HA	0.93	0.92
1:C:231:ASN:OD1	1:C:1098:TYR:HD1	1.47	0.92
1:J:12:LYS:HE3	1:A:94:HIS:HB3	1.49	0.92
1:C:83:LEU:HD12	1:C:1058:ILE:HG22	1.49	0.92
1:C:1056:SER:OG	1:C:1084:VAL:CG2	2.18	0.92
1:C:1285:TYR:CD1	1:C:1317:LEU:CG	2.53	0.92
1:C:175:LEU:CD1	1:C:1081:ILE:HD11	1.99	0.92
1:J:193:VAL:HG21	1:J:1093:ASN:OD1	1.69	0.91
1:A:130:GLU:CD	1:A:1074:THR:HG22	1.90	0.91
1:A:764:GLU:CB	1:A:765:PRO:HD3	1.94	0.91
1:J:231:ASN:ND2	1:J:1099:VAL:H	1.67	0.91
1:C:1160:ASN:HD21	1:C:1298:ASP:H	1.18	0.91
1:A:426:THR:HG22	1:A:442:PHE:CE2	2.04	0.91
1:J:228:PHE:CE1	1:J:1099:VAL:CG2	2.53	0.91
1:C:598:LYS:HD2	1:C:1000:ASN:HD22	1.32	0.91
1:J:37:ILE:HG12	1:A:114:ILE:HG12	1.51	0.91
3:D:25:VAL:HG22	3:D:54:PHE:HE1	1.34	0.91
1:A:630:PHE:CE1	1:A:879:LEU:HD21	2.07	0.90
1:A:942:PHE:CZ	1:A:995:SER:CB	2.53	0.90
1:C:790:PRO:HB3	1:C:942:PHE:HD2	1.09	0.90
3:E:37:HIS:HD2	3:E:40:LEU:HB3	0.75	0.90
1:C:534:HIS:CE1	1:C:1239:LEU:HD22	2.06	0.90
1:C:1285:TYR:CD1	1:C:1317:LEU:CD1	2.55	0.90
1:J:534:HIS:CD2	1:J:537:PHE:CD1	2.60	0.90
1:A:733:VAL:HG22	1:A:738:PRO:HA	1.51	0.90
3:E:69:ALA:O	3:E:73:THR:HG23	1.71	0.90
1:A:744:ILE:O	1:A:765:PRO:HA	1.72	0.89
1:A:1105:ASP:OD2	1:A:1169:LYS:HB2	1.72	0.89
3:D:25:VAL:HG22	3:D:54:PHE:CE1	2.07	0.89
1:A:90:LYS:HG2	1:A:119:TYR:CD1	2.07	0.89
1:J:21:THR:HG22	1:A:200:ALA:CB	2.02	0.89
1:J:22:HIS:CD2	1:J:24:LYS:H	1.89	0.89
1:C:99:ARG:NH1	1:C:111:GLN:HB3	1.86	0.89
1:J:718:PRO:CD	1:J:786:LEU:HD21	2.02	0.89
1:J:732:VAL:HG12	1:J:739:LEU:HD12	1.54	0.89
1:C:7:LEU:HD11	1:C:12:LYS:HD3	1.54	0.89
1:A:207:LEU:HD13	1:A:212:ARG:HG3	1.53	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5:49:ARG:NH2	2:5:242:CYS:SG	2.45	0.89
1:J:723:LEU:CB	1:J:772:ARG:NH2	2.36	0.88
1:J:22:HIS:CG	1:J:23:VAL:N	2.41	0.88
1:C:524:VAL:HG22	1:C:1227:ALA:HB2	1.54	0.88
1:A:598:LYS:HE2	1:A:1000:ASN:ND2	1.86	0.88
1:J:790:PRO:HB3	1:J:942:PHE:HD2	1.32	0.88
1:A:388:ASN:OD1	1:A:1043:GLU:OE1	1.91	0.88
1:A:521:PHE:CE1	1:A:532:GLU:OE1	2.26	0.88
1:A:431:LEU:CD2	1:A:436:ALA:O	2.21	0.88
1:C:752:SER:OG	3:E:46:LYS:NZ	2.07	0.88
1:C:791:ALA:O	1:C:1000:ASN:OD1	1.90	0.88
1:J:1172:CYS:SG	1:J:1261:PRO:CD	2.62	0.87
1:A:1056:SER:OG	1:A:1084:VAL:CG2	2.23	0.87
1:J:7:LEU:O	1:J:12:LYS:NZ	2.07	0.87
3:D:25:VAL:C	3:D:57:LYS:HE3	1.95	0.87
1:J:1172:CYS:SG	1:J:1261:PRO:HD2	2.12	0.87
1:A:521:PHE:CE1	1:A:532:GLU:OE2	2.27	0.87
1:J:45:ARG:NH2	1:J:46:TYR:HE2	1.72	0.87
1:C:275:SER:OG	1:C:1047:LEU:HD12	1.74	0.87
1:C:733:VAL:HG11	1:C:735:ASP:O	1.72	0.87
2:6:166:ARG:HD3	2:6:186:LEU:HD11	1.57	0.87
1:A:130:GLU:OE2	1:A:1074:THR:HG22	1.75	0.86
1:A:913:ARG:NH1	1:A:981:HIS:NE2	2.22	0.86
3:E:37:HIS:CE1	3:E:39:VAL:CG1	2.58	0.86
1:J:1015:ILE:HG22	1:J:1015:ILE:O	1.73	0.86
1:C:1035:THR:HG23	1:C:1176:LEU:HD12	0.87	0.86
1:A:942:PHE:HZ	1:A:995:SER:CB	1.87	0.86
1:C:942:PHE:HZ	1:C:995:SER:CB	1.87	0.86
3:Z:69:ALA:O	3:Z:73:THR:HG23	1.73	0.86
1:J:45:ARG:CZ	1:J:46:TYR:HE2	1.88	0.86
1:C:489:GLY:O	1:C:763:ASP:OD2	1.91	0.86
1:J:430:LEU:HD23	1:J:1325:LEU:O	1.75	0.86
1:A:431:LEU:HD23	1:A:436:ALA:O	1.75	0.86
1:C:790:PRO:HB2	1:C:942:PHE:HE2	1.36	0.86
2:6:246:ASP:CG	2:6:281:SER:HB2	1.96	0.86
1:J:440:ILE:HD13	1:J:1108:VAL:HG11	0.87	0.86
1:A:193:VAL:CG1	1:A:1093:ASN:HD21	1.89	0.86
1:C:83:LEU:CD1	1:C:1058:ILE:HG22	2.05	0.86
1:A:662:ALA:HA	1:A:671:LEU:HD11	1.54	0.85
1:J:118:LYS:HD3	1:C:32:PHE:CE1	2.11	0.85
1:A:687:ILE:HD12	1:A:1006:MET:SD	2.15	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:694:ASN:HD22	1:A:704:SER:HB3	1.40	0.85
1:A:21:THR:CG2	1:C:200:ALA:CB	2.53	0.85
3:Z:37:HIS:CE1	3:Z:39:VAL:HG13	2.02	0.85
1:J:756:ARG:NH2	1:J:886:VAL:O	2.10	0.85
1:J:1069:ARG:O	1:J:1071:ILE:N	2.08	0.85
1:A:270:SER:OG	1:A:365:LYS:HG2	1.76	0.85
1:J:1244:TYR:HB2	1:J:1266:PHE:HD2	1.42	0.85
1:A:749:HIS:NE2	1:A:769:ASP:OD1	2.10	0.85
1:C:756:ARG:NH2	1:C:886:VAL:O	2.10	0.85
1:A:1015:ILE:O	1:A:1015:ILE:HG22	1.77	0.84
1:A:1212:LYS:HG2	1:A:1216:ASP:OD2	1.76	0.84
2:5:140:VAL:O	2:5:140:VAL:HG12	1.74	0.84
3:D:26:LEU:CD1	3:D:64:LEU:HD12	2.05	0.84
2:5:253:ILE:CG2	2:5:271:LEU:HD23	2.08	0.84
2:6:19:PHE:CE2	2:6:26:LYS:NZ	2.45	0.84
1:C:733:VAL:HG22	1:C:738:PRO:HA	1.58	0.84
1:A:536:PHE:CD1	1:A:1015:ILE:HG21	2.13	0.84
1:C:888:GLU:O	1:C:919:ASN:ND2	2.10	0.84
3:E:37:HIS:NE2	3:E:39:VAL:HG13	1.92	0.84
1:A:19:PHE:HZ	1:C:1088:LEU:HD13	1.36	0.84
2:5:253:ILE:CG2	2:5:271:LEU:CD2	2.55	0.84
1:C:231:ASN:HD21	1:C:1099:VAL:H	0.84	0.84
1:J:181:GLN:NE2	1:J:384:PRO:HB3	1.93	0.83
1:A:231:ASN:HD21	1:A:1099:VAL:H	1.26	0.83
1:C:1285:TYR:CG	1:C:1317:LEU:CD2	2.60	0.83
1:C:662:ALA:HA	1:C:671:LEU:HD11	1.61	0.83
1:A:715:LEU:HA	1:A:914:GLN:HE22	1.41	0.83
2:4:239:LEU:O	2:4:251:ARG:NH1	2.11	0.83
1:A:207:LEU:CD1	1:A:212:ARG:CG	2.19	0.83
1:A:388:ASN:ND2	1:A:1043:GLU:OE2	2.12	0.83
1:A:534:HIS:HE1	1:A:1239:LEU:HD22	1.44	0.83
1:J:231:ASN:HD21	1:J:1099:VAL:N	1.75	0.83
1:A:130:GLU:OE2	1:A:1074:THR:CG2	2.26	0.82
1:J:36:ARG:NH2	1:A:115:MET:CE	2.42	0.82
1:J:1327:THR:HG22	1:J:1355:VAL:HG13	1.61	0.82
1:J:440:ILE:HD11	1:J:1108:VAL:HG22	1.61	0.82
1:A:388:ASN:HD21	1:A:1043:GLU:CD	1.83	0.82
1:C:764:GLU:HG3	1:C:765:PRO:CD	1.98	0.82
2:5:140:VAL:HG21	2:5:158:HIS:NE2	1.95	0.82
1:J:723:LEU:CG	1:J:772:ARG:NH2	2.42	0.82
1:C:627:ILE:HD11	1:C:882:ALA:HB2	1.62	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:448:THR:CG2	1:J:1111:GLN:O	2.27	0.82
1:A:534:HIS:CE1	1:A:1239:LEU:HD13	2.15	0.82
2:5:267:LEU:O	2:5:271:LEU:HG	1.79	0.82
1:J:718:PRO:CD	1:J:786:LEU:CD2	2.58	0.81
1:A:27:ALA:HB1	1:A:35:LEU:HD21	1.62	0.81
1:C:433:ARG:NH1	1:C:1166:HIS:O	2.14	0.81
2:6:49:ARG:HH22	2:6:242:CYS:HB2	1.44	0.81
1:J:344:LEU:HD21	1:J:1086:MET:SD	2.20	0.81
1:J:799:GLY:O	1:J:937:VAL:HG13	1.81	0.81
3:D:26:LEU:CD1	3:D:64:LEU:HD11	1.94	0.81
3:D:47:TYR:HE2	3:D:64:LEU:CD2	1.87	0.81
1:J:2:GLU:OE1	1:A:90:LYS:NZ	2.12	0.81
1:A:668:PRO:O	1:A:672:PHE:CE2	2.33	0.81
1:A:1016:SER:O	1:A:1019:SER:OG	1.97	0.81
1:J:36:ARG:NH2	1:A:115:MET:HE1	1.95	0.81
1:J:228:PHE:CD1	1:J:1099:VAL:CG2	2.64	0.81
1:C:633:ARG:HH22	1:C:870:THR:CG2	1.78	0.81
1:C:1285:TYR:CB	1:C:1317:LEU:HD21	2.11	0.81
1:J:207:LEU:HD11	1:J:212:ARG:CG	2.04	0.80
1:J:181:GLN:HE22	1:J:384:PRO:HB3	1.46	0.80
1:A:207:LEU:HD11	1:A:212:ARG:HG3	0.89	0.80
3:D:26:LEU:HD13	3:D:64:LEU:HD12	1.61	0.80
1:J:193:VAL:HG21	1:J:1093:ASN:ND2	1.96	0.80
1:J:785:TYR:O	1:J:943:TYR:OH	1.97	0.80
1:J:1239:LEU:O	1:J:1239:LEU:HD12	1.82	0.80
3:E:37:HIS:CD2	3:E:40:LEU:H	1.99	0.80
1:C:1285:TYR:HD1	1:C:1317:LEU:HD21	1.41	0.80
1:J:228:PHE:CZ	1:J:1099:VAL:HG21	2.15	0.80
1:C:9:LEU:HD13	1:C:45:ARG:HG3	1.64	0.80
2:6:19:PHE:HE2	2:6:26:LYS:NZ	1.79	0.80
1:A:231:ASN:OD1	1:A:1098:TYR:CD1	2.35	0.80
2:5:156:PHE:HB3	2:5:159:LEU:HD12	1.64	0.80
1:A:130:GLU:CG	1:A:1074:THR:HG22	2.12	0.79
1:A:1092:SER:O	1:A:1093:ASN:OD1	2.00	0.79
3:E:24:VAL:O	3:E:57:LYS:NZ	2.14	0.79
1:A:426:THR:HG22	1:A:442:PHE:CD2	2.17	0.79
1:C:9:LEU:HD12	1:C:45:ARG:HD2	1.63	0.79
1:C:800:LEU:HG	1:C:923:VAL:HG21	1.64	0.79
1:C:1064:VAL:HG22	1:C:1077:VAL:HG12	1.64	0.79
1:J:118:LYS:NZ	1:C:32:PHE:CE1	2.50	0.79
1:A:601:VAL:HG12	1:A:793:THR:HG22	1.63	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1067:GLU:OE1	1:C:1076:HIS:NE2	2.15	0.79
1:C:1160:ASN:ND2	1:C:1298:ASP:N	2.29	0.79
1:J:18:ASP:O	1:J:19:PHE:CD1	2.36	0.79
1:J:687:ILE:CG2	1:J:1006:MET:CE	2.60	0.79
1:C:764:GLU:CG	1:C:765:PRO:CD	2.47	0.79
1:C:800:LEU:CG	1:C:923:VAL:HG21	2.13	0.79
1:A:1105:ASP:OD2	1:A:1169:LYS:HB3	1.81	0.78
1:C:1015:ILE:O	1:C:1015:ILE:HG22	1.80	0.78
2:4:181:VAL:HG12	2:4:183:PRO:HD3	1.63	0.78
3:D:43:MET:CE	3:D:67:MET:HG3	2.14	0.78
1:A:9:LEU:CD1	1:A:45:ARG:HG3	2.13	0.78
1:C:275:SER:HG	1:C:1047:LEU:HD13	1.35	0.78
1:A:747:ARG:NE	1:A:749:HIS:HE1	1.80	0.78
1:C:207:LEU:HD22	1:C:211:GLN:OE1	1.84	0.78
1:C:733:VAL:HG12	1:C:735:ASP:O	1.81	0.78
1:J:723:LEU:CB	1:J:772:ARG:HH21	1.96	0.78
1:A:747:ARG:NE	1:A:749:HIS:CE1	2.52	0.78
1:A:212:ARG:CZ	1:A:1204:PRO:HD3	2.12	0.78
1:A:521:PHE:CE1	1:A:532:GLU:CD	2.57	0.78
1:A:800:LEU:HD23	1:A:923:VAL:HG21	0.86	0.78
1:C:472:GLU:OE1	1:C:1218:ARG:CZ	2.31	0.78
1:C:942:PHE:HZ	1:C:995:SER:HB2	1.47	0.78
1:J:601:VAL:HG12	1:J:793:THR:HG22	1.66	0.78
1:A:400:TYR:HE1	1:A:573:LEU:HD12	1.48	0.78
2:5:88:ALA:HB2	2:5:109:LEU:HD22	1.64	0.78
1:C:1285:TYR:CD2	1:C:1317:LEU:CD1	2.67	0.78
1:J:534:HIS:HD2	1:J:537:PHE:HD1	1.27	0.77
2:6:248:ASN:O	2:6:252:ASN:ND2	2.18	0.77
1:J:94:HIS:HB3	1:C:12:LYS:HE3	1.66	0.77
2:4:69:HIS:O	2:4:179:PHE:CE1	2.37	0.77
1:C:1244:TYR:HB2	1:C:1266:PHE:HD2	1.47	0.77
3:D:47:TYR:CE2	3:D:64:LEU:CD2	2.64	0.77
1:A:231:ASN:OD1	1:A:1098:TYR:CE1	2.38	0.77
2:6:166:ARG:HD3	2:6:186:LEU:CD1	2.14	0.77
1:C:186:LYS:HZ2	1:C:1055:THR:HG21	0.87	0.77
1:C:431:LEU:HD23	1:C:437:VAL:HA	1.65	0.77
1:J:45:ARG:CZ	1:J:46:TYR:CE2	2.67	0.77
1:A:668:PRO:C	1:A:672:PHE:CD2	2.58	0.77
1:A:795:ASN:OD1	1:A:942:PHE:CZ	2.37	0.77
1:J:315:ALA:HB2	1:J:321:ILE:HD11	1.66	0.76
1:A:431:LEU:HD23	1:A:437:VAL:HA	1.66	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:231:ASN:OD1	1:C:1098:TYR:CE1	2.38	0.76
1:J:22:HIS:HD2	1:J:24:LYS:H	1.33	0.76
1:C:203:ALA:HB1	1:C:207:LEU:HD23	1.62	0.76
1:A:130:GLU:HG2	1:A:1074:THR:HA	1.67	0.76
1:J:888:GLU:O	1:J:919:ASN:ND2	2.19	0.76
1:J:1044:VAL:HG11	1:J:1096:VAL:CG1	2.15	0.76
1:C:1044:VAL:HG11	1:C:1096:VAL:HG13	1.66	0.76
1:C:1285:TYR:CE1	1:C:1317:LEU:CG	2.69	0.76
1:A:130:GLU:HG2	1:A:1074:THR:HG22	1.66	0.76
2:4:77:LEU:CD1	2:4:114:PHE:CD1	2.49	0.76
3:D:25:VAL:O	3:D:57:LYS:HE2	1.85	0.75
1:A:790:PRO:HB2	1:A:942:PHE:HE2	1.45	0.75
1:C:175:LEU:CD1	1:C:1081:ILE:CD1	2.63	0.75
1:J:27:ALA:HB1	1:J:35:LEU:CD2	2.16	0.75
1:J:119:TYR:CZ	1:C:2:GLU:OE2	2.40	0.75
1:J:388:ASN:OD1	1:J:1311:ILE:CG1	2.33	0.75
1:J:1092:SER:O	1:J:1093:ASN:OD1	2.05	0.75
1:A:785:TYR:O	1:A:943:TYR:OH	2.04	0.75
1:A:795:ASN:CG	1:A:942:PHE:CE1	2.59	0.75
2:4:69:HIS:O	2:4:179:PHE:HE1	1.67	0.75
1:J:275:SER:HB3	1:J:1047:LEU:HD13	1.68	0.75
1:J:983:TYR:O	1:J:988:ARG:NH2	2.20	0.75
1:J:80:PHE:CE2	1:J:86:LEU:CD2	2.70	0.75
1:J:130:GLU:HB3	1:J:1074:THR:HG22	1.68	0.75
1:C:924:VAL:HG12	1:C:925:THR:HG23	1.69	0.75
1:A:521:PHE:CZ	1:A:532:GLU:CD	2.59	0.74
1:C:1160:ASN:HD21	1:C:1298:ASP:N	1.83	0.74
1:A:448:THR:CG2	1:A:1111:GLN:O	2.35	0.74
1:A:753:ASP:O	1:A:757:LEU:HG	1.87	0.74
1:C:764:GLU:CB	1:C:765:PRO:HD2	1.92	0.74
1:C:942:PHE:HE1	1:C:992:SER:HA	1.52	0.74
1:C:1044:VAL:HG22	1:C:1099:VAL:CG2	2.18	0.74
2:4:77:LEU:HD12	2:4:114:PHE:CZ	2.23	0.74
1:C:186:LYS:HZ3	1:C:1055:THR:HG21	1.50	0.74
1:C:633:ARG:CZ	1:C:870:THR:CG2	2.59	0.74
1:J:344:LEU:CD2	1:J:1086:MET:SD	2.76	0.74
1:A:79:LYS:NZ	1:A:1061:ASN:OD1	2.19	0.74
1:A:424:LEU:HD23	1:A:577:GLU:CD	2.06	0.74
1:A:20:LEU:HD13	1:C:197:VAL:HG22	1.70	0.74
1:A:284:MET:SD	1:A:291:ILE:CD1	2.74	0.74
1:A:388:ASN:ND2	1:A:1043:GLU:CD	2.40	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1160:ASN:CG	1:C:1298:ASP:H	1.89	0.74
2:4:178:MET:HB2	2:4:213:VAL:HG13	1.70	0.74
2:5:253:ILE:HG22	2:5:271:LEU:HD21	1.68	0.73
1:J:118:LYS:NZ	1:C:32:PHE:HE1	1.84	0.73
1:J:1175:ILE:HB	1:J:1239:LEU:HD21	1.69	0.73
1:A:431:LEU:CD2	1:A:437:VAL:HA	2.18	0.73
1:C:1172:CYS:SG	1:C:1173:GLU:N	2.61	0.73
1:C:798:CYS:O	1:C:923:VAL:HB	1.89	0.73
2:6:167:ILE:HG22	2:6:184:LEU:CD1	2.17	0.73
1:C:1195:ARG:NH1	1:C:1227:ALA:O	2.21	0.73
1:A:534:HIS:CE1	1:A:1239:LEU:CD2	2.67	0.73
3:D:25:VAL:CG2	3:D:54:PHE:HE1	2.00	0.73
1:A:1179:VAL:O	1:A:1179:VAL:HG12	1.87	0.73
1:J:193:VAL:CG1	1:J:1093:ASN:ND2	2.32	0.73
1:C:263:THR:HB	1:C:267:ALA:HB3	1.69	0.73
1:J:80:PHE:HE2	1:J:86:LEU:HD23	1.48	0.73
1:A:598:LYS:HZ2	1:A:793:THR:HA	1.52	0.73
1:C:733:VAL:HG13	1:C:735:ASP:O	1.86	0.73
1:C:1056:SER:OG	1:C:1084:VAL:HG23	1.86	0.73
1:J:638:MET:SD	1:J:642:ARG:NH2	2.61	0.72
1:C:388:ASN:OD1	1:C:1043:GLU:OE1	2.06	0.72
1:A:9:LEU:HD11	1:A:45:ARG:HG2	1.70	0.72
1:A:967:HIS:CD2	1:A:967:HIS:O	2.43	0.72
1:J:1069:ARG:HG3	1:J:1069:ARG:NH1	2.00	0.72
3:D:25:VAL:CA	3:D:57:LYS:HE3	2.19	0.72
1:C:8:GLU:HB2	1:C:45:ARG:HD3	1.71	0.72
1:C:231:ASN:ND2	1:C:1099:VAL:HB	2.05	0.72
1:C:1285:TYR:CG	1:C:1317:LEU:CD1	2.72	0.72
1:J:598:LYS:HD2	1:J:1000:ASN:HB3	1.71	0.72
1:A:440:ILE:HB	1:A:1108:VAL:HG11	1.70	0.72
1:J:710:LEU:HD12	1:J:1012:LEU:CD1	2.20	0.72
1:C:800:LEU:HD12	1:C:800:LEU:O	1.90	0.72
1:C:1327:THR:HG22	1:C:1355:VAL:HG13	1.71	0.72
2:6:170:ASN:HD22	2:6:184:LEU:CD2	2.02	0.72
1:J:800:LEU:CD2	1:J:923:VAL:HG21	2.20	0.72
1:J:1174:LEU:O	1:J:1176:LEU:HG	1.90	0.72
1:A:598:LYS:CE	1:A:792:MET:O	2.38	0.72
1:A:668:PRO:C	1:A:672:PHE:CE2	2.64	0.72
1:A:1102:VAL:CG2	1:A:1366:MET:CE	2.68	0.72
3:E:45:SER:O	3:E:49:ARG:NH1	2.23	0.72
1:A:1205:TYR:HE2	1:A:1277:THR:HG23	1.55	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:942:PHE:CE1	1:C:992:SER:HA	2.25	0.71
1:C:698:LEU:HB2	1:C:706:TYR:HE2	1.54	0.71
1:C:1148:ILE:O	1:C:1152:THR:OG1	2.06	0.71
1:J:19:PHE:CE2	1:A:1088:LEU:HD22	1.99	0.71
1:J:430:LEU:HD22	1:J:1325:LEU:O	1.89	0.71
1:C:431:LEU:HG	1:C:1333:MET:CE	2.20	0.71
1:C:524:VAL:CG2	1:C:1227:ALA:HB2	2.19	0.71
1:J:727:MET:HB2	1:J:730:VAL:HB	1.73	0.71
1:J:800:LEU:HA	1:J:937:VAL:HG12	1.72	0.71
1:J:1044:VAL:HG11	1:J:1096:VAL:HG12	1.73	0.71
1:A:35:LEU:HD13	1:C:116:VAL:CG1	2.21	0.71
1:A:1034:LEU:HD21	1:A:1173:GLU:OE2	1.91	0.71
1:C:1035:THR:HG21	1:C:1176:LEU:HD13	1.70	0.71
1:J:27:ALA:CB	1:J:35:LEU:HD21	2.18	0.71
1:A:1064:VAL:HG22	1:A:1077:VAL:HG12	1.73	0.71
1:J:231:ASN:OD1	1:J:1098:TYR:HD1	1.73	0.71
1:J:534:HIS:HD2	1:J:537:PHE:CD1	2.06	0.71
1:J:207:LEU:HB2	1:J:211:GLN:HB2	1.72	0.71
1:A:942:PHE:CE1	1:A:992:SER:HA	2.25	0.71
1:C:426:THR:CA	1:C:442:PHE:HE2	2.03	0.70
1:J:116:VAL:HG13	1:C:35:LEU:HD13	1.73	0.70
1:A:7:LEU:O	1:A:12:LYS:NZ	2.24	0.70
1:J:487:PRO:O	1:J:494:ARG:NH2	2.24	0.70
1:A:764:GLU:CB	1:A:765:PRO:HD2	2.20	0.70
1:A:967:HIS:CD2	1:A:969:HIS:HE1	2.09	0.70
3:E:37:HIS:CD2	3:E:40:LEU:N	2.59	0.70
1:J:41:ASP:CG	1:J:45:ARG:HH12	1.95	0.70
1:A:945:ASN:HD22	1:A:948:ILE:HD13	1.56	0.70
