



Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2020 – 07:10 pm BST

PDB ID : 2OAE
Title : Crystal structure of rat dipeptidyl peptidase (DPPIV) with thiazole-based peptide mimetic #31
Authors : Longenecker, K.L.; Shuai, Q.; Patel, J.; Wiedeman, P.
Deposited on : 2006-12-15
Resolution : 3.00 Å(reported)

This is a Full wwPDB X-ray Structure 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/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

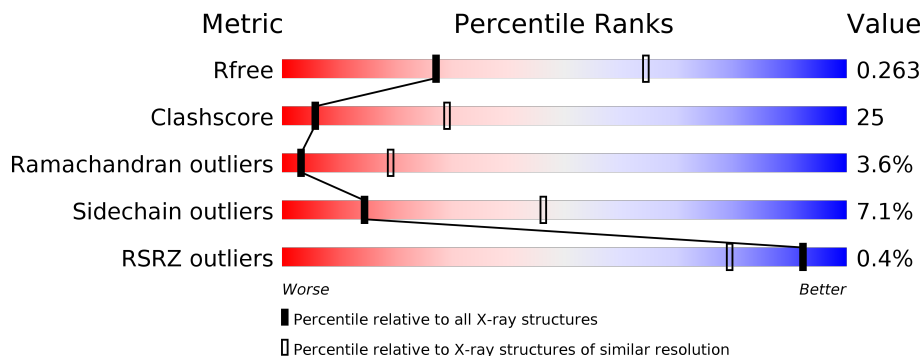
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	730	
1	B	730	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 11866 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 Dipeptidyl peptidase 4.

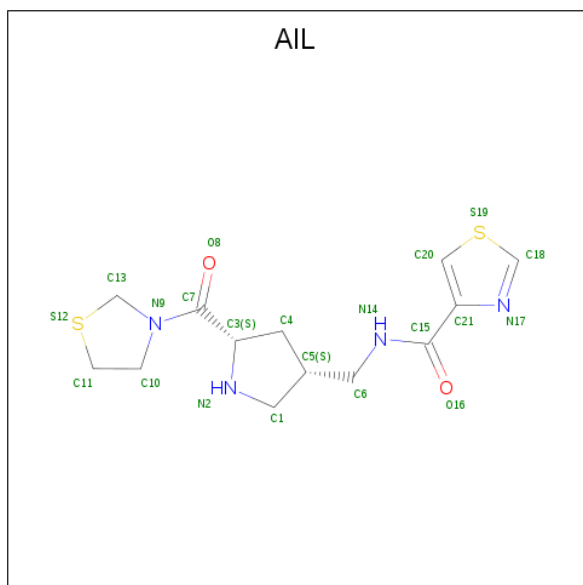
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	730	Total 5920	C 3789	N 981	O 1124	S 26	0	0	0
1	B	730	Total 5920	C 3789	N 981	O 1124	S 26	0	0	0

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
2	A	1	Total 5	O 4	S 1	0	0

- Molecule 3 is N-[[[(3S,5S)-5-(1,3-THIAZOLIDIN-3-YLCARBONYL)PYRROLIDIN-3-YL]METHYL]-1,3-THIAZOLE-4-CARBOXAMIDE (three-letter code: AIL) (formula: C₁₃H₁₈N₄O₂S₂).

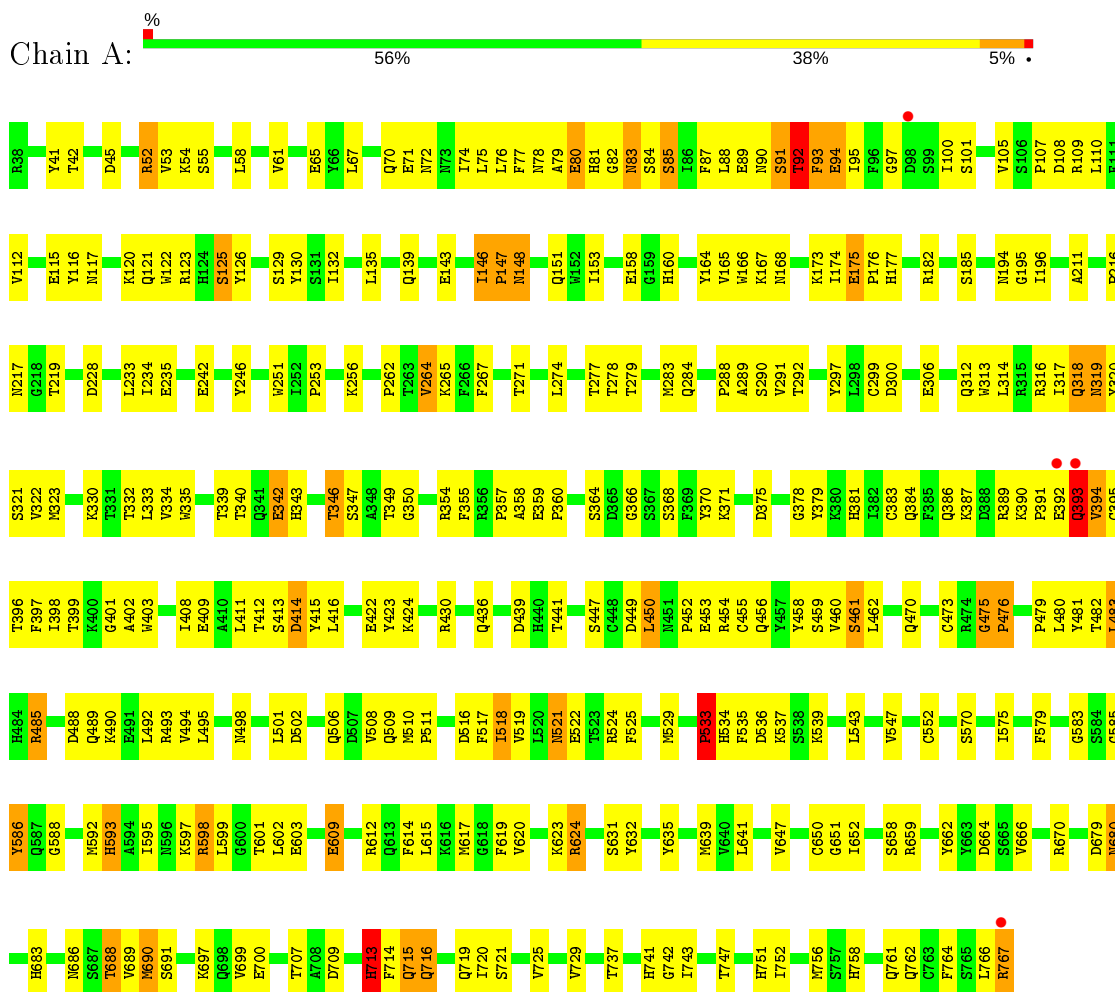


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
3	A	1	21	13	4	2	2	0	0

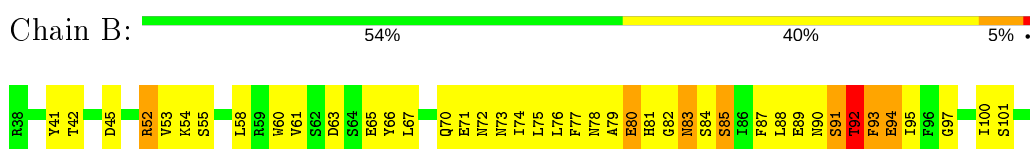
3 Residue-property plots

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

- Molecule 1: Dipeptidyl peptidase 4



- Molecule 1: Dipeptidyl peptidase 4



Q761	G650	V547	G475	K383	R316	I110
Q762	G651	G552	F476	V394	I317	F111
C763	G652	G552	P479	C395	Q318	V112
F764	G658	T566	L480	T396	N319	E115
S765	G659	V567	Y481	F397	Y320	P216
L766	R659	V567	T482	I398	S321	Y116
R767	V662	L568	L483	T399	V322	N117
	V663	A569	L483	K400	M323	K120
	D664	S570	H484	G401	D228	Q121
	T665	T571	R485	A402	W122	W122
	S665	E572	S486	W403	S125	S125
	V666	V575	T487	W403	Y126	Y126
	R670	V575	D488	L408	S129	S129
	D679	F579	Q489	E409	Y130	Y130
	N680	F579	Q490	E410	S131	S131
	N680	E491	L411	L411	I132	I132
	H683	G583	L492	T412	L135	L135
	H683	S584	R493	T412	Q139	Q139
	H686	G585	V494	S413	E143	E143
	S687	V586	L495	D414	I146	I146
	T688	Q587	M498	Y415	P147	P147
	V689	G588	N498	L416	N148	N148
	N690	S592	L501	I419	Q151	Q151
	S691	H593	D502	L419	W152	W152
	G697	L595	Q506	E422	I153	I153
	Q698	N596	D507	Y423	E158	E158
	V699	K597	V508	R424	G159	G159
	E700	R598	W509	Y424	K161	K161
	T707	L599	M510	E424	Y164	Y164
	A708	G600	P511	Q436	V165	V165
	D709	T601	K514	L437	K167	K167
	H713	L602	L515	T438	M168	M168
	F714	E603	D516	D439	S174	S174
	Q715	E609	F517	H440	E175	E175
	Q716	R612	L518	T441	P176	P176
	I719	G613	L520	E442	H177	H177
	I720	F614	M521	Y443	L178	L178
	S721	L615	E522	E443	R182	R182
	K722	L616	T523	R454	S185	S185
	V725	H617	R524	R454	M194	M194
	D726	G618	F525	C455	G195	G195
	V729	V620	M529	Q456	I196	I196
	H741	R624	L530	Y457	I205	I205
	G742	Y632	L531	Y458	A283	A283
	I743	V635	P532	H381	Q284	Q284
	I752	V639	P532	H382	P288	P288
	H756	L641	H534	T382	A289	A289
	S757	V647	F535	C383	S290	S290
	H758		L462	Q384	V291	V291
			D465	F385	T292	T292
			K537	L462	Y297	Y297
			S538	L462	L298	L298
			K539	E465	C299	C299
			L543	Q470	D300	D300
				C473	W303	W303
				R474	E306	E306
					Q312	Q312
					W313	W313
					L314	L314
					R315	R315

