



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 04:12 PM UTC

PDB ID : 3ZZT / pdb_00003zzt
Title : Crystal structure of Staphylococcus aureus elongation factor G with a fusidic
-acid-resistant mutation F88L
Authors : Koripella, R.K.; Chen, Y.; Selmer, M.; Sanyal, S.
Deposited on : 2011-09-05
Resolution : 2.95 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 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:

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

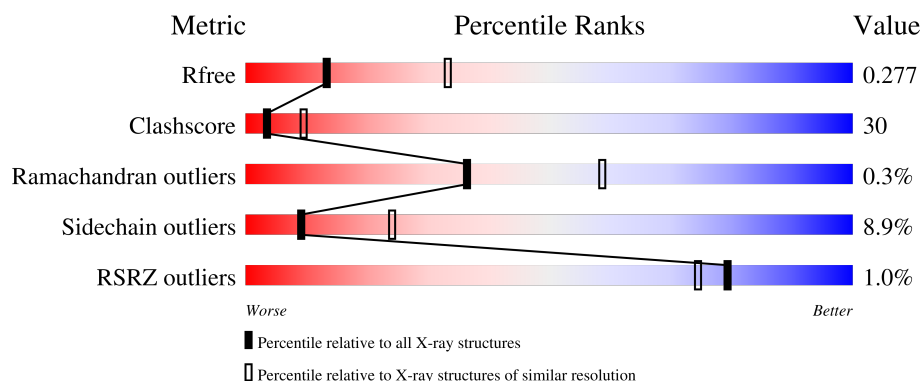
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.95 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}	180053	1130 (2.98-2.94)
Clashscore	190562	1157 (2.98-2.94)
Ramachandran outliers	187476	1101 (2.98-2.94)
Sidechain outliers	187428	1101 (2.98-2.94)
RSRZ outliers	180081	1130 (2.98-2.94)

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 of 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	693	52%36%6%6%
1	B	693	45%43%5%6%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 10059 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 ELONGATION FACTOR G.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	649	Total	C	N	O	S	0	0	1
			5018	3150	841	1000	27			
1	B	649	Total	C	N	O	S	0	0	1
			5018	3150	841	1000	27			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	88	LEU	PHE	engineered mutation	UNP P68790
B	88	LEU	PHE	engineered mutation	UNP P68790

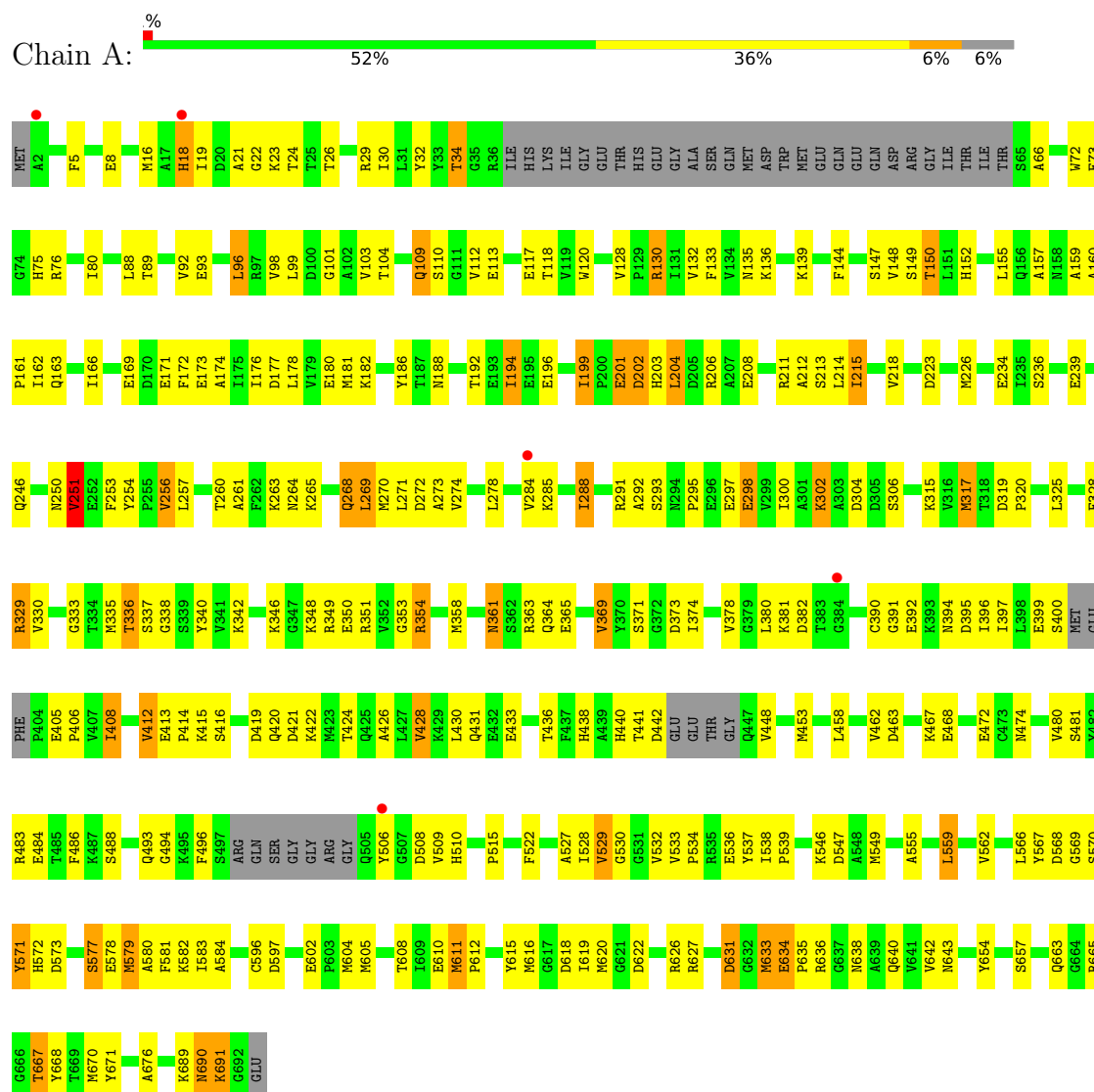
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	17	Total	O	0	0
			17	17		
2	B	6	Total	O	0	0
			6	6		