1:C:510:ASN:OD1	1:C:982:GLU:OE2	2.09	0.70
2:5:253:ILE:CG2	2:5:271:LEU:HD21	2.21	0.70
1:J:435:ARG:HG3	1:J:1367:LEU:HD13	1.73	0.70
1:A:534:HIS:ND1	1:A:1239:LEU:HD22	2.06	0.70
1:A:601:VAL:CG1	1:A:793:THR:HG22	2.21	0.70
3:Z:37:HIS:CD2	3:Z:40:LEU:N	2.59	0.70
1:J:895:VAL:HB	1:J:914:GLN:HB2	1.74	0.70
1:A:9:LEU:HD11	1:A:45:ARG:CG	2.21	0.70
2:6:156:PHE:HB3	2:6:159:LEU:HD12	1.73	0.70
1:A:942:PHE:HE1	1:A:992:SER:HA	1.56	0.70
1:C:983:TYR:O	1:C:988:ARG:NH2	2.25	0.70
1:J:83:LEU:HD12	1:J:1058:ILE:HG22	1.74	0.70
1:J:146:THR:O	1:J:149:ASP:N	2.25	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:274:VAL:HG11	1:J:372:LEU:HD12	1.74	0.70
1:J:693:LEU:HD11	1:J:1026:ALA:HB2	1.73	0.70
1:C:489:GLY:HA3	1:C:763:ASP:OD2	1.87	0.70
1:C:1336:LYS:NZ	1:C:1346:THR:O	2.25	0.70
1:J:733:VAL:HG22	1:J:738:PRO:HA	1.74	0.70
1:C:27:ALA:CB	1:C:35:LEU:CD2	2.62	0.70
1:C:343:SER:HA	1:C:346:GLN:HB2	1.72	0.70
1:A:380:ASP:OD1	1:A:380:ASP:O	2.10	0.69
2:6:26:LYS:HE2	2:6:34:HIS:NE2	2.05	0.69
1:A:487:PRO:O	1:A:494:ARG:NH2	2.25	0.69
1:A:668:PRO:CB	1:A:672:PHE:HE2	2.03	0.69
1:C:766:LEU:CD2	1:C:891:LYS:CD	2.70	0.69
1:J:45:ARG:NE	1:J:46:TYR:CE2	2.60	0.69
1:J:662:ALA:HA	1:J:671:LEU:HD11	1.73	0.69
1:J:800:LEU:HD21	1:J:923:VAL:HG21	1.73	0.69
1:C:1044:VAL:HG11	1:C:1096:VAL:CG1	2.22	0.69
2:4:101:LYS:O	2:4:104:ASP:CG	2.29	0.69
1:A:9:LEU:CD1	1:A:45:ARG:CG	2.70	0.69
1:A:727:MET:HB2	1:A:730:VAL:HB	1.73	0.69
3:Z:37:HIS:NE2	3:Z:39:VAL:CG1	2.40	0.69
1:A:1102:VAL:HG23	1:A:1366:MET:HE2	1.74	0.69
1:C:737:GLN:HE22	2:4:143:THR:H	1.40	0.69
3:Z:37:HIS:CD2	3:Z:40:LEU:H	2.11	0.69
1:J:628:ARG:HH21	3:Z:75:ARG:HH22	1.41	0.69
3:Z:19:ARG:O	3:Z:23:ASN:HB2	1.93	0.69
1:J:118:LYS:HZ2	1:C:32:PHE:HE1	1.27	0.69
1:A:454:LEU:HD12	1:A:1239:LEU:HD11	1.73	0.69
1:A:798:CYS:O	1:A:923:VAL:HB	1.92	0.69
1:C:447:LYS:HD2	1:C:1112:ASP:HB3	1.73	0.69
1:J:445:ALA:HA	1:J:1110:VAL:HG21	1.73	0.69
1:J:970:ASP:OD2	1:J:993:ARG:NH2	2.24	0.69
1:J:597:PHE:CE1	1:J:601:VAL:HG21	2.28	0.68
1:J:99:ARG:NH1	1:J:111:GLN:HB3	2.07	0.68
1:J:440:ILE:CG1	1:J:1108:VAL:HG11	2.18	0.68
1:A:36:ARG:NH2	1:A:42:ASP:OD2	2.26	0.68
1:A:1344:PHE:H	1:A:1364:GLN:NE2	1.91	0.68
1:C:942:PHE:CZ	1:C:995:SER:HB2	2.22	0.68
1:J:18:ASP:O	1:J:19:PHE:HD1	1.73	0.68
1:J:440:ILE:HG13	1:J:1108:VAL:HG21	1.74	0.68
2:6:26:LYS:HE2	2:6:34:HIS:CE1	2.28	0.68
3:D:43:MET:HE2	3:D:67:MET:HG3	1.73	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:102:SER:HB3	1:J:108:THR:HG22	1.75	0.68
1:A:263:THR:HB	1:A:267:ALA:HB3	1.75	0.68
1:J:1034:LEU:HG	1:J:1173:GLU:OE2	1.93	0.68
1:C:718:PRO:HD3	1:C:786:LEU:HD21	1.73	0.68
1:J:601:VAL:CG1	1:J:793:THR:HG22	2.23	0.68
1:J:1244:TYR:HB2	1:J:1266:PHE:CD2	2.28	0.68
1:C:598:LYS:CD	1:C:1000:ASN:HD22	2.06	0.68
1:C:819:LEU:HD11	3:E:32:ILE:HD12	1.74	0.68
1:C:895:VAL:HB	1:C:914:GLN:HB2	1.74	0.68
2:5:73:LEU:HD23	2:5:210:ILE:HD13	1.75	0.68
1:C:440:ILE:HD12	1:C:1108:VAL:HG12	1.72	0.68
1:J:538:ASP:OD1	1:J:555:ARG:NE	2.27	0.68
1:J:723:LEU:CG	1:J:772:ARG:HH22	2.04	0.68
1:J:723:LEU:HD12	1:J:772:ARG:NH2	2.09	0.68
3:E:68:VAL:O	3:E:71:SER:OG	2.07	0.68
1:J:941:ARG:HG3	1:J:992:SER:HB3	1.75	0.68
1:J:1195:ARG:NH1	1:J:1227:ALA:O	2.27	0.68
1:J:118:LYS:HD3	1:C:32:PHE:HE1	1.59	0.67
1:A:647:PHE:HD2	1:A:653:LEU:HD13	1.58	0.67
1:C:601:VAL:HG12	1:C:793:THR:HG22	1.75	0.67
1:C:718:PRO:HD3	1:C:786:LEU:CD2	2.24	0.67
1:C:130:GLU:HB3	1:C:1074:THR:HG22	1.76	0.67
1:J:942:PHE:HE1	1:J:992:SER:HA	1.59	0.67
1:A:21:THR:CG2	1:C:200:ALA:CA	2.35	0.67
1:A:908:PRO:HG3	1:A:1123:ARG:HH12	1.59	0.67
1:C:785:TYR:O	1:C:943:TYR:OH	2.07	0.67
1:C:532:GLU:OE2	1:C:555:ARG:NH1	2.27	0.67
1:J:748:HIS:O	1:J:756:ARG:NH1	2.28	0.67
1:C:536:PHE:CD1	1:C:1015:ILE:HG21	2.30	0.67
3:E:29:PRO:HG2	3:E:32:ILE:HG12	1.74	0.67
1:J:942:PHE:CZ	1:J:995:SER:CB	2.78	0.67
1:A:431:LEU:CD2	1:A:437:VAL:N	2.58	0.67
1:A:741:PRO:HB2	1:A:744:ILE:HG13	1.76	0.67
1:J:115:MET:O	1:C:35:LEU:HD13	1.90	0.67
1:J:790:PRO:HB2	1:J:942:PHE:HE2	1.53	0.67
1:C:999:PRO:O	1:C:1004:SER:OG	2.05	0.67
2:6:167:ILE:HG22	2:6:184:LEU:HD13	1.76	0.67
1:A:231:ASN:ND2	1:A:1099:VAL:H	1.93	0.67
1:C:514:GLN:HB3	1:C:993:ARG:NH2	2.10	0.67
1:J:433:ARG:NH1	1:J:1166:HIS:O	2.28	0.67
1:C:8:GLU:HB2	1:C:45:ARG:CD	2.25	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:646:VAL:HG12	1:C:647:PHE:N	2.10	0.67
1:C:1221:ASP:OD1	1:C:1222:ALA:N	2.27	0.67
2:5:140:VAL:O	2:5:140:VAL:CG1	2.43	0.66
1:A:747:ARG:CD	1:A:749:HIS:CE1	2.77	0.66
2:5:267:LEU:HG	2:5:271:LEU:HD11	1.76	0.66
3:D:39:VAL:O	3:D:43:MET:HG2	1.94	0.66
1:J:35:LEU:CD1	1:A:116:VAL:HG12	2.12	0.66
1:J:118:LYS:CD	1:C:32:PHE:CE1	2.78	0.66
1:C:19:PHE:CE1	1:C:22:HIS:C	2.45	0.66
1:C:1285:TYR:CE1	1:C:1317:LEU:HG	2.31	0.66
1:C:435:ARG:HG3	1:C:1367:LEU:HD13	1.78	0.66
1:C:514:GLN:CB	1:C:993:ARG:HH22	1.90	0.66
2:4:137:LYS:HB3	2:4:142:GLU:HB2	1.78	0.66
1:A:93:PHE:HE1	1:A:118:LYS:HG2	1.60	0.66
1:A:130:GLU:HG2	1:A:1074:THR:CA	2.26	0.66
2:5:267:LEU:HG	2:5:271:LEU:CD1	2.25	0.66
1:C:800:LEU:HD12	1:C:800:LEU:C	2.16	0.66
1:J:1044:VAL:HG22	1:J:1099:VAL:HG22	1.77	0.66
1:A:1048:LEU:HD12	1:A:1094:THR:HG22	1.78	0.66
1:C:812:PHE:HB2	3:E:65:LEU:HD21	1.78	0.66
1:J:207:LEU:HD12	1:J:207:LEU:O	1.96	0.66
1:J:518:VAL:HG11	1:J:567:PRO:HG3	1.76	0.66
1:C:186:LYS:HZ2	1:C:1055:THR:CG2	1.81	0.66
1:J:430:LEU:HD21	1:J:1326:SER:HB2	1.78	0.66
1:J:849:GLN:HB2	1:J:873:LEU:HD13	1.77	0.66
1:A:431:LEU:HD22	1:A:436:ALA:CA	2.26	0.66
1:A:502:ARG:HD3	1:A:962:GLU:HG3	1.78	0.66
1:A:1291:ASP:OD2	1:A:1313:ASN:ND2	2.27	0.66
1:C:782:LYS:O	1:C:786:LEU:HB2	1.96	0.66
1:C:1214:ILE:HD13	1:C:1268:THR:HG23	1.78	0.66
1:J:274:VAL:HG12	1:J:385:LEU:HD11	1.77	0.65
1:J:723:LEU:HG	1:J:772:ARG:NH2	2.10	0.65
1:C:440:ILE:CD1	1:C:1108:VAL:HG11	2.24	0.65
2:4:104:ASP:OD1	2:4:105:HIS:N	2.30	0.65
1:J:647:PHE:HD2	1:J:653:LEU:HD13	1.61	0.65
1:A:212:ARG:HH12	1:A:1204:PRO:HG3	1.60	0.65
1:J:275:SER:HB3	1:J:1047:LEU:CD1	2.25	0.65
1:A:1290:LYS:HB3	1:A:1310:LEU:HB3	1.76	0.65
1:A:311:ASN:HB3	1:A:321:ILE:HD12	1.78	0.65
1:C:598:LYS:HD3	1:C:1000:ASN:CB	2.26	0.65
1:C:687:ILE:HD13	1:C:1006:MET:SD	2.32	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:36:ARG:NH2	1:A:115:MET:HE3	2.11	0.65
1:J:710:LEU:HD12	1:J:1012:LEU:HD12	1.76	0.65
1:J:862:GLU:HG3	1:J:863:ASP:H	1.61	0.65
1:J:723:LEU:HG	1:J:772:ARG:HH22	1.61	0.65
1:A:21:THR:HG22	1:C:200:ALA:HB2	1.74	0.65
1:A:388:ASN:OD1	1:A:1043:GLU:CD	2.34	0.65
1:C:1285:TYR:HB2	1:C:1317:LEU:CD2	2.26	0.65
1:A:193:VAL:CG2	1:A:1093:ASN:ND2	2.59	0.65
1:A:800:LEU:HD12	1:A:800:LEU:C	2.17	0.65
1:A:1056:SER:HG	1:A:1084:VAL:HG22	1.60	0.65
1:C:617:VAL:HG12	1:C:619:GLY:H	1.62	0.65
1:A:443:VAL:O	1:A:446:LEU:HB2	1.97	0.64
1:C:508:THR:CB	1:C:982:GLU:OE1	2.45	0.64
1:C:719:PHE:HE1	1:C:939:PHE:HZ	1.43	0.64
1:C:894:GLU:OE2	1:C:915:HIS:NE2	2.31	0.64
1:A:388:ASN:ND2	1:A:1043:GLU:OE1	2.29	0.64
1:A:431:LEU:HD22	1:A:436:ALA:O	1.92	0.64
1:C:411:GLU:HG2	1:C:1350:HIS:HE1	1.61	0.64
1:A:388:ASN:OD1	1:A:1043:GLU:CA	2.38	0.64
1:A:431:LEU:HD22	1:A:436:ALA:N	2.12	0.64
1:A:1174:LEU:HD21	1:A:1266:PHE:HZ	1.63	0.64
1:J:371:ASN:OD1	1:J:372:LEU:N	2.30	0.64
1:A:598:LYS:NZ	1:A:793:THR:HA	2.11	0.64
1:C:7:LEU:HD11	1:C:12:LYS:CD	2.26	0.64
1:J:518:VAL:HB	1:J:1179:VAL:HG11	1.80	0.64
1:A:130:GLU:HG2	1:A:1074:THR:CB	2.27	0.64
1:A:967:HIS:CD2	1:A:969:HIS:CE1	2.86	0.64
1:A:1068:GLU:HG3	1:A:1073:THR:HG22	1.78	0.64
1:A:1113:LEU:HD21	1:A:1243:LEU:HD11	1.79	0.64
1:A:1362:LEU:O	1:A:1366:MET:HG2	1.97	0.64
1:C:207:LEU:CD2	1:C:211:GLN:OE1	2.46	0.64
2:5:70:ASN:ND2	2:6:189:ASP:OD2	2.30	0.64
1:J:45:ARG:NH2	1:J:46:TYR:CE2	2.60	0.64
1:A:19:PHE:HZ	1:C:1088:LEU:HD22	1.60	0.64
2:4:140:VAL:HG11	2:4:158:HIS:HE1	1.63	0.64
1:J:22:HIS:CD2	1:J:23:VAL:N	2.60	0.64
1:J:732:VAL:CG1	1:J:739:LEU:HD12	2.26	0.64
1:A:207:LEU:HD12	1:A:207:LEU:O	1.98	0.64
1:A:650:SER:O	1:A:654:VAL:HG23	1.98	0.64
1:J:687:ILE:CG2	1:J:1006:MET:HE1	2.27	0.64
1:A:983:TYR:O	1:A:988:ARG:NH2	2.30	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:627:ILE:HD11	1:J:882:ALA:HB2	1.80	0.63
1:C:592:GLU:OE2	1:C:595:ARG:NH1	2.31	0.63
1:J:83:LEU:CD2	1:J:1080:ASN:HD21	2.07	0.63
1:J:228:PHE:CE1	1:J:1099:VAL:HG21	2.26	0.63
1:J:617:VAL:HG12	1:J:619:GLY:H	1.64	0.63
1:J:698:LEU:HB2	1:J:706:TYR:HE2	1.62	0.63
1:C:419:THR:HG22	1:C:421:ARG:H	1.62	0.63
1:J:1105:ASP:N	1:J:1168:GLN:O	2.24	0.63
1:A:27:ALA:HB1	1:A:35:LEU:HD22	1.79	0.63
1:C:485:GLN:HE21	1:C:486:GLU:H	1.44	0.63
1:A:280:MET:O	1:A:284:MET:HG2	1.98	0.63
1:C:175:LEU:HD13	1:C:1081:ILE:HD11	1.79	0.63
2:5:49:ARG:NH1	2:5:242:CYS:SG	2.71	0.63
2:5:128:ALA:O	2:5:131:SER:HB3	1.97	0.63
1:J:263:THR:HB	1:J:267:ALA:HB3	1.79	0.63
1:A:315:ALA:HB2	1:A:321:ILE:HD11	1.80	0.63
1:C:360:ILE:HD12	1:C:369:MET:SD	2.35	0.63
1:J:1069:ARG:O	1:J:1071:ILE:HG22	1.98	0.63
1:A:730:VAL:HG13	1:A:895:VAL:HG13	1.81	0.63
1:C:410:VAL:O	1:C:412:SER:N	2.32	0.63
1:J:1069:ARG:C	1:J:1071:ILE:H	2.02	0.63
1:C:770:ASP:OD1	1:C:771:TYR:N	2.32	0.63
1:A:630:PHE:CE1	1:A:879:LEU:CD2	2.76	0.63
1:J:764:GLU:HG3	1:J:765:PRO:CD	2.04	0.62
1:J:448:THR:HG21	1:J:1111:GLN:O	1.98	0.62
1:A:388:ASN:CG	1:A:1043:GLU:OE1	2.38	0.62
1:A:400:TYR:CE1	1:A:573:LEU:HD12	2.31	0.62
1:C:1035:THR:CB	1:C:1176:LEU:HD11	2.28	0.62
1:C:1044:VAL:HG22	1:C:1099:VAL:HG22	1.81	0.62
2:4:140:VAL:HG11	2:4:158:HIS:CE1	2.33	0.62
1:J:700:GLU:HG3	1:J:700:GLU:O	1.99	0.62
1:J:1039:THR:HG21	1:J:1259:TYR:HE2	1.64	0.62
1:A:90:LYS:CG	1:A:119:TYR:CE1	2.82	0.62
1:A:193:VAL:HG21	1:A:1093:ASN:HD21	1.61	0.62
1:A:558:ILE:HD12	1:A:1015:ILE:HD11	1.79	0.62
1:A:862:GLU:HG3	1:A:863:ASP:H	1.64	0.62
1:C:9:LEU:HD12	1:C:45:ARG:CD	2.29	0.62
1:C:194:GLN:OE1	1:C:245:ARG:HD3	2.00	0.62
1:J:867:ASP:OD1	1:J:868:ALA:N	2.32	0.62
1:A:90:LYS:HG2	1:A:119:TYR:CE1	2.34	0.62
1:A:130:GLU:HG2	1:A:1074:THR:CG2	2.29	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:480:GLU:O	1:A:481:CYS:SG	2.57	0.62
2:6:28:ASP:OD1	2:6:176:ARG:NH1	2.28	0.62
2:4:20:LEU:HG	2:4:65:GLU:HG2	1.82	0.62
1:A:12:LYS:HE3	1:C:94:HIS:CB	2.18	0.62
1:A:604:PRO:HA	1:A:925:THR:HG21	1.82	0.62
1:C:790:PRO:CB	1:C:942:PHE:HD2	1.89	0.62
1:C:317:SER:OG	1:C:318:TYR:CD2	2.53	0.62
1:C:534:HIS:CE1	1:C:1239:LEU:HD13	2.35	0.62
1:C:795:ASN:CG	1:C:942:PHE:CD1	2.73	0.62
1:C:1285:TYR:HB2	1:C:1317:LEU:HD21	1.78	0.62
2:5:77:LEU:HD11	2:5:114:PHE:CZ	2.35	0.62
1:J:534:HIS:NE2	1:J:537:PHE:HD1	1.98	0.62
1:A:764:GLU:O	1:A:766:LEU:HD12	2.00	0.62
1:J:633:ARG:O	1:J:637:ASN:ND2	2.25	0.62
1:J:1044:VAL:CG1	1:J:1096:VAL:HG12	2.29	0.62
1:A:710:LEU:HD21	1:A:783:VAL:HG23	1.81	0.62
1:A:1020:LEU:HD21	1:A:1032:PHE:HZ	1.64	0.62
2:6:6:ILE:HB	2:6:50:THR:HG23	1.82	0.62
1:A:259:THR:HG22	1:A:352:LEU:HD11	1.82	0.61
2:5:136:ALA:O	2:5:139:SER:HB3	2.00	0.61
1:J:718:PRO:HD3	1:J:786:LEU:CG	2.31	0.61
1:J:1214:ILE:HD13	1:J:1268:THR:HG23	1.83	0.61
2:4:66:LEU:HB3	2:4:217:TRP:CZ3	2.34	0.61
1:C:1044:VAL:HG22	1:C:1099:VAL:HG23	1.81	0.61
1:C:186:LYS:NZ	1:C:1055:THR:HG23	2.11	0.61
2:4:246:ASP:OD2	2:4:280:ASP:HB2	2.00	0.61
1:J:598:LYS:HD2	1:J:1000:ASN:HB2	1.75	0.61
1:J:812:PHE:HB2	3:Z:65:LEU:HD21	1.82	0.61
1:A:431:LEU:HD23	1:A:437:VAL:CA	2.29	0.61
1:C:800:LEU:HD21	1:C:923:VAL:HG21	1.78	0.61
1:A:1168:GLN:HA	1:A:1298:ASP:O	2.00	0.61
1:C:120:SER:HB3	1:C:1084:VAL:HG12	1.81	0.61
2:4:243:LEU:HD22	3:D:74:ARG:HA	1.82	0.61
2:4:271:LEU:O	2:4:278:TYR:OH	2.19	0.61
1:A:534:HIS:HE1	1:A:1239:LEU:CD2	2.10	0.61
1:C:315:ALA:HB2	1:C:321:ILE:HD11	1.82	0.61
1:C:1328:THR:HG21	1:C:1353:ASN:HD22	1.66	0.61
1:J:1015:ILE:O	1:J:1015:ILE:CG2	2.47	0.61
1:A:1034:LEU:HD22	1:A:1173:GLU:CD	2.19	0.61
1:C:572:GLU:OE2	1:C:994:TYR:OH	2.18	0.61
2:6:164:VAL:HA	2:6:167:ILE:HG12	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1196:ALA:HB3	1:A:1222:ALA:HB3	1.82	0.61
1:C:273:MET:HE2	1:C:1047:LEU:HD11	1.83	0.61
1:C:534:HIS:ND1	1:C:1239:LEU:HB2	2.16	0.61
1:A:7:LEU:HD12	1:A:12:LYS:HD3	1.80	0.61
1:A:417:ASN:O	1:A:422:ASN:ND2	2.27	0.61
1:A:668:PRO:CB	1:A:672:PHE:CE2	2.78	0.61
1:A:941:ARG:HG3	1:A:992:SER:HB3	1.82	0.61
1:C:231:ASN:HD21	1:C:1099:VAL:HB	1.66	0.61
1:C:1016:SER:HB3	1:C:1019:SER:H	1.65	0.61
1:C:1217:HIS:HE2	1:C:1235:GLN:HA	1.66	0.61
1:J:723:LEU:CD1	1:J:772:ARG:HH22	2.14	0.60
1:J:810:ASP:OD2	1:J:933:TYR:OH	2.17	0.60
1:A:1102:VAL:CG2	1:A:1366:MET:HE1	2.28	0.60
1:J:76:HIS:CE1	1:J:78:ILE:HD11	2.35	0.60
1:A:212:ARG:HH22	1:A:1204:PRO:HD3	0.49	0.60
1:A:733:VAL:HG22	1:A:738:PRO:CA	2.26	0.60
1:C:945:ASN:ND2	1:C:947:THR:OG1	2.34	0.60
2:6:170:ASN:HB2	2:6:184:LEU:HD21	1.82	0.60
2:6:260:ASN:O	2:6:262:ASP:N	2.34	0.60
1:J:35:LEU:CD1	1:A:115:MET:C	2.68	0.60
1:J:790:PRO:CB	1:J:942:PHE:HE2	2.06	0.60
1:A:681:LEU:HD22	1:A:783:VAL:HG12	1.83	0.60
1:A:1195:ARG:NH1	1:A:1227:ALA:O	2.34	0.60
1:C:795:ASN:OD1	1:C:942:PHE:CG	2.53	0.60
1:J:41:ASP:CG	1:J:45:ARG:NH2	2.40	0.60
1:J:1109:ARG:HD2	1:J:1169:LYS:CD	2.31	0.60
2:4:166:ARG:HH12	2:4:185:ASP:HA	1.66	0.60
1:A:1105:ASP:CG	1:A:1169:LYS:HA	2.22	0.60
1:C:1160:ASN:CG	1:C:1298:ASP:HB3	2.21	0.60
1:J:431:LEU:HG	1:J:1333:MET:CE	2.31	0.60
1:A:431:LEU:CD2	1:A:437:VAL:CA	2.78	0.60
1:A:1197:SER:HB3	1:A:1214:ILE:HG13	1.84	0.60
3:Z:69:ALA:O	3:Z:73:THR:CG2	2.46	0.60
1:J:1156:MET:SD	1:J:1294:ARG:NH1	2.74	0.60
1:C:1177:THR:O	1:C:1180:THR:OG1	2.20	0.60
1:C:78:ILE:HD12	1:C:344:LEU:HD12	1.84	0.60
2:5:118:VAL:HG12	2:6:90:ARG:HH12	1.67	0.60
2:4:91:GLY:HA3	2:4:106:LEU:HD21	1.84	0.60
1:J:2:GLU:OE1	1:A:90:LYS:HD2	2.02	0.60
1:J:1182:ASP:HB2	1:J:1186:PHE:HB2	1.84	0.59
1:A:597:PHE:O	1:A:601:VAL:HG23	2.01	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:805:LYS:H	1:A:889:HIS:HE1	1.50	0.59
1:C:426:THR:HB	1:C:442:PHE:HE2	1.66	0.59
2:5:50:THR:HG22	2:5:54:ASN:HD21	1.66	0.59
1:J:19:PHE:CE2	1:A:1088:LEU:CD2	2.51	0.59
1:A:207:LEU:HD11	1:A:212:ARG:CD	2.26	0.59
1:A:435:ARG:HG3	1:A:1367:LEU:HD13	1.83	0.59
1:C:193:VAL:HG12	1:C:249:ALA:HB1	1.84	0.59
1:J:37:ILE:CG1	1:A:114:ILE:HG12	2.29	0.59
1:J:434:ASP:HA	1:J:1367:LEU:HD11	1.83	0.59