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 3	Depositor
Cell constants a, b, c, α , β , γ	208.35Å 208.35Å 208.35Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.00 19.96 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.7 (20.00-3.00) 100.0 (19.96-3.00)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.95 (at 2.98Å)	Xtrriage
Refinement program	CNS	Depositor
R, R_{free}	0.249 , 0.280 0.234 , 0.263	Depositor DCC
R_{free} test set	3039 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	57.9	Xtrriage
Anisotropy	0.000	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 39.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.35$	Xtrriage
Estimated twinning fraction	0.001 for l,-k,h	Xtrriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	11866	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.81% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: AIL, SO4

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	0/6088	0.71	1/8278 (0.0%)
1	B	0.51	0/6088	0.71	1/8278 (0.0%)
All	All	0.50	0/12176	0.71	2/16556 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	713	HIS	N-CA-C	7.03	129.98	111.00
1	B	713	HIS	N-CA-C	6.85	129.50	111.00

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	5920	0	5632	285	0
1	B	5920	0	5632	303	0
2	A	5	0	0	1	0
3	A	21	0	18	1	0
All	All	11866	0	11282	582	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 25.

All (582) 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:A:52:ARG:HH11	1:A:52:ARG:HB2	1.10	1.11
1:B:761:GLN:HB3	1:B:767:ARG:HB3	1.30	1.11
1:B:52:ARG:HB2	1:B:52:ARG:HH11	1.12	1.09
1:A:761:GLN:HB3	1:A:767:ARG:HB3	1.27	1.09
1:B:688:THR:HG22	1:B:691:SER:H	1.23	1.03
1:B:595:ILE:HD11	1:B:603:GLU:HB3	1.39	1.03
1:B:349:THR:HB	1:B:593:HIS:HD2	1.20	1.03
1:A:349:THR:HB	1:A:593:HIS:HD2	1.22	1.02
1:A:412:THR:HG22	1:A:414:ASP:H	1.23	0.99
1:A:595:ILE:HD11	1:A:603:GLU:HB3	1.41	0.99
1:B:460:VAL:HG22	1:B:461:SER:H	1.26	0.97
1:A:688:THR:HG22	1:A:691:SER:H	1.25	0.97
1:A:52:ARG:NH1	1:A:52:ARG:HB2	1.81	0.96
1:B:412:THR:HG22	1:B:414:ASP:H	1.28	0.94
1:A:460:VAL:HG22	1:A:461:SER:H	1.26	0.94
1:B:386:GLN:HG3	1:B:390:LYS:NZ	1.82	0.94
1:A:174:ILE:H	1:A:174:ILE:HD12	1.33	0.94
1:B:52:ARG:NH1	1:B:52:ARG:HB2	1.82	0.94
1:B:174:ILE:HD12	1:B:174:ILE:H	1.32	0.94
1:A:386:GLN:HG3	1:A:390:LYS:NZ	1.84	0.92
1:B:349:THR:HB	1:B:593:HIS:CD2	2.06	0.91
1:A:349:THR:HB	1:A:593:HIS:CD2	2.08	0.89
1:A:52:ARG:HH11	1:A:52:ARG:CB	1.87	0.86
1:B:52:ARG:CB	1:B:52:ARG:HH11	1.89	0.86
1:A:383:CYS:HB3	1:A:397:PHE:HA	1.58	0.84
1:B:91:SER:HA	1:B:94:GLU:OE1	1.79	0.83
1:B:383:CYS:HB3	1:B:397:PHE:HA	1.59	0.83
1:A:91:SER:HA	1:A:94:GLU:OE1	1.79	0.82
1:A:624:ARG:HB2	1:A:624:ARG:HH11	1.45	0.81
1:A:485:ARG:HG3	1:A:485:ARG:O	1.81	0.80
1:A:761:GLN:HB3	1:A:767:ARG:CB	2.11	0.79
1:A:460:VAL:HG22	1:A:461:SER:N	1.97	0.79
1:B:485:ARG:HG3	1:B:485:ARG:O	1.81	0.79
1:A:641:LEU:HD22	1:A:699:VAL:HG11	1.65	0.79
1:B:639:MET:CE	1:B:689:VAL:HA	2.13	0.79
1:B:460:VAL:HG22	1:B:461:SER:N	1.99	0.78
1:A:639:MET:CE	1:A:689:VAL:HA	2.12	0.78
1:B:449:ASP:O	1:B:452:PRO:HD3	1.84	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:761:GLN:CB	1:A:767:ARG:HB3	2.11	0.78
1:A:518:ILE:HD13	1:A:519:VAL:H	1.50	0.76
1:A:449:ASP:O	1:A:452:PRO:HD3	1.83	0.76
1:B:624:ARG:HB2	1:B:624:ARG:HH11	1.49	0.76
1:B:234:ILE:HD13	1:B:713:HIS:CE1	2.21	0.75
1:A:234:ILE:HD13	1:A:713:HIS:CE1	2.21	0.75
1:B:767:ARG:C	1:B:767:ARG:HD2	2.06	0.75
1:B:641:LEU:HD22	1:B:699:VAL:HG11	1.68	0.75
1:B:78:ASN:HB3	1:B:83:ASN:HB3	1.69	0.75
1:B:761:GLN:CB	1:B:767:ARG:HB3	2.14	0.74
1:B:91:SER:O	1:B:93:PHE:N	2.21	0.74
1:B:518:ILE:HD13	1:B:519:VAL:H	1.53	0.74
1:A:79:ALA:O	1:A:80:GLU:HB2	1.87	0.73
1:B:652:ILE:HG21	1:B:756:MET:HE2	1.70	0.73
1:B:403:TRP:CE3	1:B:422:GLU:HB2	2.23	0.73
1:B:277:THR:HG21	1:B:279:THR:O	1.89	0.73
1:B:688:THR:HG22	1:B:691:SER:N	2.02	0.72
1:A:91:SER:O	1:A:93:PHE:N	2.22	0.72
1:A:151:GLN:NE2	1:A:167:LYS:H	1.87	0.72
1:A:688:THR:HG22	1:A:691:SER:N	2.03	0.72
1:A:318:GLN:OE1	1:A:670:ARG:HD3	1.90	0.72
1:B:761:GLN:HB3	1:B:767:ARG:CB	2.14	0.72
1:A:277:THR:HG21	1:A:279:THR:O	1.89	0.71
1:A:78:ASN:HB3	1:A:83:ASN:HB3	1.71	0.71
1:A:392:GLU:C	1:A:393:GLN:HG3	2.09	0.71
1:A:485:ARG:NH2	1:A:490:LYS:HD3	2.05	0.71
1:B:392:GLU:C	1:B:393:GLN:HG3	2.11	0.71
1:B:79:ALA:O	1:B:80:GLU:HB2	1.90	0.70
1:B:612:ARG:HH11	1:B:612:ARG:HG3	1.56	0.70
1:A:256:LYS:NZ	1:A:713:HIS:HD2	1.90	0.70
1:B:235:GLU:HG2	1:B:251:TRP:HB3	1.73	0.70
1:B:318:GLN:OE1	1:B:670:ARG:HD3	1.91	0.70
1:A:107:PRO:HG2	1:A:158:GLU:O	1.92	0.69
1:A:235:GLU:HG2	1:A:251:TRP:HB3	1.74	0.69
1:A:403:TRP:CE3	1:A:422:GLU:HB2	2.26	0.69
1:A:586:TYR:CD1	1:A:586:TYR:N	2.60	0.69
1:B:151:GLN:NE2	1:B:167:LYS:H	1.89	0.69
1:B:256:LYS:NZ	1:B:713:HIS:HD2	1.90	0.69
1:B:483:LEU:HB3	1:B:495:LEU:HD11	1.74	0.69
1:A:386:GLN:HG3	1:A:390:LYS:HZ2	1.55	0.69
1:A:612:ARG:HG3	1:A:612:ARG:HH11	1.58	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:386:GLN:HG3	1:B:390:LYS:HZ2	1.58	0.68
1:B:485:ARG:NH2	1:B:490:LYS:HD3	2.08	0.68
1:A:483:LEU:HB3	1:A:495:LEU:HD11	1.76	0.68
1:B:107:PRO:HG2	1:B:158:GLU:O	1.93	0.68
1:A:658:SER:H	1:A:716:GLN:NE2	1.93	0.67
1:A:652:ILE:HG21	1:A:756:MET:HE2	1.77	0.67
1:B:235:GLU:OE2	1:B:251:TRP:HB3	1.95	0.67
1:B:460:VAL:CG2	1:B:461:SER:H	2.05	0.67
1:A:601:THR:HG22	1:A:602:LEU:N	2.10	0.66
1:A:332:THR:O	1:A:334:VAL:HG23	1.96	0.66
1:A:767:ARG:HD2	1:A:767:ARG:C	2.16	0.66
1:A:54:LYS:H	1:A:498:ASN:HD21	1.43	0.65
1:B:473:CYS:O	1:B:479:PRO:HA	1.96	0.65
1:A:235:GLU:OE2	1:A:251:TRP:HB3	1.97	0.65
1:B:586:TYR:N	1:B:586:TYR:CD1	2.62	0.65
1:B:219:THR:O	1:B:271:THR:HB	1.96	0.65
1:A:381:HIS:CD2	1:A:399:THR:HG22	2.32	0.64
1:A:473:CYS:O	1:A:479:PRO:HA	1.98	0.64
1:A:412:THR:HG22	1:A:414:ASP:N	2.06	0.64
1:B:482:THR:HG22	1:B:494:VAL:HA	1.80	0.64
1:A:146:ILE:HD12	1:A:153:ILE:HD12	1.80	0.63
1:A:121:GLN:O	1:A:125:SER:HB2	1.98	0.63
1:B:462:LEU:N	1:B:462:LEU:HD12	2.13	0.63
1:B:601:THR:HG22	1:B:602:LEU:N	2.12	0.63
1:B:658:SER:H	1:B:716:GLN:NE2	1.97	0.63
1:B:54:LYS:H	1:B:498:ASN:HD21	1.45	0.63
1:B:411:LEU:HD13	1:B:416:LEU:HD13	1.81	0.63
1:B:146:ILE:HD12	1:B:153:ILE:HD12	1.81	0.62
1:A:89:GLU:C	1:A:91:SER:N	2.49	0.62
1:B:72:ASN:O	1:B:90:ASN:HA	2.00	0.62
1:A:219:THR:O	1:A:271:THR:HB	1.98	0.62
1:B:317:ILE:HG22	1:B:319:ASN:HB2	1.82	0.62
1:B:121:GLN:O	1:B:125:SER:HB2	2.00	0.62
1:A:130:TYR:HB2	1:A:146:ILE:HD13	1.82	0.62
1:B:386:GLN:HG3	1:B:390:LYS:CE	2.29	0.62
1:B:332:THR:O	1:B:334:VAL:HG23	1.99	0.61
1:B:89:GLU:C	1:B:91:SER:N	2.50	0.61
1:A:386:GLN:HG3	1:A:390:LYS:CE	2.30	0.61
1:A:79:ALA:O	1:A:80:GLU:CB	2.48	0.61
1:A:462:LEU:N	1:A:462:LEU:HD12	2.16	0.61
1:A:72:ASN:O	1:A:90:ASN:HA	2.01	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:174:ILE:H	1:A:174:ILE:CD1	2.12	0.61