3 Residue-property plots

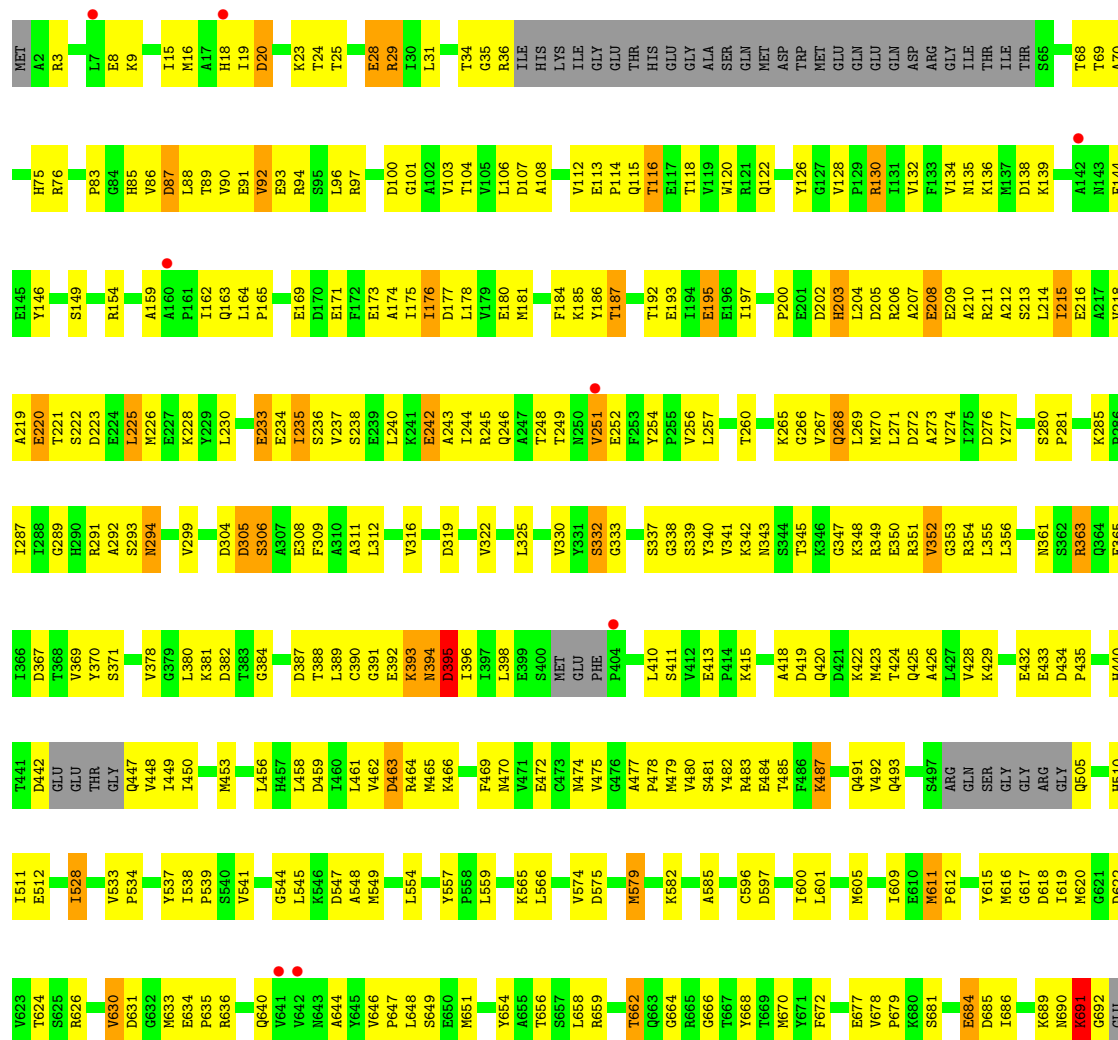
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: ELONGATION FACTOR G