1:A:1217:HIS:ND1	1:A:1228:THR:OG1	2.32	0.59
1:J:731:GLN:HB3	1:J:738:PRO:HB3	1.84	0.59
1:A:572:GLU:OE2	1:A:994:TYR:OH	2.21	0.59
1:J:502:ARG:HD2	1:J:962:GLU:HG3	1.84	0.59
1:J:538:ASP:OD1	1:J:555:ARG:NH1	2.36	0.59
1:C:635:ILE:HD11	1:C:657:ILE:HD12	1.85	0.59
1:C:795:ASN:CG	1:C:942:PHE:CE1	2.75	0.59
2:6:170:ASN:HD22	2:6:184:LEU:HG	1.67	0.59
2:4:74:SER:O	2:4:78:GLU:HG2	2.01	0.59
1:A:1221:ASP:OD1	1:A:1222:ALA:N	2.35	0.59
1:J:274:VAL:O	1:J:1047:LEU:HD12	2.03	0.59
1:J:322:LEU:HD12	1:J:322:LEU:O	2.03	0.59
1:A:1328:THR:CG2	1:A:1353:ASN:CG	2.70	0.59
1:C:538:ASP:OD1	1:C:555:ARG:NH1	2.36	0.59
1:C:1152:THR:HB	1:C:1153:PHE:HD1	1.68	0.59
2:4:245:PHE:CZ	2:4:277:ILE:HD11	2.37	0.59
1:J:193:VAL:CG2	1:J:1093:ASN:ND2	2.66	0.59
1:A:391:LEU:HD22	1:A:1042:PHE:HE2	1.67	0.59
1:A:1102:VAL:CG2	1:A:1366:MET:HE2	2.33	0.59
2:5:211:MET:O	2:5:215:ARG:HG2	2.02	0.59
1:J:723:LEU:HD12	1:J:772:ARG:HH22	1.68	0.59
1:A:1344:PHE:HB2	1:A:1364:GLN:HE21	1.64	0.59
1:C:766:LEU:CD2	1:C:891:LYS:HD3	2.32	0.59
1:J:723:LEU:CD1	1:J:772:ARG:NH2	2.66	0.59
1:C:487:PRO:O	1:C:494:ARG:NH2	2.36	0.59
2:6:98:ASP:OD1	2:6:98:ASP:N	2.35	0.59
3:D:22:VAL:HG13	3:D:28:LEU:HD12	1.83	0.59
1:J:1121:VAL:HG12	1:J:1132:ARG:HH12	1.66	0.58
1:A:130:GLU:OE2	1:A:1074:THR:HG21	2.02	0.58
1:A:1034:LEU:CD2	1:A:1175:ILE:HD13	2.32	0.58
1:C:448:THR:CG2	1:C:1111:GLN:O	2.51	0.58
1:A:800:LEU:CD2	1:A:923:VAL:CG2	2.57	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1039:THR:HG21	1:A:1259:TYR:HE2	1.68	0.58
1:J:440:ILE:CD1	1:J:1108:VAL:CB	2.58	0.58
1:J:1109:ARG:HD3	1:J:1169:LYS:HE2	1.85	0.58
1:J:234:ARG:HH22	1:J:282:ILE:HD13	1.67	0.58
1:J:799:GLY:O	1:J:937:VAL:CG1	2.50	0.58
1:A:764:GLU:HB3	1:A:765:PRO:HD2	1.71	0.58
1:C:426:THR:CB	1:C:442:PHE:HE2	2.15	0.58
3:D:33:SER:HB2	3:D:36:THR:HB	1.86	0.58
1:C:84:ASN:N	1:C:84:ASN:OD1	2.36	0.58
1:C:440:ILE:HG23	1:C:440:ILE:O	2.03	0.58
1:C:646:VAL:CG1	1:C:647:PHE:N	2.67	0.58
1:C:713:HIS:H	1:C:713:HIS:CD2	2.22	0.58
3:D:24:VAL:HG12	3:D:54:PHE:HZ	1.69	0.58
3:D:47:TYR:OH	3:D:64:LEU:HD23	2.03	0.58
1:J:311:ASN:HB3	1:J:321:ILE:HD12	1.85	0.58
1:J:478:LEU:HD11	1:J:509:VAL:HG13	1.85	0.58
1:C:443:VAL:O	1:C:446:LEU:HG	2.03	0.58
2:4:245:PHE:CE1	3:D:67:MET:HE1	2.38	0.58
1:J:274:VAL:HG11	1:J:372:LEU:CD1	2.33	0.58
1:A:1034:LEU:HD23	1:A:1175:ILE:HD13	1.84	0.58
1:A:1125:ASP:OD1	1:A:1129:ARG:NH1	2.37	0.58
1:C:489:GLY:HA2	1:C:763:ASP:CG	2.21	0.58
1:C:1160:ASN:HD21	1:C:1297:THR:CA	2.17	0.58
1:A:284:MET:CE	1:A:291:ILE:HG21	2.34	0.58
1:C:763:ASP:O	1:C:764:GLU:O	2.22	0.58
1:C:1035:THR:OG1	1:C:1176:LEU:HD11	2.03	0.58
1:J:242:PHE:HE2	1:J:1095:CYS:HG	1.52	0.58
1:A:630:PHE:CE2	1:A:879:LEU:HG	2.39	0.58
1:A:739:LEU:HG	1:A:739:LEU:O	2.04	0.58
1:C:705:ALA:HB1	1:C:712:ASP:HB3	1.86	0.58
2:5:166:ARG:HD2	2:5:186:LEU:HD11	1.86	0.58
1:J:1109:ARG:CD	1:J:1169:LYS:HD2	2.34	0.57
1:C:426:THR:CA	1:C:442:PHE:CE2	2.86	0.57
1:C:743:ASN:ND2	2:4:158:HIS:O	2.37	0.57
1:A:19:PHE:HZ	1:C:1088:LEU:CD2	2.14	0.57
1:A:598:LYS:HD2	1:A:792:MET:O	2.03	0.57
1:C:9:LEU:CD1	1:C:45:ARG:CD	2.82	0.57
1:J:83:LEU:HD22	1:J:1080:ASN:CG	2.20	0.57
1:J:274:VAL:HG12	1:J:385:LEU:CD1	2.33	0.57
1:A:801:GLY:HA3	1:A:890:VAL:HG11	1.85	0.57
1:C:1160:ASN:HD21	1:C:1297:THR:HA	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:1232:TRP:HB3	1:J:1239:LEU:HD23	1.87	0.57
1:C:572:GLU:HB3	1:C:1003:HIS:HE1	1.69	0.57
1:C:741:PRO:HB3	2:4:158:HIS:CG	2.40	0.57
1:J:78:ILE:O	1:J:1058:ILE:HA	2.05	0.57
1:C:534:HIS:HE1	1:C:1239:LEU:HD22	1.64	0.57
1:C:1268:THR:HA	1:C:1271:ILE:HG22	1.87	0.57
1:C:1285:TYR:CZ	1:C:1317:LEU:HD12	2.33	0.57
1:J:730:VAL:HG13	1:J:895:VAL:HG13	1.86	0.57
1:A:448:THR:HG23	1:A:1111:GLN:O	2.03	0.57
1:A:1015:ILE:O	1:A:1015:ILE:CG2	2.51	0.57
2:5:239:LEU:HD13	2:5:250:CYS:HB2	1.87	0.57
2:4:24:THR:HG21	2:4:69:HIS:CD2	2.40	0.57
1:J:1280:LYS:O	1:J:1284:GLU:HG2	2.04	0.57
1:A:756:ARG:NH2	1:A:886:VAL:O	2.37	0.57
1:A:1109:ARG:HH11	1:A:1169:LYS:HD3	1.70	0.57
1:C:431:LEU:CD2	1:C:437:VAL:HA	2.32	0.57
2:6:194:THR:O	2:6:198:ASN:ND2	2.37	0.57
1:J:747:ARG:HG2	1:J:748:HIS:N	2.19	0.57
1:A:845:SER:HB2	1:A:848:ALA:HB3	1.87	0.57
1:A:953:SER:HB2	1:A:956:ILE:HD12	1.85	0.57
1:C:800:LEU:HG	1:C:923:VAL:CG2	2.34	0.57
1:C:849:GLN:HB2	1:C:873:LEU:HD13	1.87	0.57
1:C:1066:LYS:HD2	1:C:1075:TYR:HE1	1.69	0.57
1:J:508:THR:OG1	1:J:511:GLU:HB2	2.04	0.57
1:C:443:VAL:HG13	1:C:446:LEU:HD11	1.87	0.57
1:J:4:TRP:O	1:J:5:SER:OG	2.19	0.56
1:J:7:LEU:HD12	1:J:12:LYS:CE	2.35	0.56
1:C:1190:ASN:OD1	1:C:1191:ASN:N	2.35	0.56
1:J:17:THR:HG21	1:A:95:VAL:HG21	1.87	0.56
1:J:440:ILE:CD1	1:J:1108:VAL:HG13	2.27	0.56
1:J:558:ILE:HD12	1:J:1015:ILE:HD11	1.86	0.56
1:A:212:ARG:NH2	1:A:1204:PRO:CD	2.18	0.56
1:A:853:VAL:CG1	1:A:873:LEU:HD23	2.35	0.56
1:A:1344:PHE:HB2	1:A:1364:GLN:CD	2.26	0.56
1:C:598:LYS:HD3	1:C:1000:ASN:HB2	1.86	0.56
1:C:1085:ASP:OD1	1:C:1086:MET:N	2.39	0.56
1:C:1196:ALA:HB3	1:C:1222:ALA:HB3	1.88	0.56
2:4:35:PRO:O	2:4:39:LYS:HG2	2.05	0.56
2:4:245:PHE:CZ	3:D:67:MET:CE	2.88	0.56
1:J:207:LEU:HD12	1:J:207:LEU:C	2.26	0.56
1:J:431:LEU:HG	1:J:1333:MET:HE1	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:536:PHE:CD1	1:J:1015:ILE:HG21	2.40	0.56
1:J:942:PHE:HZ	1:J:995:SER:CB	2.16	0.56
1:J:1109:ARG:CD	1:J:1169:LYS:CD	2.84	0.56
1:A:447:LYS:HD3	1:A:1112:ASP:HB3	1.87	0.56
1:A:1235:GLN:HB2	1:A:1238:CYS:HB3	1.88	0.56
1:J:601:VAL:CG1	1:J:793:THR:CG2	2.83	0.56
1:A:193:VAL:CG1	1:A:1093:ASN:ND2	2.57	0.56
1:C:597:PHE:HE1	1:C:648:ALA:HB1	1.70	0.56
2:6:170:ASN:HD22	2:6:184:LEU:CG	2.18	0.56
1:A:795:ASN:CG	1:A:942:PHE:CD1	2.77	0.56
1:C:739:LEU:CD2	1:C:766:LEU:HD12	2.36	0.56
3:D:29:PRO:HG2	3:D:32:ILE:HG12	1.86	0.56
1:J:118:LYS:CD	1:C:32:PHE:HE1	2.18	0.56
1:J:1365:SER:OG	1:J:1366:MET:N	2.38	0.56
1:C:1176:LEU:HD22	1:C:1230:ASN:CG	2.26	0.56
1:A:598:LYS:HE2	1:A:1000:ASN:HD21	1.71	0.56
1:C:189:PRO:HG3	1:C:1285:TYR:HE2	1.71	0.56
1:J:222:LYS:O	1:J:226:THR:OG1	2.16	0.56
1:A:805:LYS:H	1:A:889:HIS:CE1	2.24	0.56
1:C:534:HIS:CD2	1:C:537:PHE:HD1	2.24	0.56
1:J:117:THR:CG2	1:C:2:GLU:OE2	2.43	0.55
1:A:252:ASP:OD1	1:A:253:SER:N	2.38	0.55
1:C:388:ASN:OD1	1:C:1043:GLU:HA	2.06	0.55
1:C:739:LEU:CD2	1:C:766:LEU:CD1	2.84	0.55
1:C:1168:GLN:NE2	1:C:1294:ARG:O	2.38	0.55
1:C:1182:ASP:HB2	1:C:1186:PHE:HB2	1.88	0.55
1:J:434:ASP:N	1:J:434:ASP:OD1	2.37	0.55
1:J:723:LEU:HG	1:J:768:VAL:HG21	1.88	0.55
1:C:317:SER:OG	1:C:318:TYR:CE2	2.54	0.55
1:C:431:LEU:HG	1:C:1333:MET:HE2	1.86	0.55
1:J:115:MET:C	1:C:35:LEU:CD1	2.65	0.55
1:A:23:VAL:HG12	1:C:114:ILE:HD13	1.87	0.55
1:C:175:LEU:HD12	1:C:1081:ILE:CD1	2.37	0.55
2:4:235:LEU:HD11	2:4:282:PHE:HE1	1.70	0.55
1:A:739:LEU:CD1	1:A:744:ILE:CG2	2.84	0.55
2:5:184:LEU:HD11	2:5:205:TYR:OH	2.06	0.55
1:A:400:TYR:HE1	1:A:573:LEU:CD1	2.18	0.55
1:C:424:LEU:HD23	1:C:577:GLU:CD	2.26	0.55
1:J:718:PRO:CG	1:J:786:LEU:CD2	2.85	0.55
1:J:862:GLU:HG3	1:J:863:ASP:N	2.21	0.55
1:A:236:ARG:HH21	1:A:289:SER:HB3	1.70	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1042:PHE:HD1	1:A:1102:VAL:HG22	1.72	0.55
1:C:719:PHE:HE1	1:C:939:PHE:CZ	2.24	0.55
1:C:1118:PRO:HB2	1:C:1151:LEU:HD23	1.89	0.55
3:D:45:SER:O	3:D:49:ARG:NH1	2.40	0.55
1:J:25:THR:OG1	1:A:203:ALA:O	2.25	0.55
1:J:1246:THR:O	1:J:1250:GLU:HG3	2.07	0.55
1:C:426:THR:HA	1:C:442:PHE:CE2	2.42	0.55
1:C:1132:ARG:HB3	1:C:1137:VAL:O	2.07	0.55
1:A:431:LEU:HD22	1:A:436:ALA:H	1.72	0.55
1:C:78:ILE:CD1	1:C:344:LEU:HD12	2.37	0.55
1:C:698:LEU:O	1:C:699:ALA:HB3	2.06	0.55
2:5:248:ASN:O	2:5:252:ASN:ND2	2.40	0.55
2:6:239:LEU:HD13	2:6:250:CYS:HB2	1.89	0.55
1:J:117:THR:HG21	1:C:2:GLU:CD	2.26	0.55
1:J:1109:ARG:HD2	1:J:1169:LYS:HD2	1.87	0.55
1:A:617:VAL:HG12	1:A:619:GLY:H	1.72	0.55
1:J:95:VAL:HG21	1:C:17:THR:HG21	1.89	0.54
1:J:1290:LYS:HB3	1:J:1310:LEU:HB3	1.90	0.54
1:A:450:CYS:O	1:A:1122:TYR:OH	2.22	0.54
1:A:1042:PHE:CD1	1:A:1102:VAL:HG22	2.42	0.54
2:6:7:GLY:HA3	2:6:46:LEU:HD13	1.89	0.54
1:J:1037:VAL:HG22	1:J:1172:CYS:HB2	1.89	0.54
1:A:79:LYS:N	1:A:303:GLY:O	2.33	0.54
1:A:1214:ILE:HG21	1:A:1272:ILE:HD11	1.89	0.54
1:C:146:THR:O	1:C:149:ASP:N	2.36	0.54
1:C:186:LYS:HZ1	1:C:1055:THR:HG23	1.64	0.54
1:C:730:VAL:HG13	1:C:895:VAL:HG13	1.88	0.54
1:A:388:ASN:CG	1:A:1043:GLU:CD	2.65	0.54
1:A:715:LEU:HA	1:A:914:GLN:NE2	2.18	0.54
1:C:193:VAL:HG21	1:C:1093:ASN:HB3	1.90	0.54
1:C:597:PHE:CE1	1:C:648:ALA:HB1	2.43	0.54
1:C:1285:TYR:CD1	1:C:1317:LEU:HG	2.42	0.54
2:6:118:VAL:O	2:6:214:ARG:NH1	2.40	0.54
2:6:259:GLU:O	2:6:263:SER:HB2	2.06	0.54
1:J:93:PHE:HE1	1:J:118:LYS:HG2	1.72	0.54
1:J:760:MET:HA	1:J:888:GLU:OE1	2.08	0.54
1:J:942:PHE:CZ	1:J:995:SER:HB3	2.43	0.54
1:A:867:ASP:OD1	1:A:868:ALA:N	2.40	0.54
1:C:78:ILE:HD12	1:C:344:LEU:CD1	2.37	0.54
1:C:413:LYS:HD3	1:C:1335:THR:HG21	1.89	0.54
2:4:245:PHE:CZ	3:D:67:MET:HE1	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:4:245:PHE:HZ	3:D:67:MET:CE	2.21	0.54
1:C:966:TYR:HB3	1:C:973:PHE:HB2	1.88	0.54
2:5:33:ALA:O	2:5:35:PRO:HD3	2.08	0.54
1:A:193:VAL:HG12	1:A:249:ALA:HB1	1.88	0.54
1:A:707:VAL:HG22	1:A:1022:LEU:HD23	1.90	0.54
1:C:270:SER:OG	1:C:365:LYS:HG2	2.07	0.54
1:C:360:ILE:CG1	1:C:369:MET:SD	2.96	0.54
1:C:524:VAL:HG22	1:C:1227:ALA:CB	2.32	0.54
2:4:118:VAL:HB	2:4:214:ARG:CZ	2.37	0.54
2:4:245:PHE:HZ	2:4:277:ILE:HD11	1.72	0.54
3:E:63:ASP:O	3:E:67:MET:HG2	2.07	0.54
1:J:193:VAL:CB	1:J:1093:ASN:ND2	2.70	0.54
1:J:193:VAL:HG12	1:J:249:ALA:HB1	1.89	0.54
1:A:76:HIS:HE1	1:A:344:LEU:O	1.91	0.54
1:A:193:VAL:CB	1:A:1093:ASN:ND2	2.71	0.54
3:D:62:LEU:O	3:D:66:ARG:HG2	2.06	0.54
1:J:228:PHE:CE2	1:J:1099:VAL:HG21	2.43	0.54
1:A:1179:VAL:O	1:A:1179:VAL:CG1	2.53	0.54
1:C:19:PHE:CD1	1:C:21:THR:O	2.61	0.54
1:C:426:THR:HA	1:C:442:PHE:HE2	1.70	0.54
1:C:710:LEU:HB2	1:C:1012:LEU:HD23	1.88	0.54
3:E:37:HIS:CD2	3:E:40:LEU:CA	2.89	0.54
1:J:597:PHE:CE1	1:J:601:VAL:CG2	2.90	0.54
1:J:994:TYR:OH	1:J:1007:THR:HG21	2.07	0.54
1:A:90:LYS:HG2	1:A:119:TYR:HD1	1.69	0.54
1:A:1195:ARG:NH2	1:A:1216:ASP:O	2.41	0.54
2:5:260:ASN:O	2:5:262:ASP:N	2.41	0.54
1:J:41:ASP:OD2	1:J:45:ARG:NH2	2.34	0.54
1:A:157:MET:O	1:A:161:LEU:HG	2.08	0.54
1:A:429:TYR:HA	1:A:438:GLN:O	2.08	0.54
2:5:49:ARG:CZ	2:5:242:CYS:SG	2.96	0.54
1:J:448:THR:HG22	1:J:1113:LEU:HD13	1.90	0.53
1:A:552:CYS:SG	1:A:907:LEU:HD11	2.48	0.53
1:C:175:LEU:HD11	1:C:1081:ILE:HD11	1.89	0.53
1:C:710:LEU:HD21	1:C:783:VAL:HG23	1.90	0.53
1:J:36:ARG:HH22	1:A:115:MET:HE1	1.69	0.53
1:J:1271:ILE:HD12	1:J:1274:ALA:HB3	1.88	0.53
1:A:630:PHE:HZ	1:A:879:LEU:HD21	1.57	0.53
1:C:278:ASN:O	1:C:282:ILE:HG13	2.08	0.53
2:5:163:GLU:OE2	2:5:186:LEU:HD22	2.08	0.53
3:D:26:LEU:HD13	3:D:64:LEU:HD13	1.87	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5:246:ASP:N	2:5:246:ASP:OD1	2.40	0.53
2:6:246:ASP:OD2	2:6:281:SER:N	2.42	0.53
1:J:517:VAL:HG12	1:J:518:VAL:N	2.24	0.53
1:J:707:VAL:HG22	1:J:1022:LEU:HD23	1.89	0.53
1:C:1056:SER:OG	1:C:1084:VAL:HG22	2.07	0.53
1:C:1280:LYS:O	1:C:1284:GLU:HG3	2.08	0.53
1:J:409:THR:O	1:J:411:GLU:N	2.40	0.53
1:J:533:LEU:HB2	1:J:539:PHE:CE2	2.43	0.53
1:C:545:ASN:N	1:C:545:ASN:OD1	2.41	0.53
1:C:1043:GLU:C	1:C:1044:VAL:HG23	2.29	0.53
1:J:231:ASN:ND2	1:J:1099:VAL:HB	2.24	0.53
1:J:485:GLN:HE21	1:J:486:GLU:H	1.56	0.53
1:C:93:PHE:HB2	1:C:116:VAL:HG23	1.91	0.53
1:J:275:SER:OG	1:J:280:MET:HG2	2.09	0.53
1:J:558:ILE:HD13	1:J:1015:ILE:HG12	1.91	0.53
1:A:536:PHE:CE1	1:A:1015:ILE:HG21	2.44	0.53
1:A:1325:LEU:HD22	1:A:1344:PHE:CE2	2.43	0.53
3:Z:37:HIS:CD2	3:Z:40:LEU:CA	2.89	0.53
1:J:435:ARG:H	1:J:1367:LEU:HD11	1.74	0.53
2:4:227:ARG:O	2:4:231:ARG:HG2	2.07	0.53
1:J:743:ASN:HD21	2:6:160:LYS:HA	1.73	0.53
1:A:284:MET:HA	1:A:291:ILE:CD1	2.38	0.53
1:A:698:LEU:HD23	1:A:1127:VAL:HG22	1.91	0.53
1:C:801:GLY:HA3	1:C:890:VAL:HB	1.91	0.53
2:6:249:TYR:CE2	3:E:67:MET:HE1	2.43	0.53
1:C:311:ASN:HB3	1:C:321:ILE:HD12	1.91	0.53
2:4:167:ILE:HG13	2:4:185:ASP:OD2	2.09	0.53
1:J:12:LYS:HE3	1:A:94:HIS:CB	2.32	0.52
1:A:21:THR:HG22	1:C:200:ALA:HB1	1.82	0.52
1:A:343:SER:HA	1:A:346:GLN:HB2	1.90	0.52
1:A:633:ARG:O	1:A:637:ASN:ND2	2.39	0.52
1:C:209:ARG:HA	1:C:212:ARG:NH1	2.24	0.52
1:J:188:PRO:HG2	1:J:1093:ASN:OD1	2.09	0.52
1:A:197:VAL:O	1:A:197:VAL:HG12	2.09	0.52
1:C:269:ILE:HD13	1:C:368:ILE:HD11	1.91	0.52
3:Z:37:HIS:HE1	3:Z:39:VAL:CG1	2.14	0.52
1:A:473:PRO:HA	1:A:476:GLN:HG2	1.91	0.52
1:A:534:HIS:CE1	1:A:1239:LEU:CD1	2.90	0.52
1:A:760:MET:HB3	1:A:889:HIS:CD2	2.45	0.52
1:A:1271:ILE:HD12	1:A:1274:ALA:HB3	1.90	0.52
1:J:193:VAL:CG2	1:J:1093:ASN:OD1	2.50	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:430:LEU:HD23	1:J:1326:SER:HA	1.92	0.52
1:J:495:ILE:HG22	1:J:496:PRO:HD3	1.90	0.52
1:J:1193:ARG:NH2	1:J:1195:ARG:O	2.41	0.52
1:A:1034:LEU:CD2	1:A:1175:ILE:CD1	2.87	0.52
1:C:15:ILE:HD12	1:C:16:PRO:HD2	1.91	0.52
1:C:687:ILE:CD1	1:C:1006:MET:CE	2.86	0.52
1:C:719:PHE:CE1	1:C:939:PHE:HZ	2.24	0.52
2:5:245:PHE:CZ	2:5:277:ILE:HD11	2.44	0.52
1:J:7:LEU:CD1	1:J:12:LYS:CE	2.88	0.52
1:J:620:ASN:HB2	1:J:623:ALA:HB3	1.92	0.52
1:C:259:THR:HG22	1:C:352:LEU:HD11	1.90	0.52
2:6:245:PHE:CZ	2:6:277:ILE:HD11	2.45	0.52
1:J:718:PRO:CG	1:J:786:LEU:HD21	2.40	0.52
1:J:1290:LYS:HE3	1:J:1312:GLU:HB3	1.92	0.52
1:A:1193:ARG:NH2	1:A:1195:ARG:O	2.43	0.52
1:C:193:VAL:O	1:C:197:VAL:HG23	2.09	0.52
1:C:426:THR:HB	1:C:442:PHE:CE2	2.45	0.52
1:A:8:GLU:OE1	1:A:45:ARG:HB2	2.09	0.52
1:A:1048:LEU:HD12	1:A:1094:THR:CG2	2.40	0.52
1:C:598:LYS:HB2	1:C:792:MET:HE3	1.92	0.52
1:A:20:LEU:CD1	1:C:197:VAL:HG22	2.38	0.52
1:A:21:THR:HG21	1:C:200:ALA:HA	1.79	0.52
1:A:212:ARG:HH12	1:A:1204:PRO:CG	2.22	0.52
1:A:341:ASN:OD1	1:A:345:SER:HB3	2.09	0.52
1:A:426:THR:CG2	1:A:442:PHE:CD2	2.85	0.52
1:A:790:PRO:CB	1:A:942:PHE:HE2	2.03	0.52
1:C:203:ALA:CB	1:C:207:LEU:HD23	2.23	0.52
2:6:29:VAL:HG11	2:6:179:PHE:HE2	1.74	0.52
1:J:344:LEU:HD23	1:J:1086:MET:SD	2.49	0.52
1:J:374:ARG:NH1	1:J:374:ARG:HB3	2.25	0.52
1:J:782:LYS:O	1:J:786:LEU:HB2	2.10	0.52
2:6:246:ASP:HB2	2:6:278:TYR:HA	1.92	0.52
1:J:322:LEU:HD21	1:J:325:PHE:HD1	1.73	0.52