1:A:151:GLN:NE2	1:A:167:LYS:N	2.48	0.61
1:A:392:GLU:O	1:A:393:GLN:HG3	2.01	0.61
1:A:460:VAL:CG2	1:A:461:SER:H	2.05	0.61
1:A:624:ARG:HB2	1:A:624:ARG:NH1	2.15	0.61
1:B:713:HIS:O	1:B:714:PHE:HB3	2.01	0.61
1:B:358:ALA:O	1:B:371:LYS:HE3	2.01	0.60
1:B:511:PRO:HD3	1:B:570:SER:HB2	1.83	0.60
1:A:317:ILE:HG22	1:A:319:ASN:HB2	1.82	0.60
1:A:713:HIS:O	1:A:714:PHE:HB3	2.00	0.60
1:A:688:THR:HG23	1:A:690:MET:HG2	1.83	0.60
1:B:383:CYS:CB	1:B:397:PHE:HA	2.31	0.60
1:B:151:GLN:NE2	1:B:167:LYS:N	2.50	0.60
1:A:383:CYS:CB	1:A:397:PHE:HA	2.30	0.60
1:A:168:ASN:O	1:A:194:ASN:HB2	2.02	0.59
1:B:641:LEU:HD11	1:B:651:GLY:HA3	1.84	0.59
1:B:217:ASN:HB2	1:B:306:GLU:OE1	2.02	0.59
1:A:709:ASP:OD2	1:A:741:HIS:HA	2.03	0.59
1:B:415:TYR:HD2	1:B:436:GLN:HA	1.68	0.59
1:A:641:LEU:HD11	1:A:651:GLY:HA3	1.83	0.59
1:A:688:THR:CG2	1:A:690:MET:HG2	2.32	0.59
1:B:55:SER:HA	1:B:481:TYR:CE1	2.38	0.59
1:B:709:ASP:OD2	1:B:741:HIS:HA	2.03	0.59
1:B:79:ALA:O	1:B:80:GLU:CB	2.50	0.59
1:A:411:LEU:HD13	1:A:416:LEU:HD13	1.83	0.59
1:B:595:ILE:CG2	1:B:599:LEU:HD23	2.33	0.59
1:A:267:PHE:CE2	1:A:284:GLN:HB2	2.38	0.59
1:A:511:PRO:HD3	1:A:570:SER:HB2	1.82	0.59
1:A:697:LYS:HG2	1:A:729:VAL:HG22	1.85	0.59
1:B:168:ASN:O	1:B:194:ASN:HB2	2.03	0.59
1:A:482:THR:HG22	1:A:494:VAL:HA	1.83	0.59
1:A:597:LYS:O	1:A:683:HIS:HD2	1.86	0.59
1:A:89:GLU:HB2	1:A:91:SER:HB3	1.84	0.59
1:B:339:THR:O	1:B:342:GLU:HB2	2.03	0.59
1:B:267:PHE:CE2	1:B:284:GLN:HB2	2.38	0.58
1:B:454:ARG:HH11	1:B:480:LEU:HB2	1.68	0.58
1:B:688:THR:CG2	1:B:690:MET:HG2	2.33	0.58
1:A:595:ILE:CG2	1:A:599:LEU:HD23	2.33	0.58
1:B:597:LYS:O	1:B:683:HIS:HD2	1.85	0.58
1:A:195:GLY:C	1:A:211:ALA:HB3	2.24	0.58
1:A:415:TYR:HD2	1:A:436:GLN:HA	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:631:SER:OG	3:A:901:AIL:H102	2.03	0.58
1:B:386:GLN:HG3	1:B:390:LYS:HZ1	1.66	0.58
1:B:403:TRP:CD2	1:B:422:GLU:HB2	2.38	0.58
1:B:688:THR:HG23	1:B:690:MET:HG2	1.85	0.58
1:A:454:ARG:HH11	1:A:480:LEU:HB2	1.69	0.57
1:B:690:MET:CE	1:B:720:ILE:HA	2.33	0.57
1:B:742:GLY:O	1:B:743:ILE:C	2.43	0.57
1:A:690:MET:CE	1:A:720:ILE:HA	2.34	0.57
1:B:195:GLY:C	1:B:211:ALA:HB3	2.24	0.57
1:B:697:LYS:HG2	1:B:729:VAL:HG22	1.87	0.57
1:B:89:GLU:HB2	1:B:91:SER:HB3	1.85	0.57
1:B:392:GLU:O	1:B:393:GLN:HG3	2.04	0.57
1:B:624:ARG:NH1	1:B:624:ARG:HB2	2.19	0.57
1:B:639:MET:HE3	1:B:689:VAL:HA	1.85	0.57
1:A:323:MET:O	1:A:342:GLU:O	2.23	0.57
1:A:506:GLN:HA	1:A:506:GLN:OE1	2.05	0.56
1:B:381:HIS:CD2	1:B:399:THR:HG22	2.39	0.56
1:B:101:SER:HB3	1:B:115:GLU:HG2	1.87	0.56
1:B:485:ARG:HB3	1:B:492:LEU:HD21	1.86	0.56
1:A:639:MET:HE3	1:A:689:VAL:HA	1.85	0.56
1:A:101:SER:HB3	1:A:115:GLU:HG2	1.86	0.56
1:A:339:THR:O	1:A:342:GLU:HB2	2.06	0.56
1:A:217:ASN:HB2	1:A:306:GLU:OE1	2.05	0.56
1:A:403:TRP:CD2	1:A:422:GLU:HB2	2.41	0.56
1:B:447:SER:HB2	1:B:458:TYR:CE1	2.41	0.56
1:B:767:ARG:C	1:B:767:ARG:CD	2.75	0.55
1:B:412:THR:CG2	1:B:413:SER:N	2.68	0.55
1:B:488:ASP:O	1:B:489:GLN:HB2	2.06	0.55
1:A:358:ALA:O	1:A:371:LYS:HE3	2.06	0.55
1:A:412:THR:CG2	1:A:413:SER:N	2.69	0.55
1:B:256:LYS:HZ1	1:B:713:HIS:HD2	1.53	0.55
1:B:217:ASN:HB2	1:B:306:GLU:CD	2.26	0.55
1:B:543:LEU:HD12	1:B:575:ILE:O	2.07	0.55
1:A:55:SER:HA	1:A:481:TYR:CE1	2.41	0.55
1:A:533:PRO:O	1:A:535:PHE:N	2.35	0.55
1:B:277:THR:HG22	1:B:278:THR:H	1.72	0.55
1:A:455:CYS:HA	1:A:475:GLY:HA3	1.89	0.55
1:A:742:GLY:O	1:A:743:ILE:C	2.45	0.55
1:A:256:LYS:HZ1	1:A:713:HIS:HD2	1.55	0.54
1:A:381:HIS:CD2	1:A:399:THR:CG2	2.89	0.54
1:A:662:TYR:OH	1:A:719:GLN:HG2	2.06	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:650:CYS:HB3	1:A:700:GLU:HB2	1.88	0.54
1:B:78:ASN:O	1:B:81:HIS:O	2.25	0.54
1:B:455:CYS:HA	1:B:475:GLY:HA3	1.90	0.54
1:A:485:ARG:HB3	1:A:492:LEU:HD21	1.89	0.54
1:B:662:TYR:OH	1:B:719:GLN:HG2	2.08	0.54
1:B:323:MET:O	1:B:342:GLU:O	2.26	0.54
1:B:389:ARG:HH11	1:B:389:ARG:HG2	1.73	0.54
1:A:158:GLU:HG2	1:A:217:ASN:HA	1.91	0.53
1:B:506:GLN:HA	1:B:506:GLN:OE1	2.07	0.53
1:A:447:SER:HB2	1:A:458:TYR:CE1	2.43	0.53
1:B:767:ARG:HH11	1:B:767:ARG:HG3	1.73	0.53
1:B:598:ARG:HE	1:B:601:THR:HG21	1.74	0.53
1:A:234:ILE:O	1:A:234:ILE:HG13	2.09	0.53
1:B:265:LYS:HG2	1:B:284:GLN:HE22	1.72	0.53
1:A:383:CYS:HB2	1:A:396:THR:O	2.08	0.53
1:A:389:ARG:HH11	1:A:389:ARG:HG2	1.73	0.53
1:B:277:THR:HG22	1:B:279:THR:H	1.73	0.52
1:B:650:CYS:HB3	1:B:700:GLU:HB2	1.91	0.52
1:A:439:ASP:OD1	1:A:441:THR:HB	2.10	0.52
1:A:151:GLN:HE21	1:A:167:LYS:H	1.56	0.52
1:A:342:GLU:O	1:A:343:HIS:HB2	2.09	0.52
1:A:228:ASP:OD1	1:A:262:PRO:HB3	2.10	0.52
1:B:688:THR:CG2	1:B:691:SER:H	2.10	0.52
1:A:597:LYS:NZ	1:A:679:ASP:OD1	2.43	0.52
1:A:314:LEU:HD12	1:A:321:SER:HB2	1.92	0.52
1:B:130:TYR:HB2	1:B:146:ILE:HD13	1.92	0.52
1:A:84:SER:O	1:A:85:SER:CB	2.59	0.51
1:B:439:ASP:OD1	1:B:441:THR:HB	2.10	0.51
1:A:543:LEU:HD12	1:A:575:ILE:O	2.11	0.51
1:A:70:GLN:HG2	1:A:71:GLU:HG3	1.92	0.51
1:B:379:TYR:CE2	1:B:402:ALA:HA	2.45	0.51
1:A:217:ASN:HB2	1:A:306:GLU:CD	2.30	0.51
1:B:277:THR:HG22	1:B:278:THR:N	2.25	0.51
1:B:632:TYR:O	1:B:635:TYR:HB3	2.10	0.51
1:A:384:GLN:HG3	1:A:398:ILE:HD11	1.92	0.51
1:A:454:ARG:NH1	1:A:480:LEU:HB2	2.26	0.51
1:B:320:TYR:CE2	1:B:322:VAL:HG23	2.46	0.51
1:B:384:GLN:HG3	1:B:398:ILE:HD11	1.93	0.51
1:B:65:GLU:HB3	1:B:76:LEU:HD11	1.92	0.51
1:A:529:MET:HE2	1:A:575:ILE:HG21	1.93	0.51
1:A:624:ARG:HG2	1:A:764:PHE:CD2	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:752:ILE:O	1:A:756:MET:HG3	2.11	0.51
1:B:108:ASP:OD2	1:B:110:LEU:HD12	2.10	0.51
1:B:612:ARG:HG3	1:B:612:ARG:NH1	2.24	0.51
1:A:84:SER:O	1:A:85:SER:HB2	2.11	0.51
1:B:158:GLU:HG2	1:B:217:ASN:HA	1.92	0.51
1:B:228:ASP:OD1	1:B:262:PRO:HB3	2.11	0.51
1:B:713:HIS:C	1:B:715:GLN:H	2.14	0.51
1:B:292:THR:O	1:B:292:THR:HG22	2.11	0.50
1:A:277:THR:HG22	1:A:279:THR:H	1.75	0.50
1:A:320:TYR:CE2	1:A:322:VAL:HG23	2.47	0.50
1:A:379:TYR:CE2	1:A:402:ALA:HA	2.47	0.50
1:B:624:ARG:HG2	1:B:764:PHE:CD2	2.45	0.50
1:B:699:VAL:HG12	1:B:700:GLU:N	2.26	0.50
1:A:277:THR:HG22	1:A:278:THR:H	1.76	0.50
1:A:518:ILE:HD13	1:A:519:VAL:N	2.24	0.50
1:B:84:SER:O	1:B:85:SER:CB	2.60	0.50
1:A:488:ASP:O	1:A:489:GLN:HB2	2.11	0.50
1:A:713:HIS:C	1:A:715:GLN:H	2.14	0.50
1:B:415:TYR:CD2	1:B:436:GLN:HA	2.47	0.50
1:B:84:SER:O	1:B:85:SER:HB2	2.11	0.50
1:A:346:THR:HG23	1:A:347:SER:N	2.27	0.50
1:A:78:ASN:O	1:A:81:HIS:O	2.30	0.50
1:A:751:HIS:CD2	1:B:725:VAL:HA	2.46	0.50
1:A:108:ASP:OD2	1:A:110:LEU:HD12	2.11	0.50
1:A:265:LYS:HG2	1:A:284:GLN:HE22	1.77	0.50
1:B:146:ILE:CD1	1:B:153:ILE:HD12	2.42	0.50
1:B:342:GLU:O	1:B:343:HIS:HB2	2.11	0.50
1:B:454:ARG:NH1	1:B:480:LEU:HB2	2.26	0.50
1:B:597:LYS:O	1:B:683:HIS:CD2	2.64	0.50
1:A:415:TYR:CD2	1:A:436:GLN:HA	2.47	0.50
1:A:123:ARG:NH2	2:A:801:SO4:O4	2.45	0.49
1:A:292:THR:HG22	1:A:292:THR:O	2.11	0.49