• Molecule 1: ELONGATION FACTOR G





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	65.97Å 127.93Å 107.44Å 90.00° 107.86° 90.00°	Depositor
Resolution (Å)	47.40 – 2.95 47.40 – 2.95	Depositor EDS
% Data completeness (in resolution range)	90.3 (47.40-2.95) 90.3 (47.40-2.95)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.90 (at 2.96Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.241 , 0.294 (Not available) , 0.277	Depositor DCC
R_{free} test set	1524 reflections (4.71%)	wwPDB-VP
Wilson B-factor (Å ²)	77.8	Xtriage
Anisotropy	0.213	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 79.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.032 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	10059	wwPDB-VP
Average B, all atoms (Å ²)	93.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.78% 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

5.1 Standard geometry

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	0.33	1/5103 (0.0%)	0.81	10/6900 (0.1%)
1	B	0.38	1/5103 (0.0%)	0.82	5/6900 (0.1%)
All	All	0.36	2/10206 (0.0%)	0.81	15/13800 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	691	LYS	C-N	-7.13	1.23	1.33
1	B	691	LYS	C-N	-7.05	1.23	1.33

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	571	TYR	N-CA-C	6.65	117.02	108.24
1	B	396	ILE	N-CA-C	6.39	117.82	109.58
1	B	294	ASN	CA-C-N	6.33	125.75	118.85
1	B	294	ASN	C-N-CA	6.33	125.75	118.85
1	B	395	ASP	N-CA-C	6.16	120.93	113.17
1	B	202	ASP	N-CA-C	6.09	120.44	112.89
1	A	428	VAL	CB-CA-C	-5.57	104.62	112.14
1	A	597	ASP	CA-C-N	5.54	125.45	119.85
1	A	597	ASP	C-N-CA	5.54	125.45	119.85
1	A	578	GLU	N-CA-C	-5.30	106.66	113.23
1	A	634	GLU	CA-C-N	-5.27	115.16	120.85
1	A	634	GLU	C-N-CA	-5.27	115.16	120.85
1	A	405	GLU	CA-C-N	5.21	125.37	119.90
1	A	405	GLU	C-N-CA	5.21	125.37	119.90
1	A	690	ASN	N-CA-C	-5.04	102.17	109.59

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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	5018	0	4934	254	1
1	B	5018	0	4934	337	0
2	A	17	0	0	4	0
2	B	6	0	0	1	0
All	All	10059	0	9868	590	1

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 30.