1:A:1318:THR:OG1	1:A:1320:GLU:OE2	2.18	0.52
1:C:68:THR:HA	1:C:355:LEU:CD1	2.40	0.52
1:C:869:HIS:CD2	1:C:870:THR:HG23	2.44	0.52
3:D:25:VAL:HA	3:D:57:LYS:HE3	1.90	0.52
1:J:1064:VAL:HG13	1:J:1077:VAL:HG22	1.91	0.51
1:A:359:VAL:HG12	1:A:368:ILE:HD13	1.93	0.51
1:A:1292:CYS:HB2	1:A:1310:LEU:HD23	1.92	0.51
1:C:74:ALA:HB1	1:C:1054:CYS:SG	2.50	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:601:VAL:HG11	1:J:793:THR:CG2	2.41	0.51
1:J:1268:THR:HA	1:J:1271:ILE:HG22	1.92	0.51
1:A:192:VAL:HG11	1:A:1282:ILE:HD12	1.92	0.51
2:5:30:ASP:HB3	2:5:33:ALA:HB2	1.93	0.51
2:5:267:LEU:CG	2:5:271:LEU:HD11	2.38	0.51
2:6:259:GLU:HG3	2:6:260:ASN:N	2.26	0.51
1:A:19:PHE:CZ	1:C:1088:LEU:HD22	2.43	0.51
1:C:122:LYS:HG2	1:C:1082:ASN:ND2	2.25	0.51
2:5:140:VAL:HG21	2:5:158:HIS:CD2	2.45	0.51
2:4:31:LEU:HD23	2:4:59:TRP:CZ2	2.46	0.51
1:A:410:VAL:O	1:A:412:SER:N	2.43	0.51
1:C:601:VAL:CG1	1:C:793:THR:HG22	2.40	0.51
1:C:1182:ASP:OD1	1:C:1183:VAL:N	2.43	0.51
3:D:20:HIS:CD2	3:D:24:VAL:HG21	2.45	0.51
1:J:698:LEU:HB2	1:J:706:TYR:CE2	2.44	0.51
1:J:795:ASN:OD1	1:J:942:PHE:CE1	2.63	0.51
1:J:1057:VAL:HG12	1:J:1083:THR:HG22	1.93	0.51
1:A:212:ARG:NH1	1:A:1204:PRO:HG3	2.25	0.51
1:C:457:PRO:HG3	1:C:537:PHE:CD2	2.46	0.51
1:C:633:ARG:NH1	1:C:870:THR:CB	2.73	0.51
1:C:800:LEU:HD23	1:C:923:VAL:HG21	1.85	0.51
2:4:31:LEU:HD11	2:4:58:LEU:HD21	1.93	0.51
1:J:2:GLU:OE1	1:A:90:LYS:CE	2.58	0.51
1:J:1038:ARG:HG3	1:J:1170:ALA:O	2.10	0.51
1:A:193:VAL:CG2	1:A:1093:ASN:HD21	2.21	0.51
1:C:392:THR:HA	1:C:1039:THR:HA	1.93	0.51
1:C:966:TYR:O	1:C:973:PHE:HB3	2.11	0.51
3:D:43:MET:SD	3:D:67:MET:CE	2.99	0.51
1:J:924:VAL:O	1:J:925:THR:CG2	2.58	0.51
1:A:90:LYS:CG	1:A:119:TYR:CD1	2.87	0.51
1:A:858:THR:O	1:A:862:GLU:HG2	2.11	0.51
1:C:80:PHE:CE1	1:C:305:PHE:HD2	2.28	0.51
1:C:1176:LEU:CD2	1:C:1230:ASN:CG	2.79	0.51
2:6:245:PHE:HZ	2:6:277:ILE:HD11	1.76	0.51
1:A:79:LYS:O	1:A:304:ASN:HA	2.10	0.51
1:A:706:TYR:CD1	1:A:900:ASP:OD2	2.64	0.51
1:C:375:VAL:O	1:C:375:VAL:HG12	2.11	0.51
2:4:74:SER:HA	2:4:77:LEU:HB3	1.93	0.51
1:J:83:LEU:HD22	1:J:1080:ASN:HD22	1.59	0.51
1:J:628:ARG:HG3	1:J:661:LEU:HD11	1.93	0.51
1:J:1104:THR:HG22	1:J:1106:MET:H	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:102:SER:HB3	1:A:108:THR:HG22	1.93	0.51
1:A:731:GLN:HB3	1:A:738:PRO:HB3	1.91	0.51
1:A:733:VAL:CG2	1:A:738:PRO:HA	2.34	0.51
1:A:753:ASP:O	1:A:757:LEU:CG	2.58	0.51
1:A:898:PRO:HG3	1:A:911:ILE:HG12	1.93	0.51
1:C:514:GLN:C	1:C:993:ARG:HH22	2.14	0.51
1:C:739:LEU:HD21	1:C:766:LEU:HG	1.93	0.51
1:C:1290:LYS:HB3	1:C:1310:LEU:HB3	1.92	0.51
2:6:32:GLU:HG3	2:6:59:TRP:HH2	1.76	0.51
2:4:245:PHE:HB2	3:D:71:SER:HA	1.93	0.51
1:J:205:GLN:HG3	1:C:24:LYS:HE2	1.92	0.51
1:A:1336:LYS:NZ	1:A:1346:THR:O	2.32	0.51
2:6:137:LYS:NZ	2:6:152:GLU:OE1	2.44	0.51
1:J:383:ASP:OD1	1:J:384:PRO:HD2	2.10	0.50
1:J:684:VAL:O	1:J:687:ILE:HG22	2.12	0.50
1:J:713:HIS:CD2	1:J:726:ASN:HD21	2.29	0.50
1:A:1292:CYS:HB2	1:A:1310:LEU:CD2	2.40	0.50
1:J:908:PRO:HG3	1:J:1123:ARG:HH12	1.76	0.50
1:J:1336:LYS:HE2	1:J:1355:VAL:HG11	1.94	0.50
1:A:231:ASN:HD21	1:A:1099:VAL:N	2.01	0.50
1:A:448:THR:HG21	1:A:1111:GLN:O	2.09	0.50
1:A:747:ARG:HD3	1:A:749:HIS:CE1	2.45	0.50
1:J:79:LYS:N	1:J:303:GLY:O	2.36	0.50
1:J:1054:CYS:SG	1:J:1055:THR:HG22	2.51	0.50
1:A:431:LEU:HD23	1:A:436:ALA:C	2.12	0.50
1:A:732:VAL:O	1:A:739:LEU:N	2.29	0.50
1:A:1359:ILE:HG23	1:A:1360:ILE:HG13	1.92	0.50
2:4:109:LEU:O	2:4:112:THR:HG22	2.12	0.50
1:J:514:GLN:HE22	1:J:563:ASP:H	1.58	0.50
1:J:524:VAL:HA	1:J:1227:ALA:HB2	1.92	0.50
1:A:443:VAL:HG22	1:A:1024:THR:HG22	1.93	0.50
1:A:588:PRO:HG2	1:A:683:LEU:HD11	1.94	0.50
1:A:862:GLU:HG3	1:A:863:ASP:N	2.26	0.50
1:J:19:PHE:CE2	1:J:32:PHE:HZ	2.30	0.50
1:J:653:LEU:O	1:J:657:ILE:HG12	2.12	0.50
1:A:445:ALA:HA	1:A:1110:VAL:HG21	1.94	0.50
1:C:707:VAL:HG22	1:C:1022:LEU:HD23	1.93	0.50
1:C:945:ASN:HD22	1:C:948:ILE:HD13	1.77	0.50
1:J:7:LEU:HD11	1:J:12:LYS:CD	2.38	0.50
1:J:341:ASN:HD21	1:J:345:SER:HB3	1.76	0.50
1:J:534:HIS:NE2	1:J:537:PHE:CD1	2.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:1221:ASP:HB3	1:J:1224:THR:O	2.10	0.50
1:A:4:TRP:O	1:A:5:SER:OG	2.29	0.50
1:A:853:VAL:HG13	1:A:873:LEU:CD2	2.42	0.50
1:C:188:PRO:HA	1:C:1286:LEU:HD21	1.93	0.50
1:C:384:PRO:O	1:C:387:ARG:HD3	2.11	0.50
1:C:1308:GLU:OE1	1:C:1308:GLU:N	2.44	0.50
2:5:16:LEU:HD13	2:5:58:LEU:HD21	1.94	0.50
2:4:250:CYS:SG	2:4:278:TYR:HB2	2.51	0.50
1:C:120:SER:HB3	1:C:1084:VAL:CG1	2.41	0.50
1:C:733:VAL:HG22	1:C:738:PRO:CA	2.36	0.50
1:C:801:GLY:HA3	1:C:890:VAL:CB	2.41	0.50
1:C:1055:THR:HG22	1:C:1085:ASP:HA	1.94	0.50
1:C:1193:ARG:HG3	1:C:1266:PHE:CE1	2.47	0.50
1:C:1296:ASP:OD1	1:C:1297:THR:N	2.45	0.50
1:J:144:GLU:O	1:J:146:THR:HG23	2.12	0.50
1:J:457:PRO:HG3	1:J:537:PHE:CD2	2.47	0.50
1:A:78:ILE:O	1:A:1058:ILE:HA	2.10	0.50
1:A:574:ARG:NH2	1:A:1010:ALA:O	2.43	0.50
1:A:601:VAL:CG1	1:A:793:THR:CG2	2.88	0.50
1:C:431:LEU:CG	1:C:1333:MET:CE	2.89	0.50
1:C:954:ASP:O	1:C:958:ARG:HG2	2.12	0.50
1:C:1168:GLN:HA	1:C:1298:ASP:O	2.12	0.50
3:D:47:TYR:OH	3:D:64:LEU:CD2	2.60	0.50
1:J:663:ASP:OD1	1:J:664:GLY:N	2.45	0.50
1:J:946:PRO:HG3	1:J:973:PHE:CD1	2.47	0.50
1:A:764:GLU:HB2	1:A:765:PRO:HD2	1.94	0.50
1:C:633:ARG:NH1	1:C:870:THR:HG21	2.19	0.50
1:C:1152:THR:HB	1:C:1153:PHE:CD1	2.47	0.50
2:6:249:TYR:HE2	3:E:67:MET:HE1	1.74	0.50
1:J:443:VAL:O	1:J:446:LEU:HG	2.11	0.49
1:J:1212:LYS:HB3	1:J:1219:GLU:OE1	2.12	0.49
1:A:207:LEU:HD12	1:A:207:LEU:C	2.33	0.49
2:4:243:LEU:HB3	3:D:74:ARG:HH11	1.77	0.49
1:J:118:LYS:CD	1:C:32:PHE:CD1	2.95	0.49
1:J:1121:VAL:HG12	1:J:1132:ARG:NH1	2.27	0.49
1:J:388:ASN:CG	1:J:1311:ILE:HG13	2.30	0.49
1:J:763:ASP:O	1:J:764:GLU:O	2.29	0.49
1:A:17:THR:HG21	1:C:95:VAL:HG21	1.94	0.49
1:A:343:SER:HA	1:A:346:GLN:CB	2.43	0.49
1:A:638:MET:HE3	1:A:642:ARG:HD2	1.92	0.49
1:A:1020:LEU:HD21	1:A:1032:PHE:CZ	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1291:ASP:HB3	1:A:1316:ARG:NH2	2.27	0.49
1:A:687:ILE:CD1	1:A:1006:MET:SD	2.95	0.49
1:A:1327:THR:HG22	1:A:1355:VAL:HG13	1.94	0.49
1:C:535:PRO:O	1:C:555:ARG:NH2	2.44	0.49
2:5:55:GLU:HA	2:5:58:LEU:HD12	1.95	0.49
1:J:400:TYR:HE1	1:J:573:LEU:HD12	1.76	0.49
1:J:800:LEU:C	1:J:800:LEU:HD12	2.32	0.49
1:C:227:LEU:O	1:C:1096:VAL:HB	2.13	0.49
1:C:397:VAL:HG22	1:C:428:ALA:CB	2.43	0.49
1:C:647:PHE:HD2	1:C:653:LEU:HD13	1.78	0.49
1:J:270:SER:OG	1:J:365:LYS:HG3	2.13	0.49
1:J:790:PRO:CG	1:J:942:PHE:CE2	2.93	0.49
1:A:231:ASN:HD21	1:A:1099:VAL:HB	1.77	0.49
1:A:812:PHE:HB2	3:D:65:LEU:HD21	1.93	0.49
1:C:1244:TYR:HB2	1:C:1266:PHE:CD2	2.38	0.49
1:J:15:ILE:HD12	1:J:16:PRO:HD2	1.95	0.49
1:J:485:GLN:OE1	1:J:913:ARG:NH2	2.46	0.49
1:J:651:TYR:CE2	1:J:781:GLN:HG2	2.48	0.49
1:A:538:ASP:OD1	1:A:539:PHE:N	2.46	0.49
1:A:1328:THR:HG22	1:A:1353:ASN:CG	2.33	0.49
1:J:129:PHE:CZ	1:J:1075:TYR:HD2	2.30	0.49
1:J:132:SER:O	1:J:136:LEU:HD12	2.13	0.49
1:J:397:VAL:HG22	1:J:428:ALA:CB	2.42	0.49
1:J:924:VAL:O	1:J:925:THR:HG23	2.12	0.49
1:A:967:HIS:NE2	1:A:969:HIS:HE1	2.11	0.49
1:C:710:LEU:O	1:C:782:LYS:NZ	2.33	0.49
1:C:748:HIS:O	1:C:756:ARG:NH1	2.46	0.49
1:C:1056:SER:HG	1:C:1084:VAL:CG2	2.23	0.49
1:C:1185:TYR:OH	1:C:1191:ASN:O	2.23	0.49
1:J:177:HIS:ND1	1:J:376:TYR:OH	2.27	0.49
1:A:638:MET:HB2	1:A:646:VAL:HG21	1.95	0.49
1:C:22:HIS:O	1:C:23:VAL:C	2.51	0.49
1:C:371:ASN:OD1	1:C:372:LEU:N	2.45	0.49
1:C:524:VAL:HG11	1:C:1218:ARG:O	2.12	0.49
1:C:565:LEU:HD22	1:C:1177:THR:HB	1.94	0.49
1:C:1154:GLY:HA2	1:C:1257:LYS:HD3	1.93	0.49
1:C:1291:ASP:OD1	1:C:1291:ASP:N	2.45	0.49
2:5:41:CYS:SG	2:5:55:GLU:HG3	2.52	0.49
1:J:448:THR:HG23	1:J:1111:GLN:O	2.10	0.49
1:J:698:LEU:O	1:J:699:ALA:HB3	2.12	0.49
1:A:1278:LEU:O	1:A:1282:ILE:HG23	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:553:THR:HG23	1:C:910:PHE:CE1	2.48	0.49
1:C:994:TYR:OH	1:C:1007:THR:HG21	2.13	0.49
2:5:150:GLN:HG2	2:5:150:GLN:O	2.12	0.49
2:5:225:LEU:O	2:5:229:GLN:NE2	2.45	0.49
2:6:121:ASP:HB3	2:6:214:ARG:HH12	1.77	0.49
1:A:158:HIS:O	1:A:162:ARG:HG3	2.12	0.48
1:A:603:SER:OG	1:A:644:LEU:HD22	2.13	0.48
1:A:976:PRO:HD2	1:A:979:PHE:HD2	1.77	0.48
1:A:1044:VAL:HG23	1:A:1099:VAL:HA	1.95	0.48
1:C:853:VAL:HB	1:C:857:LEU:HD23	1.94	0.48
1:J:924:VAL:HG12	1:J:925:THR:HG23	1.94	0.48
1:C:273:MET:CE	1:C:1047:LEU:HD21	2.44	0.48
1:C:362:LEU:HD22	1:C:367:VAL:HG21	1.94	0.48
1:C:534:HIS:ND1	1:C:1239:LEU:HD22	2.25	0.48
1:C:646:VAL:HG12	1:C:647:PHE:HD1	1.70	0.48
1:J:7:LEU:HD13	1:J:12:LYS:HD3	1.83	0.48
1:J:768:VAL:HG23	1:J:918:TYR:OH	2.13	0.48
1:J:941:ARG:CG	1:J:992:SER:HB3	2.40	0.48
1:J:1173:GLU:O	1:J:1244:TYR:OH	2.20	0.48
1:A:93:PHE:CE1	1:A:118:LYS:HG2	2.45	0.48
1:C:646:VAL:CG1	1:C:647:PHE:CD1	2.86	0.48
1:C:718:PRO:HD3	1:C:786:LEU:CG	2.42	0.48
1:C:867:ASP:OD1	1:C:868:ALA:N	2.46	0.48
1:C:1122:TYR:HB2	1:C:1128:ASP:HB2	1.94	0.48
2:6:217:TRP:NE1	2:6:221:GLU:OE1	2.46	0.48
2:4:115:ASP:OD1	2:4:116:THR:N	2.46	0.48
1:J:1168:GLN:NE2	1:J:1294:ARG:O	2.42	0.48
1:A:9:LEU:HD13	1:A:45:ARG:HG3	1.90	0.48
1:C:382:LYS:HD3	1:C:1309:GLN:HG3	1.94	0.48
2:4:108:VAL:HA	2:4:111:ARG:HG3	1.95	0.48
1:J:184:LEU:HD23	1:J:1048:LEU:HD13	1.96	0.48
1:A:231:ASN:ND2	1:A:1099:VAL:HB	2.28	0.48
1:A:663:ASP:OD1	1:A:664:GLY:N	2.46	0.48
1:J:231:ASN:HD21	1:J:1099:VAL:CA	2.27	0.48
1:J:535:PRO:HB3	1:J:1232:TRP:CH2	2.48	0.48
1:C:83:LEU:HD11	1:C:1058:ILE:HG22	1.89	0.48
2:6:206:THR:O	2:6:210:ILE:HG12	2.14	0.48
2:4:60:LEU:HB3	2:4:268:LEU:HD22	1.94	0.48
1:J:80:PHE:HB3	1:J:1058:ILE:CG2	2.43	0.48
1:J:397:VAL:HG22	1:J:428:ALA:HB2	1.95	0.48
1:A:397:VAL:HG22	1:A:428:ALA:CB	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:186:LYS:HZ3	1:C:1055:THR:CG2	2.14	0.48
1:C:1068:GLU:HG2	1:C:1070:ASP:H	1.79	0.48
1:J:76:HIS:HE1	1:J:78:ILE:HD11	1.79	0.48
1:C:440:ILE:HB	1:C:1108:VAL:HG11	1.96	0.48
1:C:448:THR:HG22	1:C:1113:LEU:HB2	1.95	0.48
1:C:633:ARG:HH12	1:C:870:THR:HB	1.78	0.48
1:C:681:LEU:HD22	1:C:783:VAL:HG12	1.96	0.48
1:C:1211:THR:O	1:C:1215:TYR:HB2	2.14	0.48
1:C:1271:ILE:HD12	1:C:1274:ALA:HB3	1.95	0.48
2:5:84:CYS:O	2:5:109:LEU:HD21	2.14	0.48
2:4:208:ARG:O	2:4:212:ASN:HB2	2.14	0.48
1:J:120:SER:HB3	1:J:1084:VAL:HG12	1.94	0.48
1:C:739:LEU:C	1:C:741:PRO:HD2	2.35	0.48
1:C:1160:ASN:CG	1:C:1298:ASP:CB	2.81	0.48
2:5:245:PHE:CE2	2:5:277:ILE:HD11	2.48	0.48
3:D:43:MET:SD	3:D:67:MET:HE2	2.53	0.48
1:J:228:PHE:CG	1:J:1099:VAL:HG23	2.45	0.48
1:J:924:VAL:C	1:J:925:THR:HG23	2.35	0.48
1:A:425:PRO:HB3	1:A:1328:THR:CG2	2.43	0.48
1:A:895:VAL:HB	1:A:914:GLN:HB2	1.96	0.48
1:A:1123:ARG:HE	1:A:1123:ARG:HB2	1.38	0.48
1:C:102:SER:OG	1:C:103:GLY:N	2.46	0.48
1:C:794:ASN:ND2	1:C:1000:ASN:HD21	2.12	0.48
1:C:1326:SER:O	1:C:1355:VAL:HA	2.13	0.48
3:Z:47:TYR:OH	3:Z:63:ASP:OD1	2.21	0.48
1:J:114:ILE:HG22	1:C:35:LEU:HD11	1.96	0.47
1:J:1004:SER:HA	1:J:1007:THR:HG22	1.95	0.47
1:A:597:PHE:CE1	1:A:648:ALA:HB1	2.49	0.47
1:C:287:LEU:O	1:C:291:ILE:HG13	2.13	0.47
3:Z:68:VAL:O	3:Z:71:SER:OG	2.27	0.47
1:J:21:THR:H	1:A:200:ALA:HB1	1.78	0.47
1:J:410:VAL:O	1:J:412:SER:N	2.47	0.47
1:J:598:LYS:CD	1:J:1000:ASN:CB	2.74	0.47
1:J:1221:ASP:OD1	1:J:1222:ALA:N	2.46	0.47
1:A:741:PRO:HG3	2:5:160:LYS:HE2	1.96	0.47
2:4:50:THR:OG1	2:4:283:PRO:O	2.27	0.47
1:J:2:GLU:OE1	1:A:90:LYS:CD	2.63	0.47
1:J:220:LYS:NZ	1:J:1320:GLU:OE2	2.27	0.47
1:J:431:LEU:CG	1:J:1333:MET:CE	2.92	0.47
1:A:21:THR:CG2	1:C:200:ALA:HB2	2.39	0.47
1:A:941:ARG:CG	1:A:992:SER:HB3	2.42	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:359:VAL:HG23	1:C:361:ARG:HH12	1.80	0.47
1:J:210:ILE:O	1:J:213:SER:OG	2.26	0.47
1:J:431:LEU:HA	1:J:436:ALA:O	2.15	0.47
1:J:1214:ILE:HG21	1:J:1272:ILE:HD11	1.96	0.47
1:C:801:GLY:HA3	1:C:890:VAL:HG11	1.97	0.47
2:6:88:ALA:HA	2:6:106:LEU:HD22	1.96	0.47
3:Z:29:PRO:HG2	3:Z:32:ILE:HG12	1.96	0.47
1:J:703:LEU:HA	1:J:703:LEU:HD12	1.72	0.47
1:A:970:ASP:OD1	1:A:993:ARG:HA	2.15	0.47
1:C:177:HIS:CE1	1:C:384:PRO:HD3	2.49	0.47
1:C:344:LEU:HD21	1:C:1086:MET:SD	2.54	0.47
2:6:136:ALA:O	2:6:140:VAL:HG23	2.14	0.47
2:4:164:VAL:HA	2:4:167:ILE:HG22	1.96	0.47
1:C:408:THR:HG23	1:C:1350:HIS:HA	1.97	0.47
1:C:601:VAL:HG12	1:C:601:VAL:O	2.13	0.47
1:C:734:ALA:HB2	1:C:766:LEU:HD11	1.96	0.47
1:J:83:LEU:HD23	1:J:1080:ASN:HD21	1.79	0.47
1:J:400:TYR:CE1	1:J:573:LEU:HD12	2.50	0.47
1:J:796:ARG:O	1:J:945:ASN:ND2	2.41	0.47
1:J:1196:ALA:HB3	1:J:1222:ALA:HB3	1.97	0.47
1:A:682:ARG:HD3	1:A:682:ARG:HA	1.69	0.47
1:A:967:HIS:NE2	1:A:969:HIS:CE1	2.83	0.47
1:C:8:GLU:CB	1:C:45:ARG:HD3	2.43	0.47
1:C:19:PHE:HZ	1:C:23:VAL:H	1.27	0.47
1:C:78:ILE:O	1:C:1058:ILE:HA	2.14	0.47
1:C:426:THR:C	1:C:442:PHE:CE2	2.87	0.47
1:C:431:LEU:HD11	1:C:1337:LEU:HD21	1.97	0.47
1:C:514:GLN:CB	1:C:993:ARG:HH21	1.98	0.47
1:C:694:ASN:HD22	1:C:704:SER:HB3	1.78	0.47
1:C:1004:SER:HA	1:C:1007:THR:HG22	1.95	0.47
2:6:246:ASP:OD2	2:6:281:SER:HB2	2.12	0.47
1:J:667:PRO:HD2	1:J:670:LEU:HD12	1.97	0.47
1:J:718:PRO:CG	1:J:786:LEU:HD23	2.45	0.47
1:J:718:PRO:HG2	1:J:943:TYR:HE2	1.80	0.47
1:A:390:ASP:O	1:A:391:LEU:HD12	2.15	0.47
1:A:434:ASP:HA	1:A:1367:LEU:HD11	1.96	0.47
1:A:1212:LYS:HB3	1:A:1219:GLU:OE1	2.15	0.47
1:A:1244:TYR:HB2	1:A:1266:PHE:CD2	2.49	0.47
2:4:276:ASP:OD2	3:D:49:ARG:NH2	2.48	0.47
1:J:177:HIS:O	1:J:181:GLN:HG2	2.14	0.47
1:J:1069:ARG:NH1	1:J:1069:ARG:CG	2.73	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:408:THR:HG23	1:A:1350:HIS:HA	1.97	0.47
1:A:734:ALA:CB	1:A:766:LEU:HD11	2.44	0.47
1:A:1105:ASP:N	1:A:1168:GLN:O	2.45	0.47
1:C:192:VAL:O	1:C:196:LEU:HG	2.14	0.47
1:C:1233:ALA:HA	1:C:1238:CYS:SG	2.55	0.47
1:C:1325:LEU:HD22	1:C:1344:PHE:CD2	2.49	0.47
1:J:425:PRO:HB3	1:J:1328:THR:HG21	1.97	0.47
1:A:452:PRO:HG3	1:A:1122:TYR:CE1	2.50	0.47
1:A:1109:ARG:HD2	1:A:1169:LYS:HD2	1.95	0.47
1:A:1365:SER:OG	1:A:1366:MET:N	2.48	0.47
1:C:19:PHE:CE1	1:C:21:THR:O	2.68	0.47
1:C:175:LEU:HD11	1:C:1081:ILE:CD1	2.43	0.47
1:C:504:GLU:HG2	1:C:966:TYR:OH	2.15	0.47
2:4:24:THR:HG21	2:4:69:HIS:CG	2.49	0.47
3:D:33:SER:HB2	3:D:36:THR:CB	2.45	0.47
1:J:119:TYR:HH	1:C:2:GLU:CD	2.12	0.46