1:A:598:ARG:HE	1:A:601:THR:HG21	1.76	0.49
1:B:346:THR:HG23	1:B:347:SER:N	2.27	0.49
1:B:383:CYS:HB2	1:B:396:THR:O	2.11	0.49
1:B:412:THR:HG22	1:B:414:ASP:N	2.10	0.49
1:B:680:ASN:HD21	1:B:683:HIS:CG	2.30	0.49
1:A:699:VAL:HG12	1:A:700:GLU:N	2.27	0.49
1:B:680:ASN:HD21	1:B:683:HIS:CD2	2.30	0.49
1:B:624:ARG:HG2	1:B:764:PHE:HD2	1.77	0.49
1:A:264:VAL:HG12	1:A:265:LYS:H	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:614:PHE:O	1:A:617:MET:HB2	2.11	0.49
1:A:767:ARG:HG3	1:A:767:ARG:HH11	1.77	0.49
1:B:423:TYR:CZ	1:B:424:LYS:HE3	2.46	0.49
1:B:524:ARG:HH11	1:B:524:ARG:HG2	1.77	0.49
1:A:423:TYR:CZ	1:A:424:LYS:HE3	2.47	0.49
1:B:381:HIS:CD2	1:B:399:THR:CG2	2.95	0.49
1:A:502:ASP:O	1:A:506:GLN:HG2	2.13	0.49
1:B:70:GLN:HG2	1:B:71:GLU:HG3	1.95	0.49
1:A:386:GLN:HG3	1:A:390:LYS:HE3	1.94	0.49
1:A:624:ARG:HG2	1:A:764:PHE:HD2	1.78	0.49
1:B:752:ILE:O	1:B:756:MET:HG3	2.12	0.49
1:A:65:GLU:HB3	1:A:76:LEU:HD11	1.95	0.49
1:B:767:ARG:OXT	1:B:767:ARG:HD2	2.12	0.49
1:B:767:ARG:CD	1:B:767:ARG:OXT	2.61	0.48
1:A:132:ILE:HG21	1:A:176:PRO:HB3	1.95	0.48
1:B:498:ASN:HB3	1:B:501:LEU:HB3	1.95	0.48
1:A:521:ASN:O	1:A:522:GLU:HB2	2.14	0.48
1:B:235:GLU:CG	1:B:251:TRP:HB3	2.42	0.48
1:B:41:TYR:HB2	1:B:510:MET:HE1	1.96	0.48
1:B:54:LYS:H	1:B:498:ASN:ND2	2.10	0.48
1:A:680:ASN:HD21	1:A:683:HIS:CG	2.31	0.48
1:B:277:THR:CG2	1:B:279:THR:O	2.61	0.48
1:B:401:GLY:HA3	1:B:403:TRP:NE1	2.29	0.48
1:A:378:GLY:O	1:A:588:GLY:HA2	2.13	0.48
1:A:612:ARG:NH1	1:A:612:ARG:HG3	2.27	0.48
1:A:632:TYR:O	1:A:635:TYR:HB3	2.13	0.48
1:A:386:GLN:HG3	1:A:390:LYS:HZ1	1.75	0.48
1:A:529:MET:CE	1:A:575:ILE:HG21	2.42	0.48
1:A:235:GLU:CG	1:A:251:TRP:HB3	2.43	0.48
1:A:498:ASN:HB3	1:A:501:LEU:HB3	1.96	0.48
1:A:609:GLU:O	1:A:612:ARG:HB2	2.14	0.48
1:B:234:ILE:HG13	1:B:234:ILE:O	2.12	0.48
1:B:256:LYS:HZ3	1:B:713:HIS:HD2	1.61	0.48
1:A:758:HIS:O	1:A:762:GLN:HG3	2.14	0.47
1:A:91:SER:CA	1:A:94:GLU:OE1	2.59	0.47
1:B:132:ILE:HG21	1:B:176:PRO:HB3	1.95	0.47
1:B:264:VAL:HG12	1:B:265:LYS:H	1.79	0.47
1:A:109:ARG:O	1:A:135:LEU:HD12	2.14	0.47
1:A:690:MET:HE3	1:A:720:ILE:HA	1.96	0.47
1:B:288:PRO:HD2	1:B:313:TRP:CD1	2.50	0.47
1:B:354:ARG:HB3	1:B:552:CYS:SG	2.54	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:597:LYS:O	1:A:683:HIS:CD2	2.65	0.47
1:B:597:LYS:NZ	1:B:679:ASP:OD1	2.47	0.47
1:A:242:GLU:HG3	1:B:659:ARG:NH1	2.29	0.47
1:B:54:LYS:HB2	1:B:498:ASN:HD21	1.79	0.47
1:A:314:LEU:CD1	1:A:321:SER:HB2	2.45	0.47
1:A:256:LYS:HZ3	1:A:713:HIS:HD2	1.58	0.47
1:B:93:PHE:O	1:B:100:ILE:HG13	2.13	0.47
1:B:659:ARG:HG2	1:B:662:TYR:CE2	2.49	0.47
1:A:524:ARG:HG2	1:A:524:ARG:HH11	1.79	0.47
1:A:529:MET:HE2	1:A:575:ILE:CG2	2.45	0.47
1:B:105:VAL:HG22	1:B:112:VAL:HG22	1.96	0.47
1:A:174:ILE:HD12	1:A:174:ILE:N	2.15	0.47
1:A:277:THR:HG22	1:A:278:THR:N	2.30	0.47
1:A:277:THR:CG2	1:A:279:THR:O	2.60	0.47
1:B:166:TRP:O	1:B:167:LYS:HB2	2.15	0.47
1:A:288:PRO:HD2	1:A:313:TRP:CD1	2.50	0.47
1:A:680:ASN:HD21	1:A:683:HIS:CD2	2.33	0.47
1:B:409:GLU:HG3	1:B:460:VAL:HG11	1.97	0.47
1:B:508:VAL:HG12	1:B:510:MET:HE2	1.97	0.47
1:B:690:MET:HE2	1:B:719:GLN:O	2.14	0.47
1:B:91:SER:OG	1:B:92:THR:N	2.47	0.47
1:A:166:TRP:O	1:A:167:LYS:HB2	2.14	0.47
1:A:41:TYR:HB2	1:A:510:MET:CE	2.45	0.47
1:B:158:GLU:OE2	1:B:217:ASN:N	2.48	0.47
1:B:386:GLN:HG3	1:B:390:LYS:HE3	1.95	0.47
1:A:354:ARG:HB3	1:A:552:CYS:SG	2.55	0.47
1:A:93:PHE:O	1:A:100:ILE:HG13	2.15	0.47
1:B:100:ILE:HG22	1:B:100:ILE:O	2.15	0.47
1:B:87:PHE:CZ	1:B:135:LEU:HD11	2.50	0.47
1:B:151:GLN:HE21	1:B:167:LYS:H	1.58	0.47
1:B:314:LEU:HD12	1:B:321:SER:HB2	1.96	0.47
1:B:533:PRO:O	1:B:535:PHE:N	2.38	0.47
1:B:552:CYS:HB2	1:B:592:MET:SD	2.55	0.47
1:B:529:MET:CE	1:B:575:ILE:HG21	2.45	0.47
1:A:158:GLU:OE2	1:A:217:ASN:N	2.48	0.46
1:A:536:ASP:HB3	1:A:539:LYS:NZ	2.30	0.46
1:B:41:TYR:HB2	1:B:510:MET:CE	2.45	0.46
1:A:713:HIS:O	1:A:714:PHE:CB	2.61	0.46
1:B:67:LEU:HD22	1:B:74:ILE:HG22	1.97	0.46
1:A:721:SER:O	1:A:725:VAL:HG23	2.15	0.46
1:B:378:GLY:O	1:B:588:GLY:HA2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:297:TYR:CE2	1:B:666:VAL:HG22	2.51	0.46
1:A:737:THR:HB	1:B:722:LYS:HB2	1.97	0.46
1:B:355:PHE:O	1:B:670:ARG:NH1	2.49	0.46
1:B:75:LEU:HB2	1:B:77:PHE:CE1	2.51	0.46
1:B:447:SER:HA	1:B:450:LEU:CD1	2.46	0.46
1:B:767:ARG:HG3	1:B:767:ARG:NH1	2.31	0.46
1:A:312:GLN:HG2	1:A:323:MET:HG3	1.98	0.46
1:A:383:CYS:HB2	1:A:396:THR:C	2.36	0.46
1:B:713:HIS:O	1:B:714:PHE:CB	2.62	0.46
1:B:529:MET:HE2	1:B:575:ILE:CG2	2.46	0.46
1:A:747:THR:HG21	1:B:726:ASP:HA	1.98	0.46
1:A:146:ILE:CD1	1:A:153:ILE:HD12	2.45	0.46
1:A:54:LYS:H	1:A:498:ASN:ND2	2.11	0.46
1:B:690:MET:HE3	1:B:720:ILE:HA	1.96	0.46
1:A:386:GLN:O	1:A:387:LYS:C	2.54	0.45
1:A:129:SER:HB3	1:A:148:ASN:ND2	2.31	0.45
1:A:289:ALA:C	1:A:291:VAL:H	2.19	0.45
1:A:346:THR:CG2	1:A:347:SER:N	2.79	0.45
1:A:151:GLN:HE22	1:A:167:LYS:N	2.12	0.45
1:A:355:PHE:O	1:A:670:ARG:NH1	2.50	0.45
1:A:41:TYR:HB2	1:A:510:MET:HE2	1.98	0.45
1:B:182:ARG:HH21	1:B:185:SER:HA	1.80	0.45
1:A:330:LYS:O	1:A:333:LEU:HD23	2.17	0.45
1:B:408:ILE:HG23	1:B:416:LEU:HD11	1.99	0.45
1:B:502:ASP:O	1:B:506:GLN:HG2	2.17	0.45
1:B:109:ARG:O	1:B:135:LEU:HD12	2.16	0.45
1:B:456:GLN:OE1	1:B:476:PRO:HG2	2.16	0.45
1:A:297:TYR:CE2	1:A:666:VAL:HG22	2.52	0.45
1:A:87:PHE:CZ	1:A:135:LEU:HD11	2.51	0.45
1:B:758:HIS:O	1:B:762:GLN:HG3	2.16	0.45
1:A:100:ILE:O	1:A:100:ILE:HG22	2.16	0.45
1:A:690:MET:HE2	1:A:719:GLN:O	2.16	0.45
1:B:289:ALA:C	1:B:291:VAL:H	2.20	0.45
1:B:614:PHE:O	1:B:617:MET:HB2	2.17	0.45
1:A:659:ARG:HG2	1:A:662:TYR:CE2	2.52	0.45
1:B:93:PHE:CD2	1:B:100:ILE:HG21	2.52	0.45
1:B:75:LEU:HB2	1:B:77:PHE:HE1	1.81	0.45
1:A:80:GLU:H	1:A:493:ARG:HH22	1.64	0.45
1:B:235:GLU:HG2	1:B:251:TRP:CB	2.44	0.45
1:B:306:GLU:O	1:B:306:GLU:CG	2.65	0.45
1:A:182:ARG:HH21	1:A:185:SER:HA	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:297:TYR:CE1	1:A:316:ARG:HA	2.52	0.45
1:A:598:ARG:HD3	1:A:598:ARG:O	2.17	0.45
1:B:386:GLN:O	1:B:387:LYS:C	2.55	0.45
1:B:525:PHE:HB3	1:B:579:PHE:CZ	2.52	0.45
1:A:246:TYR:CZ	1:B:232:PRO:HB2	2.52	0.44
1:B:312:GLN:HG2	1:B:323:MET:HG3	1.99	0.44
1:B:364:SER:C	1:B:366:GLY:H	2.20	0.44
1:B:518:ILE:HD13	1:B:519:VAL:N	2.27	0.44
1:A:299:CYS:SG	1:A:357:PRO:HD2	2.56	0.44
1:A:409:GLU:HG3	1:A:460:VAL:HG11	1.99	0.44
1:B:447:SER:HA	1:B:450:LEU:HD12	2.00	0.44
1:A:234:ILE:HG21	1:A:713:HIS:NE2	2.33	0.44
1:A:370:TYR:CE2	1:A:384:GLN:CG	3.00	0.44
1:A:688:THR:CG2	1:A:691:SER:H	2.12	0.44
1:A:473:CYS:HB3	1:A:480:LEU:O	2.18	0.44
1:A:306:GLU:CG	1:A:306:GLU:O	2.64	0.44
1:A:583:GLY:HA2	1:A:592:MET:O	2.16	0.44
1:A:93:PHE:CD2	1:A:100:ILE:HG21	2.52	0.44
1:B:509:GLN:O	1:B:533:PRO:HG3	2.18	0.44
1:A:235:GLU:HG2	1:A:251:TRP:CB	2.45	0.44
1:A:317:ILE:C	1:A:319:ASN:H	2.20	0.44
1:A:447:SER:HA	1:A:450:LEU:CD1	2.48	0.44
1:B:146:ILE:HG13	1:B:147:PRO:HD2	1.99	0.44