1:A:739:LEU:CD1	1:A:744:ILE:HG21	2.44	0.46
1:C:880:PHE:HE1	3:E:65:LEU:HG	1.80	0.46
1:C:1290:LYS:HD3	1:C:1312:GLU:HG2	1.97	0.46
1:J:83:LEU:HD23	1:J:1080:ASN:ND2	2.23	0.46
1:J:252:ASP:OD1	1:J:253:SER:N	2.48	0.46
1:J:322:LEU:HD21	1:J:325:PHE:CD1	2.51	0.46
1:J:371:ASN:HD21	1:J:373:ARG:HB3	1.80	0.46
1:J:710:LEU:HD21	1:J:783:VAL:HG22	1.97	0.46
1:J:740:ASN:N	1:J:741:PRO:HD2	2.31	0.46
1:J:819:LEU:HD11	3:Z:32:ILE:CD1	2.45	0.46
1:J:1043:GLU:C	1:J:1044:VAL:HG23	2.34	0.46
1:J:1083:THR:O	1:J:1083:THR:OG1	2.30	0.46
1:A:853:VAL:HG13	1:A:873:LEU:HD21	1.96	0.46
1:C:94:HIS:ND1	1:C:94:HIS:O	2.48	0.46
2:6:19:PHE:HE2	2:6:26:LYS:HZ3	1.50	0.46
2:6:41:CYS:SG	2:6:55:GLU:HG3	2.55	0.46
1:J:27:ALA:CB	1:J:35:LEU:CD2	2.88	0.46
1:J:231:ASN:OD1	1:J:1098:TYR:HE1	1.90	0.46
1:J:682:ARG:HA	1:J:685:THR:HG22	1.96	0.46
1:J:764:GLU:CG	1:J:765:PRO:CD	2.50	0.46
1:J:942:PHE:HZ	1:J:995:SER:HB2	1.79	0.46
1:J:1109:ARG:HD3	1:J:1169:LYS:CE	2.45	0.46
1:A:147:ILE:O	1:A:151:ILE:HG12	2.15	0.46
1:A:342:ASP:OD1	1:A:342:ASP:N	2.47	0.46
1:A:1057:VAL:HG12	1:A:1083:THR:HG22	1.95	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:197:VAL:O	1:C:197:VAL:HG12	2.14	0.46
1:C:510:ASN:OD1	1:C:982:GLU:CD	2.53	0.46
1:C:1015:ILE:O	1:C:1015:ILE:CG2	2.54	0.46
1:J:3:ASN:HD21	1:J:6:ALA:HB2	1.79	0.46
1:J:80:PHE:CB	1:J:1058:ILE:CG2	2.93	0.46
1:J:184:LEU:HD23	1:J:184:LEU:HA	1.81	0.46
1:J:275:SER:CB	1:J:1047:LEU:HD13	2.40	0.46
1:J:450:CYS:SG	1:J:1131:ILE:HD12	2.55	0.46
1:A:1344:PHE:H	1:A:1364:GLN:HE22	1.60	0.46
1:C:7:LEU:CD1	1:C:12:LYS:CD	2.65	0.46
1:C:475:MET:SD	1:C:1218:ARG:NH1	2.88	0.46
1:C:518:VAL:HB	1:C:1179:VAL:HG11	1.97	0.46
1:C:805:LYS:H	1:C:889:HIS:HE1	1.63	0.46
2:6:246:ASP:OD1	2:6:247:SER:N	2.48	0.46
1:J:254:ILE:HD12	1:J:1086:MET:HA	1.97	0.46
1:J:1193:ARG:HB2	1:J:1266:PHE:HE1	1.80	0.46
1:A:207:LEU:HD13	1:A:212:ARG:N	2.30	0.46
1:A:344:LEU:HD23	1:A:344:LEU:HA	1.68	0.46
2:5:35:PRO:O	2:5:39:LYS:HG2	2.16	0.46
2:5:115:ASP:HA	2:6:93:THR:HG21	1.97	0.46
2:4:6:ILE:HG22	2:4:284:GLN:HB3	1.97	0.46
2:4:73:LEU:HD21	2:4:213:VAL:HG11	1.98	0.46
1:J:621:VAL:O	1:J:625:LEU:HG	2.16	0.46
1:A:913:ARG:HH12	1:A:981:HIS:CD2	2.09	0.46
1:A:1058:ILE:HG13	1:A:1082:ASN:HB2	1.96	0.46
1:C:21:THR:O	1:C:22:HIS:C	2.53	0.46
1:C:504:GLU:HB2	1:C:963:PHE:HE2	1.81	0.46
1:C:666:LEU:HD12	1:C:666:LEU:HA	1.84	0.46
1:J:560:ASN:HA	1:J:990:PRO:HG2	1.96	0.46
1:J:808:LEU:CD2	1:J:886:VAL:HG21	2.46	0.46
1:A:464:PHE:CD1	1:A:533:LEU:HD11	2.49	0.46
1:C:408:THR:HG22	1:C:411:GLU:HB2	1.98	0.46
2:6:117:ASP:OD2	2:6:119:ARG:NH2	2.49	0.46
2:4:2:SER:OG	2:4:272:ILE:HG21	2.16	0.46
1:J:382:LYS:HG3	1:J:383:ASP:N	2.31	0.46
1:A:434:ASP:OD1	1:A:434:ASP:N	2.48	0.46
1:A:461:LEU:HD13	1:A:552:CYS:HB2	1.98	0.46
1:A:1021:VAL:O	1:A:1025:LYS:HD3	2.16	0.46
1:C:269:ILE:HD11	1:C:296:VAL:HG22	1.98	0.46
1:C:1044:VAL:HG12	1:C:1045:ASP:N	2.31	0.46
1:J:139:LEU:HD22	1:J:160:VAL:HG21	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:303:GLY:CA	1:J:348:GLY:HA3	2.46	0.46
1:J:431:LEU:HD21	1:J:1333:MET:HE2	1.97	0.46
1:C:147:ILE:O	1:C:151:ILE:HG12	2.16	0.46
1:C:795:ASN:ND2	1:C:942:PHE:CE1	2.83	0.46
2:5:206:THR:O	2:5:210:ILE:HG12	2.16	0.46
2:4:10:ARG:O	2:4:14:VAL:HG23	2.16	0.46
1:J:118:LYS:HD3	1:C:32:PHE:CD1	2.50	0.46
1:A:698:LEU:HB2	1:A:706:TYR:HE2	1.80	0.46
1:A:949:CYS:SG	1:A:956:ILE:HG21	2.55	0.46
1:C:242:PHE:HD2	1:C:243:LEU:HD23	1.81	0.46
1:C:1043:GLU:O	1:C:1044:VAL:HG23	2.16	0.46
1:J:390:ASP:O	1:J:391:LEU:HD12	2.15	0.45
1:J:682:ARG:HA	1:J:682:ARG:HD3	1.79	0.45
1:J:798:CYS:SG	1:J:799:GLY:N	2.89	0.45
1:A:18:ASP:O	1:A:19:PHE:HD1	1.98	0.45
1:A:543:GLN:OE1	1:A:548:THR:HG22	2.16	0.45
1:A:607:PRO:HG3	1:A:638:MET:HE2	1.99	0.45
1:A:766:LEU:HD21	1:A:893:LEU:CD2	2.34	0.45
1:C:341:ASN:OD1	1:C:345:SER:HB3	2.15	0.45
1:C:698:LEU:HD11	1:C:1130:TRP:CD1	2.52	0.45
1:C:1158:GLU:OE1	1:C:1299:THR:HG21	2.16	0.45
1:J:118:LYS:CE	1:C:32:PHE:HE1	2.29	0.45
1:A:795:ASN:ND2	1:A:942:PHE:CE1	2.83	0.45
1:C:360:ILE:HG22	1:C:362:LEU:CD1	2.46	0.45
1:C:1043:GLU:O	1:C:1044:VAL:CG2	2.65	0.45
2:5:67:ARG:O	2:5:70:ASN:HB2	2.16	0.45
2:6:246:ASP:OD2	2:6:281:SER:CA	2.64	0.45
1:J:597:PHE:CZ	1:J:601:VAL:HG21	2.51	0.45
1:J:601:VAL:HG12	1:J:601:VAL:O	2.16	0.45
1:A:625:LEU:HD23	3:D:75:ARG:NH1	2.31	0.45
1:A:1347:SER:O	1:A:1348:GLU:HG3	2.15	0.45
1:A:1350:HIS:O	1:A:1352:GLY:N	2.38	0.45
1:C:515:ASP:OD1	1:C:515:ASP:N	2.49	0.45
1:C:740:ASN:N	1:C:741:PRO:HD2	2.31	0.45
1:C:891:LYS:HE2	1:C:891:LYS:HB3	1.76	0.45
1:C:1042:PHE:CD1	1:C:1102:VAL:HG22	2.50	0.45
1:C:1217:HIS:CE1	1:C:1228:THR:HG1	2.32	0.45
2:5:23:LEU:HD21	2:5:62:TYR:HE1	1.81	0.45
2:5:36:LYS:HE3	2:5:40:LYS:HE2	1.97	0.45
2:6:145:VAL:HG22	2:6:152:GLU:HG2	1.99	0.45
2:4:243:LEU:HD13	3:D:74:ARG:NH1	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:76:HIS:O	1:J:78:ILE:HG13	2.17	0.45
1:J:207:LEU:HD13	1:J:212:ARG:HG3	1.90	0.45
1:A:651:TYR:CD2	1:A:781:GLN:HG2	2.51	0.45
1:C:578:ILE:HG12	1:C:1028:ILE:HD12	1.99	0.45
2:5:194:THR:O	2:5:198:ASN:ND2	2.50	0.45
1:J:341:ASN:OD1	1:J:345:SER:HB3	2.16	0.45
1:A:703:LEU:HA	1:A:703:LEU:HD12	1.69	0.45
1:A:883:VAL:O	1:A:886:VAL:HG23	2.17	0.45
1:C:22:HIS:O	1:C:25:THR:N	2.47	0.45
1:C:293:LYS:HB2	1:C:293:LYS:HE3	1.82	0.45
1:C:574:ARG:O	1:C:577:GLU:HB2	2.16	0.45
2:6:274:ASP:O	2:6:277:ILE:HG22	2.16	0.45
1:J:35:LEU:CD1	1:A:116:VAL:CG1	2.79	0.45
1:J:498:PHE:O	1:J:501:VAL:HG22	2.17	0.45
1:J:628:ARG:NH2	3:Z:75:ARG:HH12	2.14	0.45
1:J:805:LYS:H	1:J:889:HIS:HE1	1.64	0.45
1:J:1237:GLY:O	1:J:1238:CYS:O	2.33	0.45
1:J:1271:ILE:HD12	1:J:1271:ILE:HA	1.81	0.45
1:A:431:LEU:HG	1:A:1333:MET:CE	2.46	0.45
1:C:534:HIS:CD2	1:C:537:PHE:CD1	3.04	0.45
1:C:1285:TYR:CB	1:C:1317:LEU:CD2	2.84	0.45
2:5:32:GLU:OE2	2:5:227:ARG:CZ	2.65	0.45
1:J:486:GLU:HG2	1:J:487:PRO:HD2	1.98	0.45
1:J:1168:GLN:HA	1:J:1298:ASP:O	2.16	0.45
1:A:21:THR:H	1:C:200:ALA:HB1	1.82	0.45
1:A:30:GLU:HB3	1:C:1280:LYS:HD3	1.98	0.45
1:C:122:LYS:HG2	1:C:1082:ASN:HD21	1.81	0.45
1:C:247:ALA:HB1	1:C:365:LYS:HD3	1.98	0.45
1:C:731:GLN:HB3	1:C:738:PRO:HB3	1.97	0.45
1:C:941:ARG:HE	1:C:941:ARG:HB2	1.61	0.45
1:J:273:MET:CE	1:J:1047:LEU:HD21	2.47	0.45
1:J:495:ILE:HD13	1:J:937:VAL:HA	1.99	0.45
1:J:746:ALA:O	1:J:767:PHE:HA	2.17	0.45
1:A:749:HIS:CD2	1:A:769:ASP:OD1	2.69	0.45
1:A:853:VAL:CG1	1:A:873:LEU:CD2	2.94	0.45
1:C:202:LEU:HD12	1:C:203:ALA:N	2.31	0.45
2:4:66:LEU:HB3	2:4:217:TRP:HZ3	1.78	0.45
2:4:211:MET:O	2:4:215:ARG:HG2	2.16	0.45
1:J:647:PHE:O	1:J:654:VAL:CG2	2.65	0.45
1:J:953:SER:HB2	1:J:956:ILE:HD12	1.99	0.45
1:J:1218:ARG:HA	1:J:1218:ARG:HD2	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:78:ILE:HB	1:A:1058:ILE:HG22	1.99	0.45
1:A:681:LEU:HB3	1:A:780:LEU:HD22	1.99	0.45
1:A:746:ALA:O	1:A:767:PHE:HA	2.17	0.45
1:C:2:GLU:OE1	1:C:34:ALA:HB3	2.17	0.45
1:C:344:LEU:CD2	1:C:1086:MET:SD	3.05	0.45
1:C:651:TYR:CD2	1:C:781:GLN:HG2	2.52	0.45
1:C:1296:ASP:OD1	1:C:1297:THR:HG23	2.17	0.45
2:6:107:ALA:O	2:6:111:ARG:HG3	2.17	0.45
2:4:136:ALA:HB2	2:4:200:VAL:HG11	1.99	0.45
1:J:94:HIS:CB	1:C:12:LYS:HE3	2.43	0.45
1:A:132:SER:OG	1:A:135:CYS:SG	2.72	0.45
1:C:5:SER:HA	1:C:8:GLU:HG3	1.99	0.45
1:C:633:ARG:NH1	1:C:870:THR:HB	2.32	0.45
1:C:862:GLU:HG3	1:C:863:ASP:N	2.32	0.45
1:C:1105:ASP:N	1:C:1168:GLN:O	2.34	0.45
1:J:1044:VAL:CG1	1:J:1096:VAL:CG1	2.90	0.44
1:A:18:ASP:O	1:A:19:PHE:CD1	2.70	0.44
1:C:294:GLU:OE1	1:C:359:VAL:HG21	2.17	0.44
1:C:598:LYS:HD3	1:C:1000:ASN:HB3	1.96	0.44
2:6:60:LEU:HA	2:6:60:LEU:HD23	1.75	0.44
2:4:170:ASN:ND2	2:4:182:LYS:O	2.43	0.44
1:J:21:THR:CG2	1:A:200:ALA:CB	2.86	0.44
1:C:79:LYS:O	1:C:304:ASN:HA	2.17	0.44
1:C:1290:LYS:CB	1:C:1310:LEU:HB3	2.47	0.44
1:J:303:GLY:HA2	1:J:348:GLY:HA3	1.98	0.44
1:J:435:ARG:N	1:J:1367:LEU:HD11	2.32	0.44
1:J:650:SER:O	1:J:654:VAL:HG23	2.17	0.44
1:A:68:THR:HG23	1:A:355:LEU:HD13	1.99	0.44
1:A:945:ASN:HD22	1:A:948:ILE:CD1	2.26	0.44
1:C:1130:TRP:CE3	1:C:1131:ILE:HD13	2.52	0.44
1:C:1239:LEU:O	1:C:1243:LEU:HB2	2.17	0.44
2:4:243:LEU:HD22	3:D:74:ARG:HD3	1.99	0.44
3:D:24:VAL:CG1	3:D:54:PHE:HZ	2.30	0.44
1:J:37:ILE:HD11	1:A:114:ILE:HD13	2.00	0.44
1:J:341:ASN:HD21	1:J:345:SER:CB	2.30	0.44
1:J:1038:ARG:NH2	1:J:1324:ILE:HD13	2.32	0.44
1:J:1341:ALA:O	1:J:1364:GLN:NE2	2.50	0.44
1:A:35:LEU:HG	1:A:36:ARG:N	2.31	0.44
1:A:999:PRO:O	1:A:1004:SER:OG	2.36	0.44
1:C:645:LEU:HD11	1:C:674:TYR:CE2	2.52	0.44
1:C:718:PRO:HD3	1:C:786:LEU:HG	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:741:PRO:HB3	2:4:158:HIS:CD2	2.53	0.44
2:5:267:LEU:O	2:5:271:LEU:CG	2.58	0.44
3:D:37:HIS:CD2	3:D:40:LEU:H	2.35	0.44
1:J:941:ARG:HE	1:J:941:ARG:HB2	1.44	0.44
1:A:148:LEU:HD12	1:A:148:LEU:HA	1.84	0.44
1:A:275:SER:OG	1:A:280:MET:HG2	2.18	0.44
1:A:713:HIS:H	1:A:713:HIS:CD2	2.35	0.44
1:A:1240:SER:HG	1:A:1266:PHE:HE2	1.64	0.44
1:C:22:HIS:O	1:C:24:LYS:N	2.51	0.44
1:C:633:ARG:HH22	1:C:870:THR:HG22	1.72	0.44
1:C:1044:VAL:CG1	1:C:1096:VAL:HG13	2.44	0.44
2:6:92:TYR:CE1	2:6:106:LEU:HD13	2.53	0.44
1:J:205:GLN:HG3	1:C:24:LYS:CE	2.47	0.44
1:J:472:GLU:HB2	1:J:475:MET:HG2	1.99	0.44
1:J:1059:ILE:HD12	1:J:1079:GLN:HE22	1.82	0.44
1:A:31:MET:CE	1:C:1279:PHE:CE1	3.00	0.44
1:A:272:VAL:HG23	1:A:368:ILE:HB	1.98	0.44
1:A:1064:VAL:HA	1:A:1076:HIS:O	2.18	0.44
1:C:184:LEU:HD23	1:C:184:LEU:HA	1.74	0.44
1:C:611:TYR:O	1:C:615:VAL:HG23	2.18	0.44
1:C:646:VAL:CG1	1:C:647:PHE:H	2.29	0.44
2:6:244:SER:O	2:6:248:ASN:HB2	2.17	0.44
1:J:94:HIS:HD2	1:J:115:MET:HE3	1.82	0.44
1:J:1042:PHE:CD1	1:J:1102:VAL:HG22	2.53	0.44
1:J:1266:PHE:O	1:J:1268:THR:N	2.49	0.44
1:A:321:ILE:HD13	1:A:321:ILE:HA	1.71	0.44
1:A:1020:LEU:HD12	1:A:1020:LEU:HA	1.70	0.44
1:C:274:VAL:O	1:C:1047:LEU:HD12	2.18	0.44
1:C:425:PRO:HB3	1:C:1328:THR:CG2	2.48	0.44
1:C:504:GLU:HB2	1:C:963:PHE:CE2	2.53	0.44
1:C:790:PRO:O	1:C:995:SER:OG	2.36	0.44
2:5:52:LEU:HB2	2:5:235:LEU:HD13	1.98	0.44
2:6:171:LEU:O	2:6:212:ASN:ND2	2.50	0.44
1:J:128:PRO:HB3	1:J:1076:HIS:ND1	2.33	0.44
1:J:1042:PHE:O	1:J:1044:VAL:HG23	2.17	0.44
1:J:1102:VAL:HG23	1:J:1366:MET:SD	2.58	0.44
1:J:1158:GLU:HB3	1:J:1301:TYR:OH	2.17	0.44
1:A:656:LEU:HB3	1:A:660:HIS:HD2	1.82	0.44
1:C:716:TRP:CZ2	1:C:730:VAL:HG11	2.53	0.44
1:J:396:PRO:O	1:J:397:VAL:HG23	2.17	0.44
1:J:790:PRO:CG	1:J:942:PHE:HE2	2.30	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:1223:GLN:HE21	1:J:1223:GLN:HB3	1.52	0.44
1:A:278:ASN:ND2	1:A:1045:ASP:OD2	2.48	0.44
1:A:518:VAL:HB	1:A:1179:VAL:HG11	2.00	0.44
1:A:625:LEU:HD23	3:D:75:ARG:HH12	1.83	0.44
1:A:716:TRP:HZ2	1:A:730:VAL:HG11	1.83	0.44
1:C:80:PHE:HB3	1:C:1058:ILE:CG2	2.48	0.44
1:C:1217:HIS:CE1	1:C:1228:THR:OG1	2.71	0.44
2:6:26:LYS:CE	2:6:34:HIS:CE1	2.99	0.44
2:6:90:ARG:HD3	2:6:90:ARG:HA	1.40	0.44
2:4:1:MET:N	2:4:64:ARG:HH11	2.16	0.44
1:J:64:VAL:HG12	1:J:65:TYR:N	2.33	0.43
1:A:241:LYS:HA	1:A:244:THR:HG22	1.99	0.43
1:A:1307:THR:OG1	1:A:1308:GLU:OE1	2.29	0.43
1:C:307:LEU:HD23	1:C:307:LEU:HA	1.76	0.43
1:C:689:ALA:HB2	1:C:711:HIS:NE2	2.33	0.43
1:C:737:GLN:NE2	2:4:143:THR:H	2.13	0.43
1:C:1325:LEU:HD22	1:C:1344:PHE:CE2	2.53	0.43
2:5:41:CYS:SG	2:5:54:ASN:HB2	2.58	0.43
2:5:76:VAL:HG11	2:5:209:LEU:HD23	2.00	0.43
2:5:275:PHE:HA	2:5:278:TYR:CE2	2.53	0.43
1:J:268:LYS:O	1:J:366:THR:OG1	2.35	0.43
1:J:639:PHE:CG	1:J:670:LEU:HD21	2.54	0.43
1:J:754:VAL:HB	3:Z:50:MET:HE1	1.99	0.43
1:A:601:VAL:HG12	1:A:601:VAL:O	2.16	0.43
1:A:1063:ILE:O	1:A:1077:VAL:HA	2.17	0.43
1:A:1172:CYS:SG	1:A:1173:GLU:N	2.89	0.43
1:C:1109:ARG:CD	1:C:1169:LYS:HD2	2.47	0.43
2:6:267:LEU:O	2:6:271:LEU:HB2	2.18	0.43
2:4:175:ARG:HB2	2:4:212:ASN:ND2	2.32	0.43
3:D:43:MET:HE2	3:D:47:TYR:OH	2.18	0.43
1:J:37:ILE:HG12	1:A:114:ILE:CG1	2.35	0.43
1:J:86:LEU:O	1:J:86:LEU:HD12	2.18	0.43
1:J:188:PRO:HG3	1:J:1090:TYR:CG	2.53	0.43
1:J:469:PRO:HB3	1:J:479:LEU:HD11	2.00	0.43
1:J:495:ILE:HG13	1:J:976:PRO:HG2	2.01	0.43
1:J:779:THR:O	1:J:783:VAL:HG23	2.18	0.43
1:A:384:PRO:O	1:A:387:ARG:HD3	2.18	0.43
1:A:533:LEU:HB2	1:A:539:PHE:CE2	2.53	0.43
1:A:764:GLU:O	1:A:766:LEU:N	2.52	0.43
1:A:967:HIS:O	1:A:967:HIS:CG	2.71	0.43
1:C:76:HIS:CE1	1:C:78:ILE:HD11	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:359:VAL:HG12	1:C:368:ILE:HD13	2.01	0.43
2:5:118:VAL:CG1	2:6:90:ARG:HH12	2.32	0.43
2:4:161:ASP:O	2:4:165:GLN:HG2	2.18	0.43
1:J:431:LEU:HD11	1:J:1333:MET:CE	2.48	0.43
1:J:1018:VAL:HG12	1:J:1131:ILE:HD11	2.00	0.43
1:J:1109:ARG:HD2	1:J:1169:LYS:HD3	2.00	0.43
1:J:1109:ARG:HD3	1:J:1169:LYS:CD	2.47	0.43
1:A:425:PRO:HB3	1:A:1328:THR:HG21	2.00	0.43
1:A:431:LEU:HD21	1:A:437:VAL:HA	1.96	0.43
1:C:564:GLY:O	1:C:1179:VAL:HG21	2.18	0.43
1:C:1110:VAL:HA	1:C:1171:ALA:HB3	1.99	0.43
1:C:1290:LYS:H	1:C:1290:LYS:HG2	1.63	0.43
1:J:208:ASN:N	1:J:211:GLN:HG3	2.33	0.43
1:J:563:ASP:OD2	1:J:993:ARG:HG2	2.18	0.43
1:J:596:LEU:O	1:J:600:THR:HG22	2.17	0.43
1:J:1026:ALA:HB3	1:J:1028:ILE:HG12	2.01	0.43
1:C:396:PRO:HB3	1:C:1186:PHE:CZ	2.54	0.43
1:C:719:PHE:N	1:C:719:PHE:CD1	2.86	0.43
1:C:1197:SER:HB3	1:C:1214:ILE:HG13	1.99	0.43
1:J:21:THR:HG22	1:A:200:ALA:HB2	1.92	0.43
1:J:79:LYS:HB2	1:J:303:GLY:O	2.19	0.43
1:J:83:LEU:CD1	1:J:1058:ILE:HG22	2.48	0.43
1:J:558:ILE:HD12	1:J:558:ILE:HA	1.80	0.43
1:J:760:MET:SD	1:J:805:LYS:HB2	2.59	0.43
1:J:966:TYR:O	1:J:973:PHE:HB3	2.19	0.43
1:J:983:TYR:HA	1:J:988:ARG:HE	1.84	0.43
1:J:1144:ASP:O	1:J:1148:ILE:HG12	2.17	0.43
1:A:7:LEU:HD11	1:A:12:LYS:CD	2.30	0.43
1:C:529:LEU:O	1:C:1235:GLN:NE2	2.52	0.43
1:C:1257:LYS:HD2	1:C:1257:LYS:N	2.34	0.43
2:5:66:LEU:HD23	2:5:66:LEU:HA	1.71	0.43
2:5:74:SER:OG	2:6:89:ARG:NH2	2.51	0.43
1:J:535:PRO:O	1:J:555:ARG:HD2	2.18	0.43
1:J:628:ARG:NH2	3:Z:75:ARG:HH22	2.10	0.43
1:A:21:THR:N	1:C:200:ALA:HB1	2.34	0.43
1:A:399:LEU:HD23	1:A:399:LEU:HA	1.84	0.43
1:A:485:GLN:HB2	1:A:913:ARG:HH22	1.84	0.43
1:A:534:HIS:ND1	1:A:535:PRO:HD2	2.34	0.43
1:A:1034:LEU:HD23	1:A:1175:ILE:CD1	2.46	0.43
1:A:1285:TYR:O	1:A:1289:ALA:HB3	2.19	0.43
1:C:195:THR:HB	1:C:219:PHE:HE1	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:432:ASN:OD1	1:C:438:GLN:NE2	2.51	0.43
2:4:31:LEU:HD23	2:4:59:TRP:CH2	2.54	0.43
1:J:257:ASN:HB2	1:J:260:THR:HG23	2.00	0.43
1:J:597:PHE:HA	1:J:600:THR:HG22	1.99	0.43
1:J:944:SER:O	1:J:944:SER:OG	2.29	0.43
1:A:193:VAL:CB	1:A:1093:ASN:HD21	2.28	0.43
1:A:698:LEU:HB2	1:A:706:TYR:CE2	2.54	0.43
1:A:1022:LEU:HD12	1:A:1022:LEU:HA	1.69	0.43
1:C:228:PHE:O	1:C:232:ARG:HG3	2.18	0.43
1:C:383:ASP:OD1	1:C:384:PRO:HD2	2.18	0.43
1:C:610:CYS:SG	1:C:647:PHE:HA	2.59	0.43
2:6:170:ASN:HD22	2:6:184:LEU:HD21	1.79	0.43
2:4:274:ASP:OD1	2:4:274:ASP:N	2.52	0.43
1:J:475:MET:O	1:J:478:LEU:HB3	2.18	0.43
1:J:485:GLN:OE1	1:J:913:ARG:CZ	2.67	0.43
1:A:616:LEU:HD23	1:A:616:LEU:HA	1.78	0.43
1:A:1202:VAL:HG11	1:A:1210:ALA:HA	2.01	0.43
1:C:395:PHE:CD2	1:C:1324:ILE:HD11	2.54	0.43
3:D:65:LEU:HD12	3:D:65:LEU:HA	1.87	0.43
1:J:730:VAL:HG22	1:J:897:ALA:HB2	2.01	0.43
1:A:446:LEU:HD12	1:A:446:LEU:HA	1.75	0.43
1:C:19:PHE:HD1	1:C:21:THR:O	2.02	0.43
1:C:292:THR:O	1:C:359:VAL:HG22	2.19	0.43
1:C:601:VAL:CG1	1:C:793:THR:CG2	2.97	0.43
1:C:795:ASN:OD1	1:C:942:PHE:CZ	2.67	0.43
1:C:940:HIS:HB3	1:C:942:PHE:O	2.19	0.43
2:5:6:ILE:HB	2:5:50:THR:HG23	2.00	0.43
3:E:33:SER:HB2	3:E:36:THR:OG1	2.18	0.43
1:J:197:VAL:HA	1:C:20:LEU:HD13	2.00	0.42
1:J:377:LYS:HA	1:J:377:LYS:HD2	1.78	0.42
1:J:505:VAL:HG21	1:J:974:PRO:HG3	2.01	0.42
1:J:582:MET:HE1	1:J:691:PRO:HD2	2.01	0.42
1:J:1328:THR:HB	1:J:1353:ASN:HB3	2.01	0.42
1:A:464:PHE:HD1	1:A:533:LEU:HD11	1.84	0.42
1:A:647:PHE:CD2	1:A:653:LEU:HD13	2.48	0.42
1:A:765:PRO:O	1:A:767:PHE:CD2	2.72	0.42
1:C:280:MET:O	1:C:284:MET:HG2	2.19	0.42
1:C:359:VAL:CG2	1:C:361:ARG:HH12	2.32	0.42
1:C:780:LEU:HD23	1:C:780:LEU:HA	1.85	0.42
2:4:7:GLY:HA3	2:4:46:LEU:HD22	2.00	0.42
3:Z:37:HIS:CE1	3:Z:39:VAL:HG11	2.39	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:504:GLU:HB2	1:J:963:PHE:CE2	2.54	0.42
1:J:1207:THR:O	1:J:1211:THR:HG22	2.19	0.42
1:A:73:ALA:HA	1:A:261:TYR:CZ	2.54	0.42
1:A:1012:LEU:HD12	1:A:1012:LEU:HA	1.70	0.42
1:C:186:LYS:HB2	1:C:186:LYS:HE2	1.60	0.42
1:C:277:ALA:HB2	1:C:371:ASN:HD21	1.84	0.42
1:C:1246:THR:O	1:C:1250:GLU:HG3	2.19	0.42
1:C:1336:LYS:NZ	1:C:1346:THR:HG23	2.34	0.42
2:6:64:ARG:NH1	2:6:268:LEU:HD23	2.34	0.42
1:J:149:ASP:OD2	1:J:153:ASN:ND2	2.53	0.42
1:J:231:ASN:HD21	1:J:1099:VAL:HB	1.85	0.42
1:J:446:LEU:HD21	1:J:1024:THR:HG21	2.00	0.42
1:J:554:PRO:HD3	1:J:907:LEU:HD12	2.02	0.42
1:J:598:LYS:O	1:J:602:THR:HG23	2.20	0.42
1:J:813:TYR:H	3:Z:65:LEU:HD11	1.82	0.42
1:A:452:PRO:O	1:A:456:GLU:HG2	2.19	0.42
1:A:480:GLU:O	1:A:480:GLU:HG3	2.19	0.42
1:A:1131:ILE:HD13	1:A:1131:ILE:HA	1.77	0.42
1:C:273:MET:CE	1:C:1047:LEU:HD11	2.46	0.42
1:C:443:VAL:HG13	1:C:446:LEU:CD1	2.48	0.42
1:C:1007:THR:O	1:C:1011:MET:HG3	2.19	0.42
3:Z:22:VAL:HG13	3:Z:28:LEU:HD12	2.02	0.42
1:J:342:ASP:OD1	1:J:342:ASP:N	2.45	0.42
1:J:947:THR:HG22	1:J:967:HIS:NE2	2.33	0.42
1:A:710:LEU:HB2	1:A:1012:LEU:HD23	2.01	0.42
1:C:431:LEU:HD22	1:C:436:ALA:C	2.40	0.42
1:C:544:GLU:O	1:C:546:SER:N	2.52	0.42
1:C:1044:VAL:CG2	1:C:1099:VAL:CG2	2.95	0.42
1:C:1336:LYS:HE3	1:C:1355:VAL:HG11	2.00	0.42
1:J:80:PHE:CD2	1:J:86:LEU:CD2	3.02	0.42
1:A:627:ILE:O	1:A:631:VAL:HG12	2.19	0.42
1:C:270:SER:OG	1:C:365:LYS:CG	2.67	0.42
1:C:360:ILE:O	1:C:366:THR:HA	2.20	0.42
1:C:1090:TYR:HE2	1:C:1282:ILE:HD11	1.84	0.42
2:5:84:CYS:SG	2:5:112:THR:HG21	2.59	0.42
2:6:175:ARG:HG3	2:6:216:SER:OG	2.20	0.42
1:J:431:LEU:HG	1:J:1333:MET:HE2	2.00	0.42
1:J:598:LYS:CD	1:J:1000:ASN:HB2	2.46	0.42
1:J:742:ALA:HB3	2:6:192:ALA:HB1	2.00	0.42
1:J:808:LEU:HD23	1:J:883:VAL:HG13	2.01	0.42
1:A:208:ASN:OD1	1:A:209:ARG:N	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:694:ASN:OD1	1:A:694:ASN:N	2.52	0.42
1:A:1105:ASP:OD1	1:A:1169:LYS:HA	2.19	0.42
1:C:445:ALA:HA	1:C:1110:VAL:HG21	2.01	0.42
2:6:260:ASN:O	2:6:263:SER:N	2.38	0.42
1:J:99:ARG:HD2	1:J:109:SER:O	2.19	0.42
1:J:175:LEU:HD13	1:J:1081:ILE:HD11	2.02	0.42
1:J:443:VAL:HG13	1:J:446:LEU:CD1	2.49	0.42
1:J:596:LEU:HD23	1:J:673:HIS:CD2	2.55	0.42
1:J:661:LEU:HD23	1:J:666:LEU:HD13	2.01	0.42
1:A:234:ARG:HH12	1:A:282:ILE:HD13	1.85	0.42
1:A:601:VAL:HG11	1:A:793:THR:CG2	2.50	0.42
1:A:1124:HIS:HE1	1:A:1126:GLU:HB3	1.84	0.42
1:C:157:MET:O	1:C:161:LEU:HG	2.20	0.42
1:C:447:LYS:HB2	1:C:447:LYS:HE3	1.78	0.42
2:6:160:LYS:HE3	2:6:160:LYS:HB2	1.83	0.42
2:4:235:LEU:HD23	2:4:254:LEU:HD21	2.02	0.42
1:J:343:SER:HA	1:J:346:GLN:CB	2.50	0.42
1:J:1008:LEU:O	1:J:1012:LEU:HG	2.20	0.42
1:J:1239:LEU:HD12	1:J:1239:LEU:C	2.38	0.42
1:J:1291:ASP:N	1:J:1291:ASP:OD1	2.51	0.42
1:A:958:ARG:HA	1:A:961:THR:HG22	2.02	0.42
1:C:639:PHE:CG	1:C:670:LEU:HD21	2.54	0.42
1:C:746:ALA:O	1:C:767:PHE:HD1	2.03	0.42
1:C:894:GLU:HG2	1:C:915:HIS:CD2	2.55	0.42
2:4:66:LEU:HB3	2:4:217:TRP:CH2	2.54	0.42
1:J:372:LEU:O	1:J:375:VAL:HG22	2.19	0.42
1:J:514:GLN:NE2	1:J:563:ASP:H	2.17	0.42
1:J:517:VAL:CG1	1:J:518:VAL:N	2.82	0.42
1:J:770:ASP:OD1	1:J:771:TYR:N	2.52	0.42
1:J:1073:THR:O	1:J:1073:THR:OG1	2.38	0.42
1:A:210:ILE:O	1:A:213:SER:OG	2.18	0.42
1:A:426:THR:O	1:A:442:PHE:CE2	2.73	0.42
1:A:638:MET:SD	1:A:642:ARG:NH2	2.93	0.42
1:A:1054:CYS:HB2	1:A:1091:THR:OG1	2.19	0.42
1:C:698:LEU:HB2	1:C:706:TYR:CE2	2.44	0.42
1:C:1202:VAL:HG11	1:C:1210:ALA:HB2	2.02	0.42
1:C:1358:GLU:OE2	1:C:1361:PRO:HA	2.20	0.42
1:A:676:ASN:O	1:A:680:VAL:HG23	2.20	0.42
1:A:709:ALA:HB2	1:A:1014:LYS:HG2	2.01	0.42
1:A:1291:ASP:OD1	1:A:1291:ASP:N	2.52	0.42
1:C:1193:ARG:HG3	1:C:1266:PHE:HE1	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1200:LEU:HA	1:C:1200:LEU:HD23	1.84	0.42
1:J:396:PRO:HD3	1:J:1186:PHE:CD2	2.55	0.41
1:J:417:ASN:O	1:J:422:ASN:ND2	2.42	0.41
1:J:582:MET:SD	1:J:691:PRO:HD2	2.60	0.41
1:J:1087:GLY:HA3	1:J:1091:THR:HG21	2.02	0.41
1:A:628:ARG:HG3	1:A:661:LEU:HD11	2.03	0.41
1:A:710:LEU:HD12	1:A:1012:LEU:HD23	2.02	0.41
1:A:1268:THR:O	1:A:1272:ILE:HG12	2.20	0.41
1:C:91:MET:O	1:C:117:THR:HA	2.20	0.41
1:C:651:TYR:HA	1:C:654:VAL:HG12	2.02	0.41
1:C:719:PHE:HE2	1:C:922:CYS:CA	2.33	0.41
1:C:801:GLY:HA3	1:C:890:VAL:CG1	2.49	0.41
2:5:285:SER:O	2:5:285:SER:OG	2.36	0.41
1:J:218:SER:O	1:J:222:LYS:HG2	2.20	0.41
1:J:343:SER:HA	1:J:346:GLN:HB3	2.02	0.41
1:J:558:ILE:N	1:J:1013:TYR:O	2.49	0.41
1:J:1123:ARG:HE	1:J:1123:ARG:HB2	1.58	0.41
1:J:1336:LYS:NZ	1:J:1346:THR:O	2.45	0.41
1:A:457:PRO:HD3	1:A:537:PHE:CZ	2.55	0.41
1:A:553:THR:HG23	1:A:910:PHE:CE1	2.56	0.41
1:C:687:ILE:HD12	1:C:1006:MET:CE	2.39	0.41
2:6:170:ASN:CB	2:6:184:LEU:HD21	2.49	0.41
2:4:56:LEU:HD21	2:4:232:CYS:SG	2.60	0.41
3:D:47:TYR:CZ	3:D:64:LEU:CD2	3.02	0.41
1:J:632:ALA:O	1:J:636:VAL:HG12	2.20	0.41
1:A:435:ARG:HH21	1:A:1364:GLN:HA	1.85	0.41
1:C:424:LEU:HD12	1:C:425:PRO:HD2	2.02	0.41
1:C:1131:ILE:HD13	1:C:1131:ILE:HA	1.82	0.41
1:C:1350:HIS:C	1:C:1352:GLY:H	2.22	0.41
3:Z:20:HIS:O	3:Z:24:VAL:N	2.45	0.41
1:J:37:ILE:CG2	1:A:112:THR:CG2	2.98	0.41
1:J:442:PHE:CE2	1:J:1030:PRO:HD2	2.55	0.41
1:J:1251:ARG:H	1:J:1251:ARG:HD2	1.84	0.41
1:J:1347:SER:C	1:J:1348:GLU:HG3	2.41	0.41
1:A:438:GLN:HE22	1:A:1107:GLY:HA2	1.84	0.41
1:A:513:LYS:HZ1	1:A:531:THR:HG22	1.86	0.41
1:A:661:LEU:HD23	1:A:666:LEU:HD13	2.02	0.41
1:C:79:LYS:HA	1:C:1059:ILE:O	2.21	0.41
1:C:396:PRO:HD3	1:C:1186:PHE:CD1	2.55	0.41
1:C:449:LEU:HB3	1:C:1020:LEU:HD23	2.02	0.41
1:C:458:ALA:HB3	1:C:459:PRO:HD3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:638:MET:CE	1:C:642:ARG:HD2	2.50	0.41
1:C:1160:ASN:OD1	1:C:1298:ASP:CB	2.55	0.41
1:A:207:LEU:HD11	1:A:212:ARG:NE	2.35	0.41
1:A:867:ASP:HB3	1:A:870:THR:HG23	2.01	0.41
1:A:1110:VAL:HA	1:A:1171:ALA:HB3	2.03	0.41
1:C:291:ILE:HG12	1:C:360:ILE:HG12	2.03	0.41
1:C:343:SER:HA	1:C:346:GLN:CB	2.45	0.41
1:C:463:THR:O	1:C:467:ARG:NH1	2.53	0.41
1:C:598:LYS:CD	1:C:1000:ASN:HB2	2.50	0.41
1:C:727:MET:HB2	1:C:730:VAL:HB	2.02	0.41
2:5:235:LEU:O	2:5:239:LEU:HG	2.21	0.41
1:J:604:PRO:C	1:J:606:TYR:H	2.24	0.41
1:A:536:PHE:CD1	1:A:1015:ILE:CG2	2.97	0.41
2:6:234:LEU:O	2:6:238:GLU:HG2	2.21	0.41
1:J:274:VAL:CG1	1:J:385:LEU:HD11	2.45	0.41
1:J:544:GLU:CD	1:J:549:VAL:HG21	2.41	0.41
1:J:677:LEU:HD23	1:J:677:LEU:HA	1.88	0.41
1:A:75:ALA:HB1	1:A:1057:VAL:HG22	2.03	0.41
1:C:80:PHE:O	1:C:83:LEU:HB2	2.20	0.41
1:C:276:THR:OG1	1:C:1045:ASP:OD2	2.39	0.41
1:C:746:ALA:O	1:C:767:PHE:HA	2.21	0.41
1:C:989:SER:N	1:C:990:PRO:HD2	2.36	0.41
1:C:1109:ARG:HD2	1:C:1169:LYS:HD2	2.02	0.41
1:C:1174:LEU:O	1:C:1176:LEU:HG	2.20	0.41
2:6:71:PRO:HD3	2:6:179:PHE:HE1	1.86	0.41
2:4:41:CYS:SG	2:4:55:GLU:HG3	2.61	0.41
3:Z:44:LEU:HD23	3:Z:44:LEU:HA	1.93	0.41
1:J:272:VAL:HG23	1:J:368:ILE:HB	2.01	0.41
1:J:322:LEU:HD11	1:J:325:PHE:HA	2.01	0.41
1:J:384:PRO:O	1:J:387:ARG:HD3	2.20	0.41
1:J:1232:TRP:CD1	1:J:1232:TRP:N	2.88	0.41
1:A:207:LEU:HB2	1:A:211:GLN:HB2	2.03	0.41
1:A:457:PRO:HG3	1:A:537:PHE:CD2	2.56	0.41
1:A:1132:ARG:HD3	1:A:1132:ARG:HA	1.90	0.41
1:C:227:LEU:HD12	1:C:227:LEU:HA	1.71	0.41
1:C:540:THR:OG1	1:C:541:HIS:N	2.54	0.41
1:C:995:SER:HA	1:C:998:CYS:SG	2.61	0.41
2:5:189:ASP:OD1	2:5:198:ASN:HB3	2.21	0.41
2:6:171:LEU:HD23	2:6:171:LEU:HA	1.93	0.41
1:J:291:ILE:HA	1:J:359:VAL:O	2.21	0.41
1:J:291:ILE:HG12	1:J:360:ILE:HG23	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:652:ALA:O	1:J:656:LEU:HG	2.21	0.41
1:J:1131:ILE:HD13	1:J:1131:ILE:HA	1.78	0.41
1:J:1279:PHE:HA	1:J:1282:ILE:HG12	2.02	0.41
1:J:1280:LYS:HA	1:J:1280:LYS:HD2	1.94	0.41
1:A:23:VAL:HG12	1:C:114:ILE:CD1	2.51	0.41
1:A:193:VAL:CG2	1:A:1093:ASN:OD1	2.54	0.41
1:A:630:PHE:CZ	1:A:879:LEU:CG	3.02	0.41
1:A:633:ARG:NH1	1:A:870:THR:HG21	2.36	0.41
1:A:716:TRP:CZ2	1:A:730:VAL:HG11	2.56	0.41
1:A:747:ARG:CZ	1:A:749:HIS:HE1	2.33	0.41
1:A:760:MET:HB3	1:A:889:HIS:HD2	1.86	0.41
1:A:780:LEU:HD23	1:A:780:LEU:HA	1.85	0.41
1:A:1109:ARG:HH11	1:A:1169:LYS:CD	2.33	0.41
1:A:1132:ARG:HB3	1:A:1137:VAL:O	2.20	0.41
1:C:79:LYS:HB2	1:C:303:GLY:O	2.21	0.41
1:C:495:ILE:HD13	1:C:937:VAL:HA	2.02	0.41
1:C:941:ARG:HG3	1:C:992:SER:HB3	2.03	0.41
1:C:1359:ILE:HG23	1:C:1360:ILE:HG13	2.03	0.41
2:5:152:GLU:O	2:5:153:PRO:C	2.55	0.41
2:6:17:VAL:O	2:6:21:ARG:HG3	2.20	0.41
3:E:69:ALA:O	3:E:73:THR:CG2	2.57	0.41
1:J:431:LEU:CD2	1:J:1333:MET:HE2	2.50	0.41
1:J:549:VAL:H	1:J:549:VAL:HG22	1.61	0.41
1:J:957:LYS:HE3	1:J:957:LYS:HB2	1.76	0.41
1:A:21:THR:CA	1:C:200:ALA:HB1	2.51	0.41
1:A:488:MET:SD	1:A:894:GLU:HB2	2.61	0.41
1:A:1344:PHE:CB	1:A:1364:GLN:NE2	2.67	0.41
1:C:4:TRP:O	1:C:7:LEU:HB3	2.21	0.41
1:C:855:GLU:O	1:C:859:GLU:HG2	2.21	0.41
1:C:945:ASN:HD22	1:C:948:ILE:CD1	2.34	0.41
1:J:448:THR:CG2	1:J:1113:LEU:HD13	2.50	0.40
1:J:480:GLU:H	1:J:480:GLU:HG3	1.67	0.40
1:J:672:PHE:HD1	1:J:672:PHE:HA	1.69	0.40
1:J:741:PRO:HB3	2:6:158:HIS:ND1	2.35	0.40
1:J:813:TYR:OH	3:Z:28:LEU:HD23	2.21	0.40
1:J:1268:THR:O	1:J:1272:ILE:HG12	2.21	0.40
1:A:7:LEU:HD23	1:C:115:MET:SD	2.60	0.40
1:A:20:LEU:HD13	1:C:197:VAL:CG2	2.47	0.40
2:6:81:GLU:OE2	2:6:113:GLU:HA	2.21	0.40
2:4:225:LEU:HA	2:4:225:LEU:HD23	1.71	0.40
2:4:271:LEU:O	2:4:271:LEU:HD23	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:66:ARG:O	3:D:70:VAL:HG23	2.22	0.40
1:J:1288:ARG:O	1:J:1290:LYS:N	2.54	0.40
1:J:1350:HIS:C	1:J:1352:GLY:H	2.23	0.40
1:A:394:PHE:HB2	1:A:1037:VAL:HG12	2.03	0.40
1:A:706:TYR:HD1	1:A:900:ASP:OD2	2.04	0.40
1:A:807:LEU:HD13	1:A:933:TYR:CD2	2.57	0.40
1:C:734:ALA:CB	1:C:766:LEU:HD21	2.51	0.40
1:J:11:PRO:HB2	1:A:339:LEU:HD13	2.03	0.40
1:J:649:HIS:HD2	1:J:922:CYS:O	2.04	0.40
1:J:688:SER:CB	1:J:708:ASN:HD22	2.34	0.40
1:J:1038:ARG:NH1	1:J:1106:MET:O	2.54	0.40
1:A:227:LEU:HD12	1:A:227:LEU:HA	1.76	0.40
1:A:519:THR:O	1:A:523:LYS:NZ	2.54	0.40
1:C:533:LEU:HB2	1:C:539:PHE:CE2	2.56	0.40
1:C:947:THR:HG22	1:C:967:HIS:CE1	2.56	0.40
1:C:1112:ASP:OD1	1:C:1112:ASP:N	2.52	0.40
2:5:167:ILE:HD11	2:5:205:TYR:CD1	2.56	0.40
2:6:19:PHE:CE2	2:6:37:ILE:HG13	2.56	0.40
2:6:71:PRO:HD3	2:6:179:PHE:CE1	2.55	0.40
2:6:121:ASP:OD2	2:6:214:ARG:NH2	2.54	0.40
1:J:114:ILE:CG2	1:C:35:LEU:HD11	2.52	0.40
1:J:396:PRO:O	1:J:397:VAL:CG2	2.70	0.40
1:J:719:PHE:HD1	1:J:917:LEU:HD23	1.86	0.40
1:J:1175:ILE:HD13	1:J:1175:ILE:HA	1.91	0.40
1:J:1238:CYS:SG	1:J:1241:ASP:HB2	2.61	0.40
1:J:1325:LEU:HA	1:J:1356:VAL:O	2.21	0.40
1:A:454:LEU:HD12	1:A:454:LEU:HA	1.52	0.40
1:A:703:LEU:HG	1:A:1022:LEU:HD21	2.03	0.40
1:A:860:LEU:O	1:A:864:VAL:HB	2.22	0.40
1:A:1266:PHE:HD1	1:A:1266:PHE:N	2.20	0.40
1:C:354:PRO:O	1:C:355:LEU:HG	2.21	0.40
1:C:508:THR:CG2	1:C:982:GLU:OE1	2.70	0.40
1:C:1199:MET:HB3	1:C:1275:ASN:HB3	2.04	0.40
2:5:190:ARG:HB2	2:5:193:ASN:ND2	2.37	0.40
1:J:202:LEU:HD12	1:J:203:ALA:N	2.36	0.40
1:J:411:GLU:O	1:J:411:GLU:HG2	2.20	0.40
1:J:647:PHE:CD2	1:J:653:LEU:HD13	2.50	0.40
1:J:1279:PHE:HD1	1:J:1282:ILE:HD11	1.86	0.40
1:A:450:CYS:SG	1:A:1131:ILE:HD12	2.61	0.40
1:A:487:PRO:HB3	1:A:736:ARG:HG3	2.04	0.40
1:A:1251:ARG:HD2	1:A:1251:ARG:H	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:263:THR:HG22	1:C:264:SER:O	2.21	0.40
1:C:388:ASN:OD1	1:C:1043:GLU:CD	2.60	0.40
1:C:435:ARG:H	1:C:1367:LEU:HD11	1.85	0.40
1:C:739:LEU:HD21	1:C:766:LEU:CD1	2.52	0.40
1:C:1037:VAL:HG22	1:C:1172:CYS:HB3	2.03	0.40
1:C:1365:SER:O	1:C:1369:ASN:CB	2.69	0.40
2:5:159:LEU:HD23	2:5:159:LEU:HA	1.91	0.40
2:4:42:GLY:HA2	2:4:45:ARG:NH2	2.36	0.40
3:D:26:LEU:HD23	3:D:26:LEU:HA	1.66	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	1322/1370 (96%)	1242 (94%)	73 (6%)	7 (0%)	29	68
1	C	1344/1370 (98%)	1255 (93%)	78 (6%)	11 (1%)	19	59
1	J	1344/1370 (98%)	1262 (94%)	71 (5%)	11 (1%)	19	59
2	4	283/285 (99%)	273 (96%)	10 (4%)	0	100	100
2	5	283/285 (99%)	271 (96%)	11 (4%)	1 (0%)	34	71
2	6	283/285 (99%)	274 (97%)	8 (3%)	1 (0%)	34	71
3	D	61/75 (81%)	60 (98%)	1 (2%)	0	100	100
3	E	61/75 (81%)	60 (98%)	1 (2%)	0	100	100
3	Z	61/75 (81%)	59 (97%)	2 (3%)	0	100	100
4	p	288/290 (99%)	273 (95%)	13 (4%)	2 (1%)	22	61
5	q	239/306 (78%)	231 (97%)	7 (3%)	1 (0%)	34	71
5	r	302/306 (99%)	288 (95%)	14 (5%)	0	100	100
All	All	5871/6092 (96%)	5548 (94%)	289 (5%)	34 (1%)	29	64