1:A:390:LYS:H	1:A:394:VAL:HG13	1.83	0.44
1:B:346:THR:CG2	1:B:347:SER:N	2.79	0.44
1:B:299:CYS:SG	1:B:357:PRO:HD2	2.56	0.44
1:B:91:SER:CA	1:B:94:GLU:OE1	2.57	0.44
1:A:120:LYS:CG	1:A:121:GLN:N	2.80	0.44
1:A:508:VAL:HG12	1:A:510:MET:HE3	1.99	0.44
1:B:317:ILE:C	1:B:319:ASN:H	2.21	0.44
1:B:482:THR:HG22	1:B:494:VAL:HG22	1.99	0.44
1:A:116:TYR:O	1:A:117:ASN:HB2	2.18	0.44
1:A:299:CYS:SG	1:A:314:LEU:HB2	2.57	0.44
1:A:615:LEU:HD23	1:A:620:VAL:CG1	2.48	0.44
1:B:529:MET:HE2	1:B:575:ILE:HG21	1.98	0.44
1:A:105:VAL:HG22	1:A:112:VAL:HG22	2.00	0.43
1:B:383:CYS:HB2	1:B:396:THR:C	2.39	0.43
1:B:42:THR:O	1:B:45:ASP:HB2	2.17	0.43
1:B:609:GLU:O	1:B:612:ARG:HB2	2.17	0.43
1:B:647:VAL:O	1:B:647:VAL:HG12	2.17	0.43
1:A:509:GLN:O	1:A:533:PRO:HG3	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:120:LYS:CG	1:B:121:GLN:N	2.80	0.43
1:B:598:ARG:NE	1:B:601:THR:HG21	2.33	0.43
1:B:95:ILE:C	1:B:97:GLY:H	2.21	0.43
1:A:525:PHE:HB3	1:A:579:PHE:CZ	2.53	0.43
1:A:61:VAL:HG21	1:A:67:LEU:HG	2.01	0.43
1:B:334:VAL:HG12	1:B:335:TRP:N	2.34	0.43
1:B:390:LYS:H	1:B:394:VAL:HG13	1.82	0.43
1:B:521:ASN:O	1:B:522:GLU:HB2	2.19	0.43
1:B:116:TYR:O	1:B:117:ASN:HB2	2.17	0.43
1:B:216:PRO:O	1:B:217:ASN:HB2	2.18	0.43
1:B:399:THR:CG2	1:B:403:TRP:CH2	3.02	0.43
1:B:618:GLY:O	1:B:620:VAL:N	2.45	0.43
1:B:61:VAL:HG21	1:B:67:LEU:HG	2.00	0.43
1:B:721:SER:O	1:B:725:VAL:HG23	2.18	0.43
1:A:125:SER:O	1:A:126:TYR:HB3	2.18	0.43
1:B:330:LYS:O	1:B:333:LEU:HD23	2.19	0.43
1:B:419:ILE:HD11	1:B:460:VAL:HG12	2.01	0.43
1:A:42:THR:O	1:A:45:ASP:HB2	2.19	0.43
1:B:639:MET:HE3	1:B:689:VAL:CA	2.48	0.43
1:A:148:ASN:HD22	1:A:148:ASN:HA	1.60	0.43
1:A:767:ARG:NH1	1:A:767:ARG:HG3	2.34	0.43
1:A:91:SER:OG	1:A:92:THR:N	2.50	0.43
1:B:125:SER:O	1:B:126:TYR:HB3	2.18	0.43
1:B:89:GLU:C	1:B:91:SER:H	2.22	0.43
1:A:552:CYS:HB2	1:A:592:MET:SD	2.59	0.43
1:B:174:ILE:H	1:B:174:ILE:CD1	2.11	0.43
1:A:53:VAL:CG1	1:A:479:PRO:HG3	2.48	0.43
1:A:601:THR:HG22	1:A:602:LEU:H	1.84	0.43
1:A:67:LEU:HD22	1:A:74:ILE:HG22	2.01	0.43
1:A:401:GLY:HA3	1:A:403:TRP:NE1	2.34	0.42
1:A:598:ARG:NE	1:A:601:THR:HG21	2.34	0.42
1:B:297:TYR:CE1	1:B:316:ARG:HA	2.53	0.42
1:A:370:TYR:CE2	1:A:384:GLN:HG2	2.54	0.42
1:A:456:GLN:OE1	1:A:476:PRO:HG2	2.18	0.42
1:A:95:ILE:C	1:A:97:GLY:H	2.22	0.42
1:B:41:TYR:CD2	1:B:566:THR:HG22	2.54	0.42
1:A:233:LEU:HD23	1:A:253:PRO:HA	2.02	0.42
1:A:75:LEU:HB2	1:A:77:PHE:HE1	1.85	0.42
1:A:88:LEU:HD23	1:A:88:LEU:HA	1.93	0.42
1:B:314:LEU:CD1	1:B:321:SER:HB2	2.50	0.42
1:B:460:VAL:CG2	1:B:461:SER:N	2.70	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:173:LYS:HE3	1:A:173:LYS:HB3	1.78	0.42
1:A:647:VAL:HG12	1:A:647:VAL:O	2.19	0.42
1:B:568:LEU:O	1:B:572:GLU:HB2	2.19	0.42
1:B:598:ARG:HD3	1:B:598:ARG:O	2.18	0.42
1:A:334:VAL:HG12	1:A:335:TRP:N	2.33	0.42
1:A:354:ARG:HD3	1:A:552:CYS:SG	2.59	0.42
1:A:767:ARG:HD2	1:A:767:ARG:OXT	2.18	0.42
1:A:165:VAL:HG21	1:A:196:ILE:HG23	2.00	0.42
1:A:54:LYS:HB2	1:A:498:ASN:HD21	1.84	0.42
1:B:306:GLU:O	1:B:306:GLU:HG2	2.20	0.42
1:A:364:SER:C	1:A:366:GLY:H	2.23	0.42
1:A:398:ILE:HG22	1:A:398:ILE:O	2.18	0.42
1:B:215:SER:HB3	1:B:303:TRP:CZ2	2.55	0.42
1:A:120:LYS:HG2	1:A:121:GLN:N	2.35	0.42
1:A:147:PRO:HB2	1:A:166:TRP:CD1	2.55	0.42
1:A:306:GLU:HG2	1:A:306:GLU:O	2.20	0.42
1:B:299:CYS:SG	1:B:314:LEU:HB2	2.60	0.42
1:B:53:VAL:CG1	1:B:479:PRO:HG3	2.49	0.42
1:A:175:GLU:OE2	1:A:177:HIS:CD2	2.72	0.42
1:B:121:GLN:O	1:B:122:TRP:HB2	2.19	0.42
1:B:441:THR:O	1:B:443:LYS:N	2.42	0.42
1:B:532:PRO:O	1:B:533:PRO:O	2.37	0.42
1:A:121:GLN:O	1:A:122:TRP:HB2	2.20	0.41
1:B:108:ASP:O	1:B:110:LEU:HG	2.20	0.41
1:B:129:SER:HB3	1:B:148:ASN:ND2	2.35	0.41
1:B:437:LEU:O	1:B:440:HIS:CE1	2.73	0.41
1:B:485:ARG:HD2	1:B:487:THR:HB	2.02	0.41
1:B:536:ASP:HB3	1:B:539:LYS:NZ	2.35	0.41
1:B:571:THR:HG22	1:B:571:THR:O	2.20	0.41
1:B:659:ARG:HG2	1:B:662:TYR:CD2	2.55	0.41
1:B:690:MET:HE2	1:B:719:GLN:C	2.40	0.41
1:A:408:ILE:HG23	1:A:416:LEU:HD11	2.01	0.41
1:A:267:PHE:CD2	1:A:284:GLN:HB2	2.55	0.41
1:B:583:GLY:HA2	1:B:592:MET:O	2.20	0.41
1:A:533:PRO:CD	1:A:570:SER:HA	2.51	0.41
1:A:61:VAL:CG2	1:A:67:LEU:HG	2.50	0.41
1:A:75:LEU:HB2	1:A:77:PHE:CE1	2.55	0.41
1:B:398:ILE:HG22	1:B:398:ILE:O	2.20	0.41
1:B:147:PRO:HG3	1:B:164:TYR:CE1	2.56	0.41
1:B:165:VAL:HG21	1:B:196:ILE:HG23	2.03	0.41
1:B:234:ILE:HG21	1:B:713:HIS:NE2	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:61:VAL:CG2	1:B:67:LEU:HG	2.50	0.41
1:A:690:MET:HE2	1:A:719:GLN:C	2.41	0.41
1:A:89:GLU:C	1:A:91:SER:H	2.21	0.41
1:B:161:LYS:NZ	1:B:271:THR:HG21	2.36	0.41
1:B:267:PHE:CD2	1:B:284:GLN:HB2	2.55	0.41
1:A:612:ARG:O	1:A:615:LEU:HB2	2.21	0.41
1:B:151:GLN:HE22	1:B:167:LYS:N	2.16	0.41
1:B:175:GLU:HB3	1:B:178:LEU:HD12	2.02	0.41
1:B:482:THR:OG1	1:B:484:HIS:HE1	2.04	0.41
1:B:615:LEU:HD23	1:B:620:VAL:CG1	2.50	0.41
1:B:205:ILE:CD1	1:B:666:VAL:HG11	2.51	0.41
1:B:699:VAL:CG1	1:B:700:GLU:N	2.84	0.41
1:A:359:GLU:HG3	1:A:360:PRO:HD2	2.03	0.41
1:A:375:ASP:HA	1:A:397:PHE:CZ	2.56	0.41
1:A:447:SER:HA	1:A:450:LEU:HD12	2.03	0.41
1:A:517:PHE:CZ	1:A:524:ARG:NH1	2.89	0.41
1:A:639:MET:HE3	1:A:689:VAL:CA	2.48	0.41
1:B:120:LYS:HG2	1:B:121:GLN:N	2.35	0.41
1:B:354:ARG:HD3	1:B:552:CYS:SG	2.61	0.41
1:A:623:LYS:HA	1:A:623:LYS:HD3	1.88	0.41
1:B:233:LEU:HD23	1:B:253:PRO:HA	2.02	0.41
1:B:449:ASP:O	1:B:450:LEU:C	2.59	0.41
1:B:82:GLY:O	1:B:83:ASN:C	2.58	0.41
1:A:256:LYS:HZ3	1:A:713:HIS:CD2	2.38	0.41
1:B:63:ASP:CG	1:B:465:GLU:HB2	2.41	0.41
1:B:533:PRO:CD	1:B:570:SER:HA	2.51	0.41
1:B:70:GLN:O	1:B:73:ASN:HB2	2.21	0.41
1:B:766:LEU:O	1:B:767:ARG:O	2.38	0.41
1:A:583:GLY:HA3	1:A:595:ILE:HD12	2.03	0.41
1:A:349:THR:HG22	1:A:593:HIS:HB3	2.03	0.41
1:A:658:SER:H	1:A:716:GLN:HE21	1.68	0.41
1:A:82:GLY:O	1:A:83:ASN:C	2.59	0.41
1:B:462:LEU:H	1:B:462:LEU:HD12	1.84	0.41
1:B:514:LYS:HE3	1:B:531:LEU:HD11	2.03	0.41
1:B:690:MET:HE3	1:B:720:ILE:HG12	2.03	0.41
1:B:714:PHE:C	1:B:716:GLN:N	2.73	0.40
1:B:73:ASN:OD1	1:B:90:ASN:N	2.53	0.40
1:A:147:PRO:HG3	1:A:164:TYR:CE1	2.57	0.40
1:A:482:THR:HG22	1:A:494:VAL:HG22	2.03	0.40
1:B:205:ILE:HG21	1:B:298:LEU:O	2.22	0.40
1:A:216:PRO:O	1:A:217:ASN:HB2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:430:ARG:HA	1:A:430:ARG:HD3	1.92	0.40
1:B:147:PRO:HB2	1:B:166:TRP:CD1	2.57	0.40
1:B:175:GLU:OE2	1:B:177:HIS:CD2	2.75	0.40
1:B:231:VAL:HA	1:B:232:PRO:HD3	1.89	0.40
1:B:370:TYR:CE2	1:B:384:GLN:CG	3.04	0.40
1:B:473:CYS:HB3	1:B:480:LEU:O	2.21	0.40
1:B:412:THR:HG22	1:B:413:SER:N	2.35	0.40
1:A:751:HIS:HD2	1:B:725:VAL:HA	1.86	0.40
1:B:88:LEU:HD23	1:B:88:LEU:HA	1.94	0.40
1:B:359:GLU:HG3	1:B:360:PRO:HD2	2.04	0.40
1:B:60:TRP:CE3	1:B:66:TYR:HB3	2.57	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 X-ray entries followed by that with respect to entries of similar resolution.

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	728/730 (100%)	624 (86%)	78 (11%)	26 (4%)	3	19
1	B	728/730 (100%)	628 (86%)	74 (10%)	26 (4%)	3	19
All	All	1456/1460 (100%)	1252 (86%)	152 (10%)	52 (4%)	3	19

All (52) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	80	GLU
1	A	85	SER
1	A	91	SER
1	A	92	THR
1	A	143	GLU
1	A	450	LEU
1	A	461	SER

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Mol	Chain	Res	Type
1	A	533	PRO
1	A	585	GLY
1	A	619	PHE
1	A	713	HIS
1	B	80	GLU
1	B	85	SER
1	B	91	SER
1	B	92	THR
1	B	450	LEU
1	B	461	SER
1	B	475	GLY
1	B	533	PRO
1	B	585	GLY
1	B	619	PHE
1	B	713	HIS
1	A	318	GLN
1	A	393	GLN
1	A	475	GLY
1	A	521	ASN
1	A	534	HIS
1	B	143	GLU
1	B	318	GLN
1	B	393	GLN
1	B	534	HIS
1	A	147	PRO
1	A	391	PRO
1	A	537	LYS
1	B	93	PHE
1	B	147	PRO
1	B	391	PRO
1	B	521	ASN
1	B	537	LYS
1	A	83	ASN
1	A	93	PHE
1	A	274	LEU
1	A	766	LEU
1	B	274	LEU
1	B	766	LEU
1	A	290	SER
1	B	83	ASN
1	B	442	ASN
1	A	476	PRO