All (34) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	J	409	THR
1	J	410	VAL
1	J	764	GLU
1	J	1070	ASP
1	J	1238	CYS
1	A	764	GLU
1	A	1222	ALA
1	C	409	THR
1	C	764	GLU
1	C	1222	ALA
1	J	1222	ALA
1	A	409	THR
1	A	410	VAL
1	A	411	GLU
1	C	410	VAL
1	C	411	GLU
1	C	1159	ARG
1	C	1160	ASN
2	5	261	GLY
2	6	261	GLY
4	p	73	GLY
1	J	411	GLU
1	J	1352	GLY
1	C	545	ASN
1	C	970	ASP
1	C	1352	GLY
5	q	239	MET
1	J	605	ASN
1	J	736	ARG
1	A	1352	GLY
4	p	244	CYS
1	C	23	VAL
1	J	147	ILE
1	A	765	PRO

5.3.2 Protein sidechains

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	1155/1192 (97%)	1137 (98%)	18 (2%)	62	83
1	C	1174/1192 (98%)	1156 (98%)	18 (2%)	65	84
1	J	1174/1192 (98%)	1149 (98%)	25 (2%)	53	78
2	4	256/257 (100%)	254 (99%)	2 (1%)	81	91
2	5	256/257 (100%)	255 (100%)	1 (0%)	91	97
2	6	256/257 (100%)	256 (100%)	0	100	100
3	D	59/68 (87%)	59 (100%)	0	100	100
3	E	59/68 (87%)	59 (100%)	0	100	100
3	Z	59/68 (87%)	59 (100%)	0	100	100
4	p	252/252 (100%)	249 (99%)	3 (1%)	71	87
5	q	214/273 (78%)	213 (100%)	1 (0%)	88	95
5	r	272/273 (100%)	272 (100%)	0	100	100
All	All	5186/5349 (97%)	5118 (99%)	68 (1%)	70	86

All (68) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	J	20	LEU
1	J	260	THR
1	J	360	ILE
1	J	480	GLU
1	J	497	HIS
1	J	510	ASN
1	J	549	VAL
1	J	553	THR
1	J	671	LEU
1	J	764	GLU
1	J	766	LEU
1	J	811	LEU
1	J	953	SER
1	J	1057	VAL
1	J	1069	ARG
1	J	1096	VAL
1	J	1149	SER
1	J	1164	THR
1	J	1239	LEU
1	J	1242	VAL

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Mol	Chain	Res	Type
1	J	1256	SER
1	J	1303	CYS
1	J	1329	THR
1	J	1353	ASN
1	J	1365	SER
1	A	83	LEU
1	A	259	THR
1	A	375	VAL
1	A	394	PHE
1	A	440	ILE
1	A	549	VAL
1	A	771	TYR
1	A	800	LEU
1	A	949	CYS
1	A	1077	VAL
1	A	1095	CYS
1	A	1099	VAL
1	A	1282	ILE
1	A	1320	GLU
1	A	1324	ILE
1	A	1328	THR
1	A	1362	LEU
1	A	1365	SER
1	C	405	ARG
1	C	480	GLU
1	C	654	VAL
1	C	727	MET
1	C	764	GLU
1	C	772	ARG
1	C	798	CYS
1	C	1002	LEU
1	C	1059	ILE
1	C	1099	VAL
1	C	1152	THR
1	C	1180	THR
1	C	1240	SER
1	C	1249	ARG
1	C	1292	CYS
1	C	1303	CYS
1	C	1324	ILE
1	C	1328	THR
2	5	182	LYS

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Mol	Chain	Res	Type
2	4	178	MET
2	4	212	ASN
4	p	28	ARG
4	p	118	LEU
4	p	158	LEU
5	q	114	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (93) such sidechains are listed below:

Mol	Chain	Res	Type
1	J	3	ASN
1	J	22	HIS
1	J	76	HIS
1	J	94	HIS
1	J	181	GLN
1	J	231	ASN
1	J	514	GLN
1	J	649	HIS
1	J	713	HIS
1	J	722	HIS
1	J	889	HIS
1	J	901	HIS
1	J	903	GLN
1	J	985	ASN
1	J	1029	HIS
1	J	1080	ASN
1	J	1093	ASN
1	J	1111	GLN
1	J	1141	GLN
1	J	1166	HIS
1	J	1223	GLN
1	A	76	HIS
1	A	181	GLN
1	A	205	GLN
1	A	231	ASN
1	A	438	GLN
1	A	649	HIS
1	A	713	HIS
1	A	722	HIS
1	A	794	ASN
1	A	889	HIS
1	A	901	HIS

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Mol	Chain	Res	Type
1	A	903	GLN
1	A	914	GLN
1	A	915	HIS
1	A	945	ASN
1	A	969	HIS
1	A	985	ASN
1	A	1000	ASN
1	A	1093	ASN
1	A	1111	GLN
1	A	1364	GLN
1	C	3	ASN
1	C	181	GLN
1	C	205	GLN
1	C	231	ASN
1	C	311	ASN
1	C	438	GLN
1	C	485	GLN
1	C	534	HIS
1	C	673	HIS
1	C	713	HIS
1	C	722	HIS
1	C	737	GLN
1	C	794	ASN
1	C	869	HIS
1	C	889	HIS
1	C	901	HIS
1	C	903	GLN
1	C	914	GLN
1	C	985	ASN
1	C	1000	ASN
1	C	1003	HIS
1	C	1029	HIS
1	C	1141	GLN
1	C	1160	ASN
1	C	1223	GLN
1	C	1350	HIS
1	C	1353	ASN
1	C	1364	GLN
2	5	22	HIS
2	5	34	HIS
2	5	54	ASN
2	5	229	GLN

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Mol	Chain	Res	Type
2	5	252	ASN
2	6	170	ASN
2	6	252	ASN
2	6	260	ASN
2	4	158	HIS
2	4	252	ASN
3	Z	37	HIS
3	D	20	HIS
3	E	37	HIS
4	p	183	GLN
4	p	266	HIS
5	q	39	HIS
5	q	50	GLN
5	q	54	HIS
5	q	147	ASN
5	q	192	HIS
5	q	235	GLN
5	r	50	GLN
5	r	191	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](#)

There are no non-standard protein/DNA/RNA residues in this entry.

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

There are no chain breaks in this entry.