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Mol	Chain	Res	Type
1	B	350	GLY
1	A	350	GLY
1	B	476	PRO

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	643/651 (99%)	598 (93%)	45 (7%)	15	47
1	B	643/651 (99%)	597 (93%)	46 (7%)	14	45
All	All	1286/1302 (99%)	1195 (93%)	91 (7%)	14	46

All (91) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	52	ARG
1	A	58	LEU
1	A	92	THR
1	A	94	GLU
1	A	125	SER
1	A	139	GLN
1	A	146	ILE
1	A	148	ASN
1	A	160	HIS
1	A	175	GLU
1	A	264	VAL
1	A	283	MET
1	A	300	ASP
1	A	319	ASN
1	A	340	THR
1	A	342	GLU
1	A	346	THR
1	A	368	SER
1	A	393	GLN
1	A	394	VAL

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Mol	Chain	Res	Type
1	A	395	CYS
1	A	414	ASP
1	A	453	GLU
1	A	459	SER
1	A	470	GLN
1	A	483	LEU
1	A	485	ARG
1	A	516	ASP
1	A	518	ILE
1	A	533	PRO
1	A	547	VAL
1	A	586	TYR
1	A	593	HIS
1	A	598	ARG
1	A	609	GLU
1	A	624	ARG
1	A	664	ASP
1	A	680	ASN
1	A	686	ASN
1	A	688	THR
1	A	690	MET
1	A	707	THR
1	A	715	GLN
1	A	716	GLN
1	A	767	ARG
1	B	52	ARG
1	B	58	LEU
1	B	92	THR
1	B	94	GLU
1	B	125	SER
1	B	139	GLN
1	B	146	ILE
1	B	148	ASN
1	B	160	HIS
1	B	175	GLU
1	B	264	VAL
1	B	283	MET
1	B	300	ASP
1	B	319	ASN
1	B	340	THR
1	B	342	GLU
1	B	346	THR

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Mol	Chain	Res	Type
1	B	349	THR
1	B	368	SER
1	B	393	GLN
1	B	394	VAL
1	B	395	CYS
1	B	414	ASP
1	B	453	GLU
1	B	459	SER
1	B	470	GLN
1	B	483	LEU
1	B	485	ARG
1	B	516	ASP
1	B	518	ILE
1	B	533	PRO
1	B	547	VAL
1	B	586	TYR
1	B	593	HIS
1	B	598	ARG
1	B	609	GLU
1	B	624	ARG
1	B	664	ASP
1	B	680	ASN
1	B	686	ASN
1	B	688	THR
1	B	690	MET
1	B	707	THR
1	B	715	GLN
1	B	716	GLN
1	B	767	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (46) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	90	ASN
1	A	148	ASN
1	A	151	GLN
1	A	217	ASN
1	A	284	GLN
1	A	319	ASN
1	A	336	ASN
1	A	341	GLN
1	A	381	HIS

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Mol	Chain	Res	Type
1	A	384	GLN
1	A	440	HIS
1	A	470	GLN
1	A	484	HIS
1	A	498	ASN
1	A	593	HIS
1	A	680	ASN
1	A	683	HIS
1	A	698	GLN
1	A	713	HIS
1	A	715	GLN
1	A	716	GLN
1	A	719	GLN
1	A	749	HIS
1	B	90	ASN
1	B	148	ASN
1	B	151	GLN
1	B	217	ASN
1	B	284	GLN
1	B	319	ASN
1	B	336	ASN
1	B	341	GLN
1	B	381	HIS
1	B	384	GLN
1	B	440	HIS
1	B	470	GLN
1	B	484	HIS
1	B	498	ASN
1	B	593	HIS
1	B	680	ASN
1	B	683	HIS
1	B	698	GLN
1	B	713	HIS
1	B	715	GLN
1	B	716	GLN
1	B	719	GLN
1	B	749	HIS

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	AIL	A	901	-	19,23,23	1.26	1 (5%)	21,31,31	1.50	3 (14%)
2	SO4	A	801	-	4,4,4	0.66	0	6,6,6	0.26	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	AIL	A	901	-	-	0/13/33/33	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	901	AIL	C21-C15	-4.13	1.40	1.50

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	901	AIL	C7-C3-N2	-3.85	104.77	111.74
3	A	901	AIL	C5-C6-N14	-2.72	107.61	112.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	901	AIL	C4-C3-C7	2.14	115.99	111.53

There are no chirality outliers.

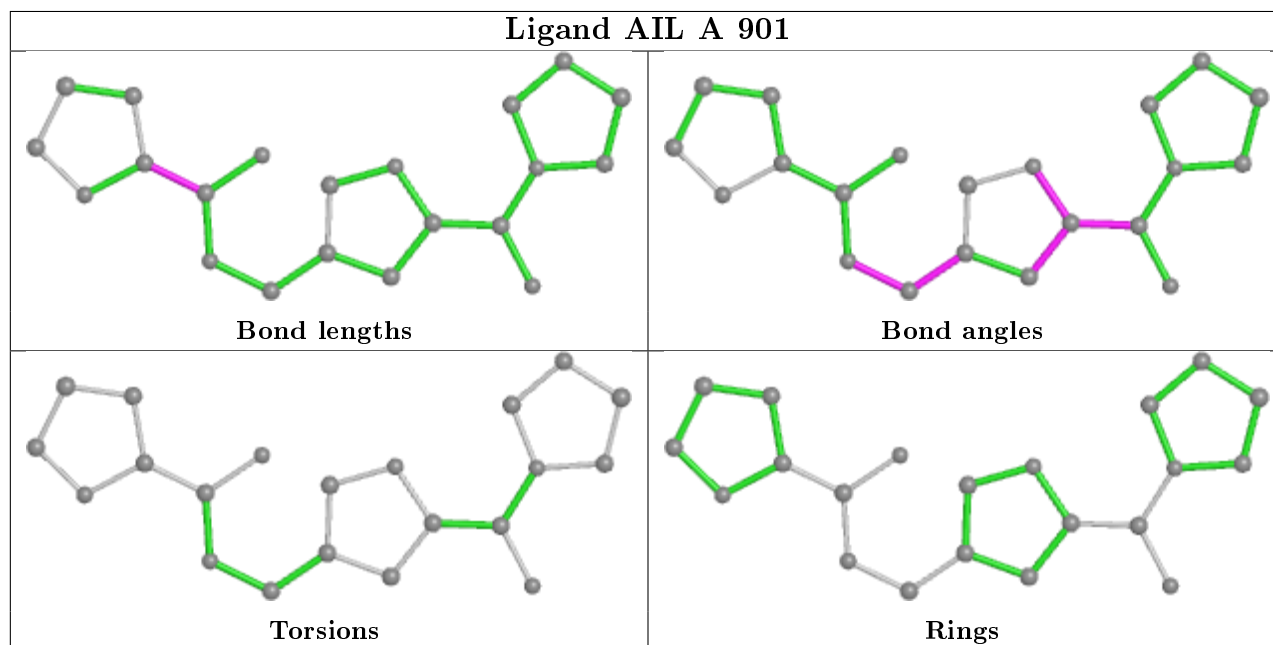
There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	901	AIL	1	0
2	A	801	SO4	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled '#RSRZ > 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q < 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	730/730 (100%)	-0.45	4 (0%) 91 75	22, 42, 73, 144	0
1	B	730/730 (100%)	-0.35	2 (0%) 94 84	25, 49, 84, 151	0
All	All	1460/1460 (100%)	-0.40	6 (0%) 92 79	22, 46, 80, 151	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	767	ARG	6.6
1	B	392	GLU	3.6
1	B	393	GLN	3.5
1	A	393	GLN	2.3
1	A	392	GLU	2.3
1	A	98	ASP	2.1

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

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

6.3 Carbohydrates [i](#)

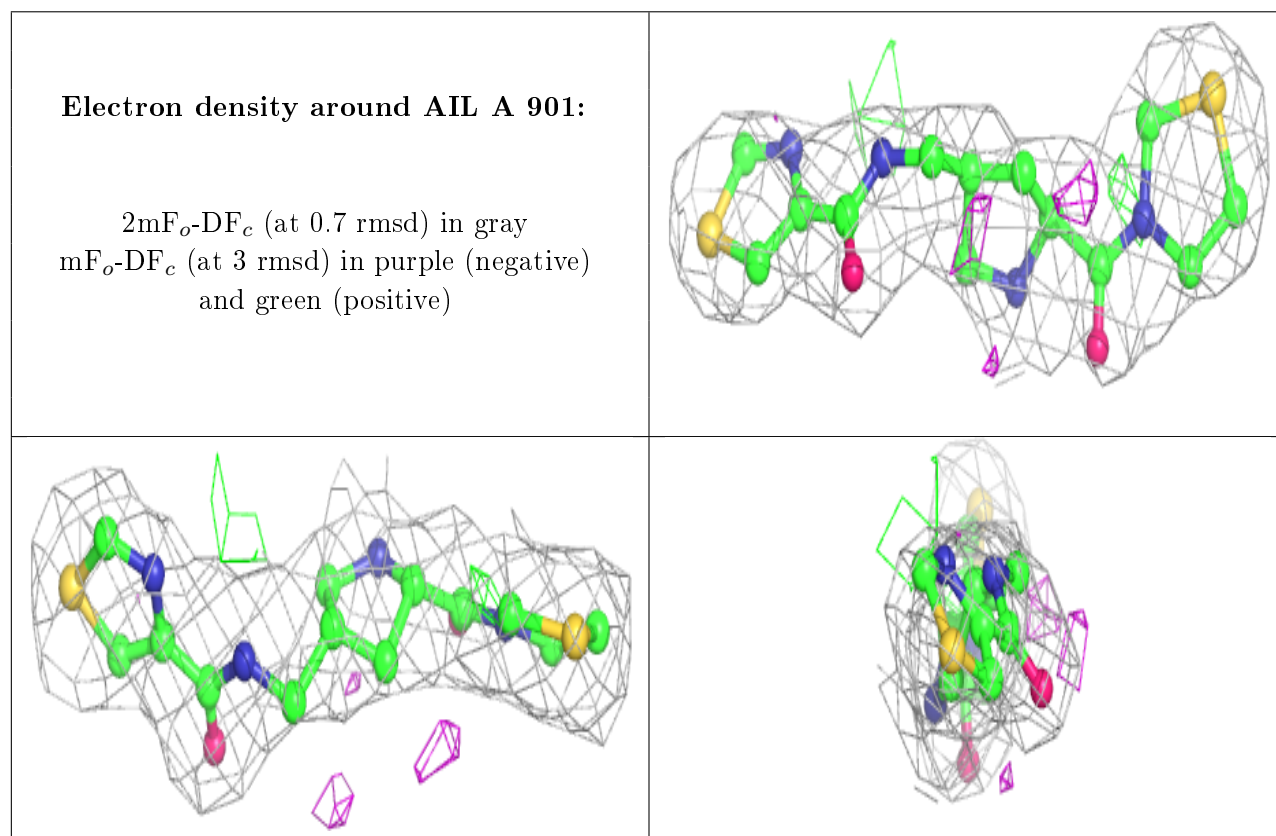
There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	SO4	A	801	5/5	0.91	0.31	47,47,47,47	0
3	AIL	A	901	21/21	0.92	0.22	47,47,47,47	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



6.5 Other polymers [i](#)

There are no such residues in this entry.