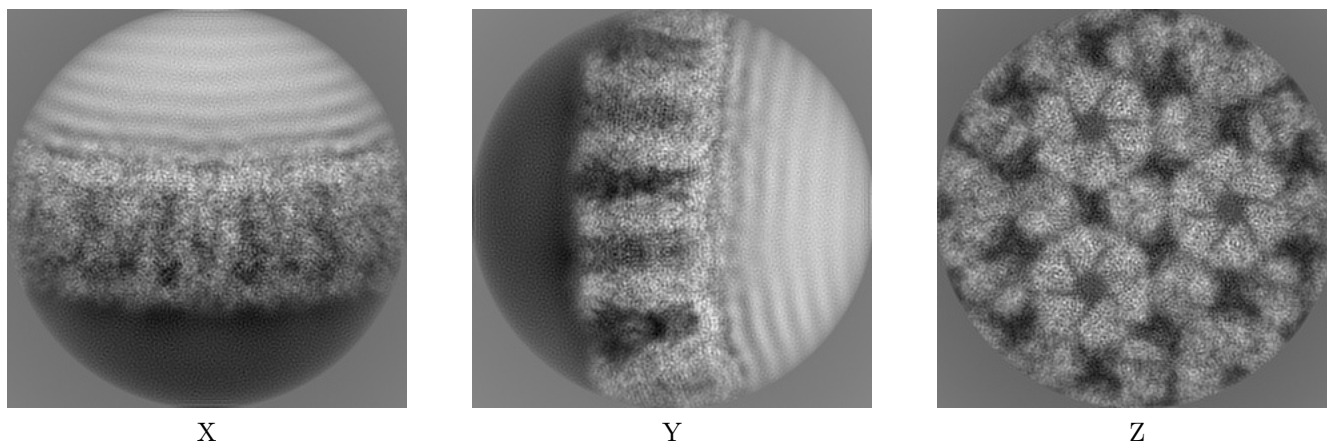
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23386. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

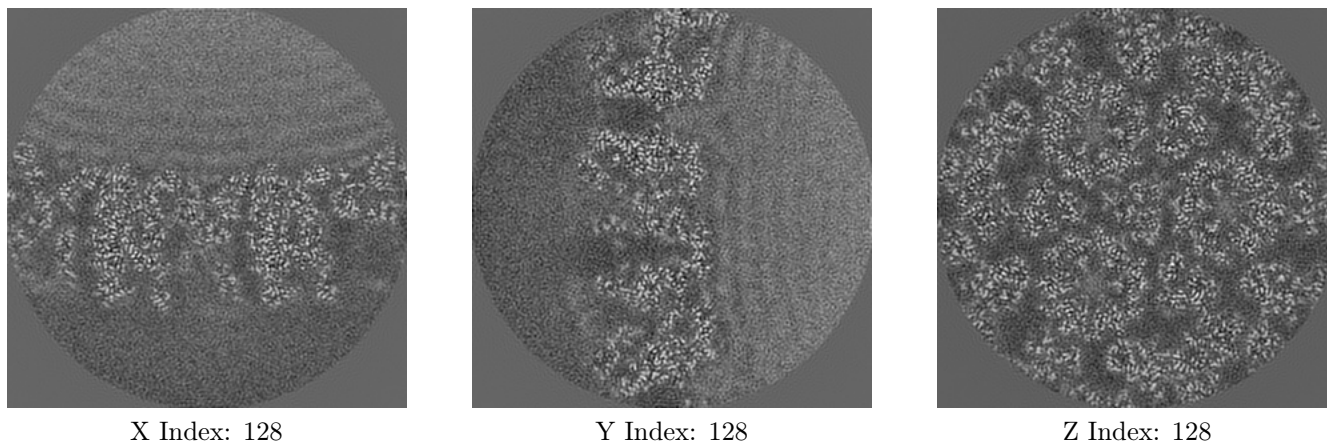
6.1.1 Primary map



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

6.2 Central slices [i](#)

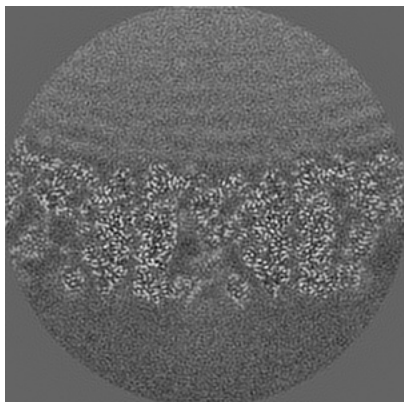
6.2.1 Primary map



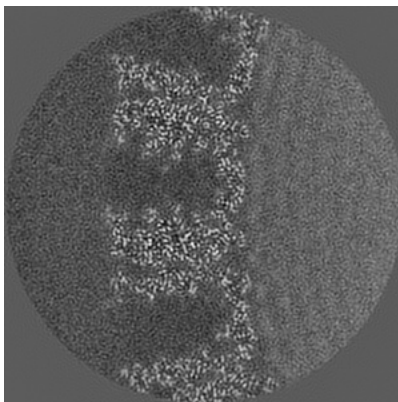
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

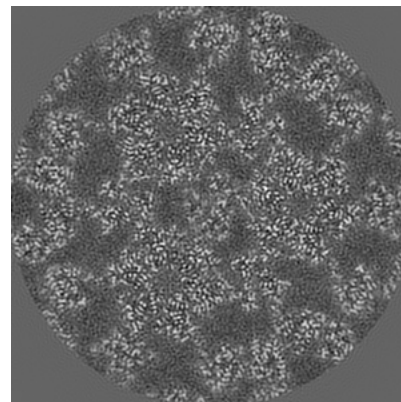
6.3.1 Primary map



X Index: 119



Y Index: 153

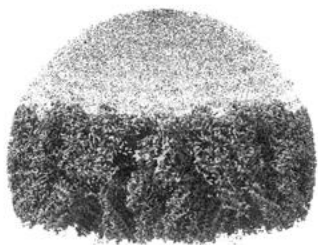


Z Index: 121

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

6.4 Orthogonal surface views [i](#)

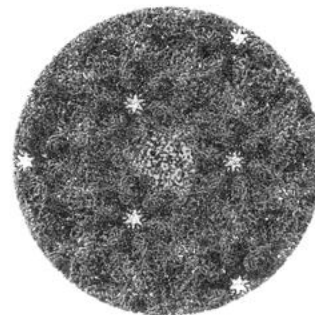
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

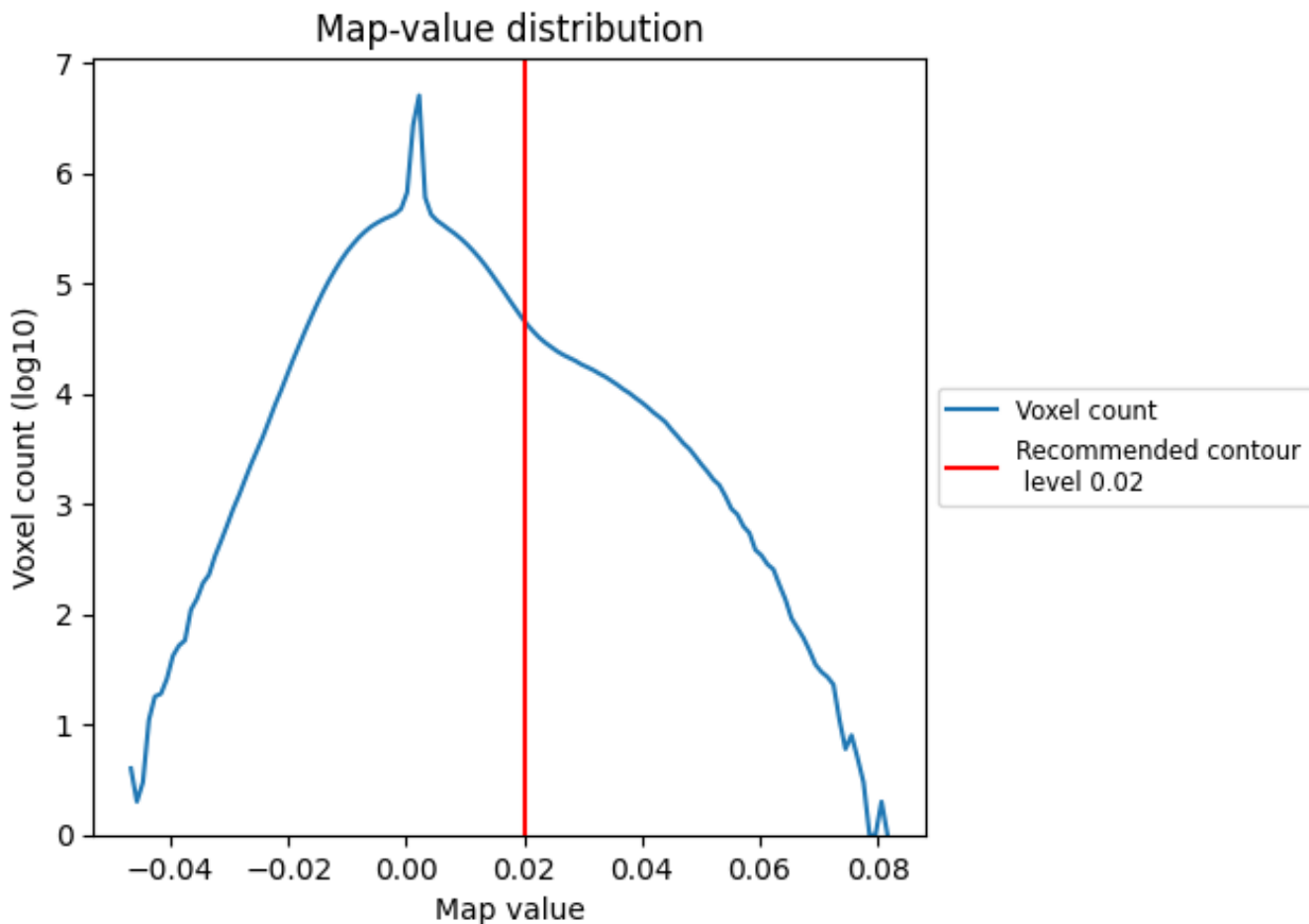
6.5 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

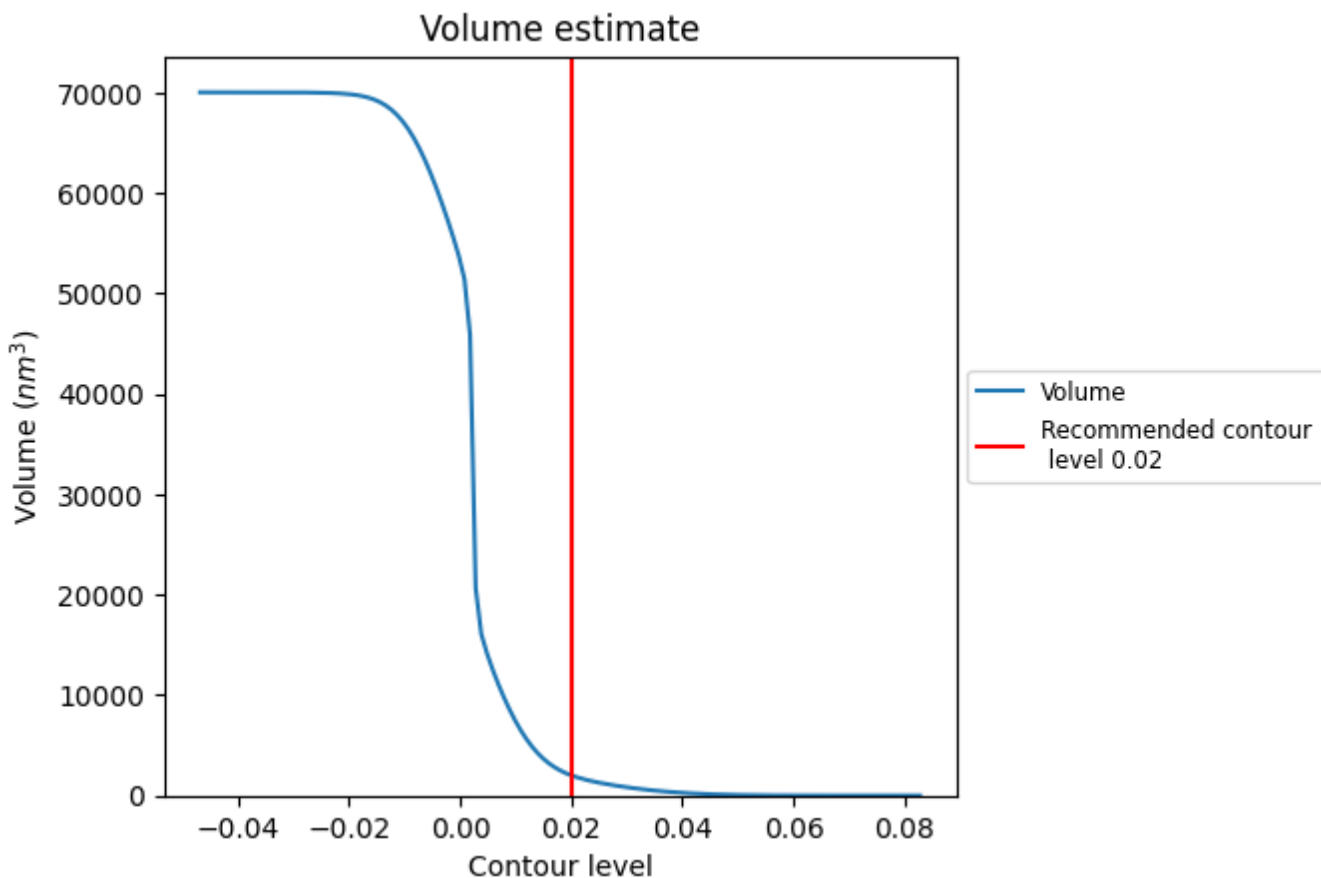
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

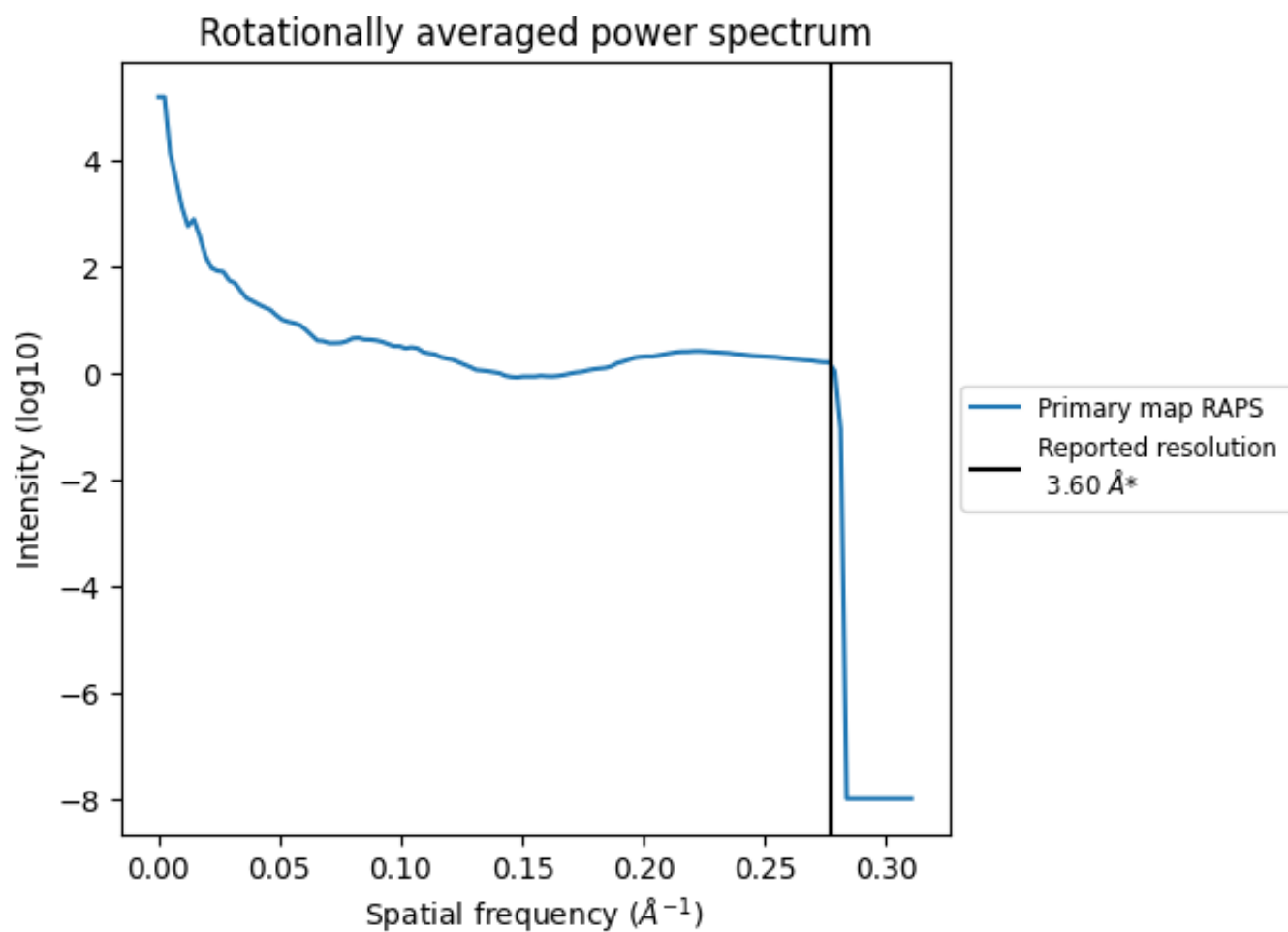
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2015 nm³; this corresponds to an approximate mass of 1820 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum i



*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

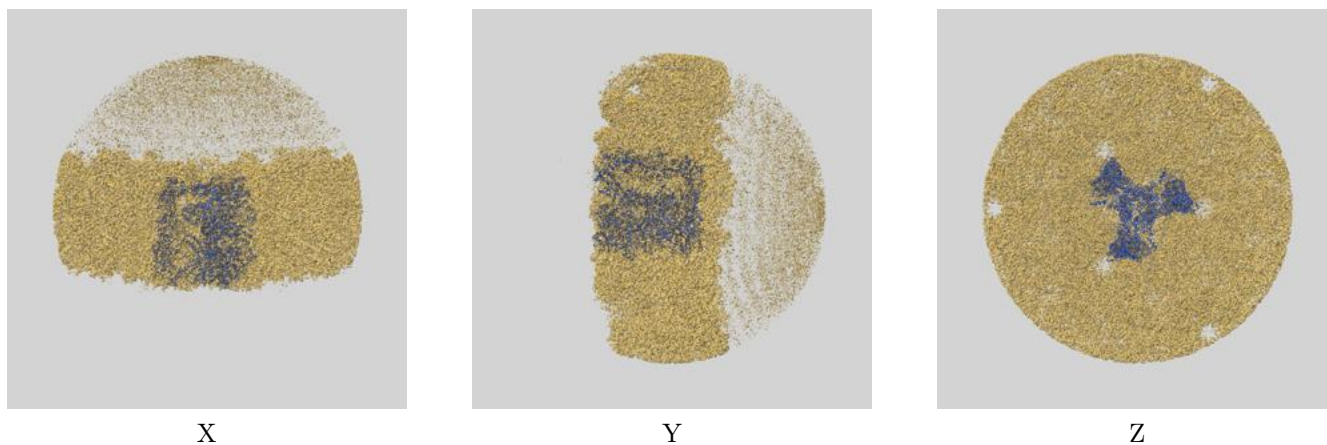
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

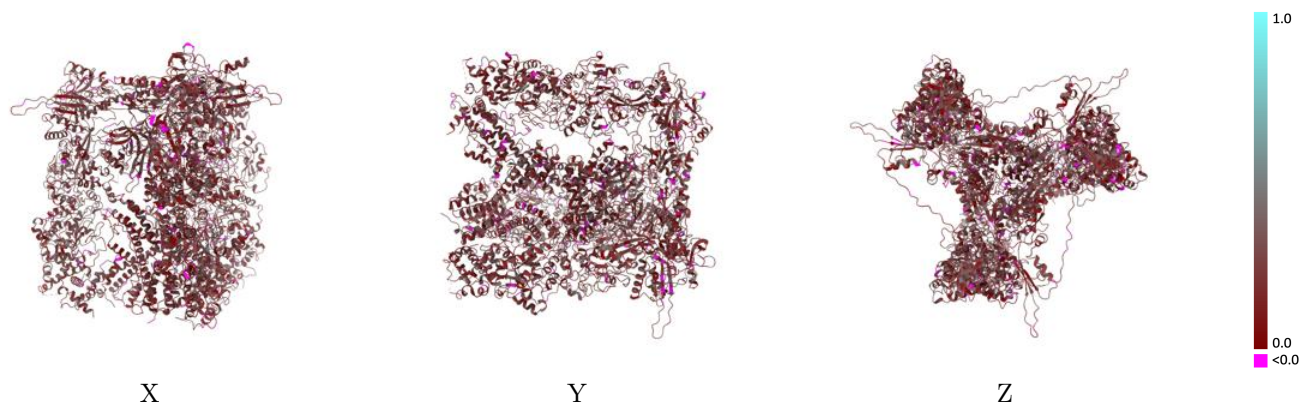
This section contains information regarding the fit between EMDB map EMD-23386 and PDB model 7LIV. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)



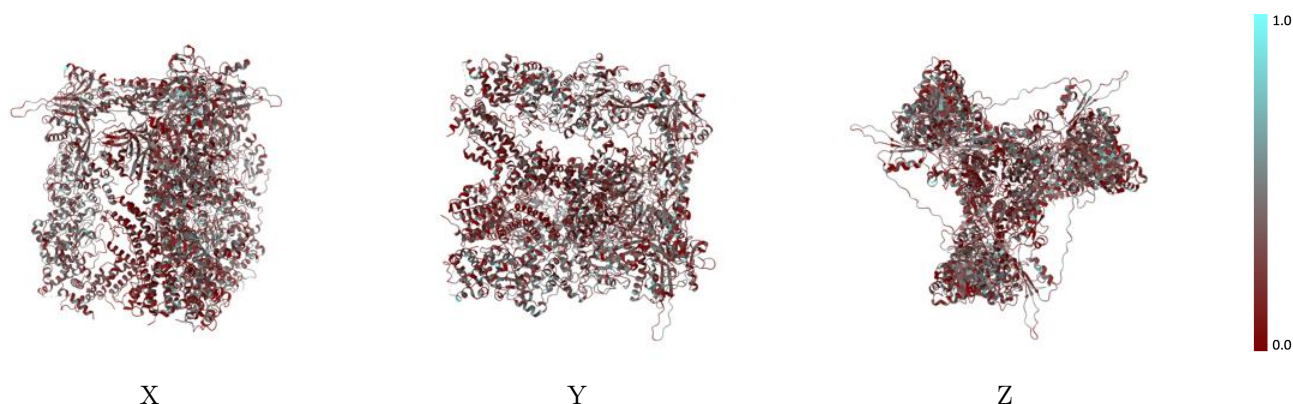
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



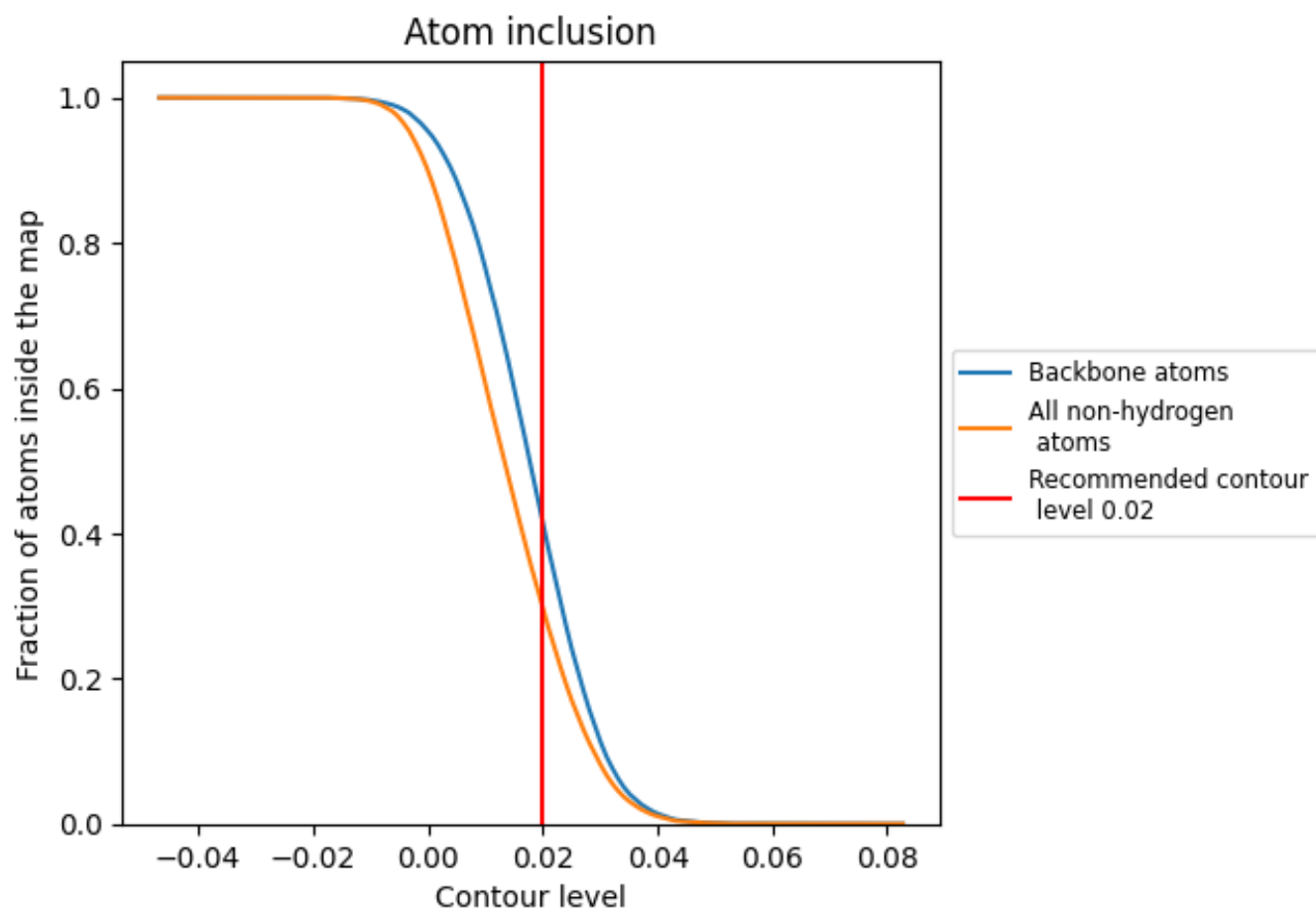
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.02).



























9.4 Atom inclusion [i](#)



At the recommended contour level, 42% of all backbone atoms, 30% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary [i](#)

The table lists the average atom inclusion at the recommended contour level (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.2976	 0.2310
4	 0.1420	 0.2040
5	 0.1787	 0.2130
6	 0.2366	 0.2360
A	 0.3338	 0.2400
C	 0.3416	 0.2380
D	 0.2550	 0.2280
E	 0.2711	 0.2290
J	 0.3306	 0.2290
Z	 0.2570	 0.2250
p	 0.2283	 0.2260
q	 0.2696	 0.2350
r	 0.2319	 0.2150