All (590) 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:B:363:ARG:HG3	1:B:363:ARG:HH11	1.01	1.17
1:B:268:GLN:N	1:B:268:GLN:OE1	1.86	1.09
1:B:186:TYR:OH	1:B:268:GLN:NE2	1.86	1.07
1:B:242:GLU:N	1:B:242:GLU:OE1	1.91	1.03
1:B:128:VAL:O	1:B:130:ARG:NH1	1.92	1.02
1:A:128:VAL:O	1:A:130:ARG:NH1	1.93	1.00
1:A:428:VAL:O	1:A:431:GLN:NE2	1.91	1.00
1:B:222:SER:HB3	1:B:225:LEU:HD23	1.44	0.99
1:B:28:GLU:OE1	1:B:28:GLU:N	1.97	0.97
1:B:28:GLU:O	1:B:31:LEU:N	1.98	0.96
1:A:130:ARG:HG3	1:A:130:ARG:HH11	1.30	0.96
1:B:208:GLU:CD	1:B:208:GLU:H	1.74	0.93
1:B:413:GLU:HB3	1:B:474:ASN:OD1	1.68	0.93
1:B:363:ARG:HG3	1:B:363:ARG:NH1	1.78	0.92
1:B:651:MET:HE2	1:B:651:MET:HA	1.51	0.92
1:B:612:PRO:HG2	1:B:615:TYR:HE2	1.35	0.91
1:A:506:TYR:HE1	1:A:571:TYR:HA	1.32	0.91
1:A:568:ASP:OD1	1:A:569:GLY:N	2.05	0.89
1:B:242:GLU:HA	1:B:245:ARG:HB3	1.54	0.87
1:A:364:GLN:NE2	1:A:365:GLU:O	2.07	0.87
1:B:88:LEU:O	1:B:88:LEU:HD12	1.72	0.87
1:B:616:MET:SD	1:B:633:MET:HE1	2.15	0.86
1:B:612:PRO:HG2	1:B:615:TYR:CE2	2.10	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:342:LYS:NZ	1:A:394:ASN:O	2.08	0.85
1:B:195:GLU:OE1	1:B:195:GLU:N	2.10	0.85
1:B:415:LYS:HZ3	1:B:474:ASN:HB3	1.42	0.85
1:B:208:GLU:OE1	1:B:208:GLU:N	2.10	0.84
1:A:610:GLU:OE1	1:A:636:ARG:NH2	2.09	0.84
1:B:691:LYS:HG3	1:B:692:GLY:N	1.93	0.82
1:B:384:GLY:N	1:B:387:ASP:OD2	2.12	0.81
1:A:506:TYR:CE1	1:A:571:TYR:HA	2.16	0.80
1:B:333:GLY:O	1:B:371:SER:OG	1.98	0.80
1:A:284:VAL:HG22	1:A:285:LYS:H	1.47	0.80
1:B:410:LEU:HG	1:B:458:LEU:HD13	1.64	0.80
1:B:425:GLN:O	1:B:428:VAL:HG12	1.82	0.79
1:A:440:HIS:NE2	1:A:442:ASP:HB3	1.97	0.79
1:B:363:ARG:HH11	1:B:363:ARG:CG	1.89	0.79
1:A:496:PHE:O	1:A:506:TYR:HA	1.82	0.78
1:B:113:GLU:N	1:B:116:THR:OG1	2.17	0.78
1:A:135:ASN:OD1	1:A:136:LYS:N	2.17	0.77
1:A:19:ILE:O	1:A:22:GLY:N	2.13	0.77
1:B:459:ASP:HA	1:B:462:VAL:HG12	1.67	0.76
1:A:346:LYS:NZ	1:A:382:ASP:O	2.19	0.76
1:B:292:ALA:N	1:B:395:ASP:O	2.17	0.76
1:A:611:MET:HE1	1:A:642:VAL:HG23	1.66	0.76
1:B:204:LEU:HD23	1:B:204:LEU:O	1.84	0.76
1:A:246:GLN:O	1:A:250:ASN:ND2	2.18	0.75
1:B:208:GLU:CD	1:B:209:GLU:H	1.93	0.75
1:B:656:THR:HG23	1:B:659:ARG:HH22	1.51	0.75
1:A:112:VAL:HG12	1:A:150:THR:HB	1.68	0.75
1:B:87:ASP:OD1	1:B:87:ASP:N	2.15	0.74
1:A:611:MET:N	1:A:611:MET:SD	2.60	0.74
1:A:581:PHE:O	1:A:584:ALA:N	2.21	0.74
1:B:107:ASP:OD1	1:B:139:LYS:HE3	1.86	0.74
1:B:415:LYS:NZ	1:B:474:ASN:HB3	2.02	0.74
1:B:395:ASP:OD1	1:B:395:ASP:N	2.21	0.73
1:A:30:ILE:O	1:A:34:THR:OG1	2.05	0.73
1:B:662:THR:HG21	1:B:666:GLY:HA3	1.69	0.73
1:A:8:GLU:OE1	1:A:8:GLU:N	2.20	0.73
1:A:130:ARG:NH1	1:A:130:ARG:HG3	1.96	0.73
1:A:349:ARG:O	1:A:381:LYS:NZ	2.17	0.73
1:A:390:CYS:SG	1:A:394:ASN:HB3	2.29	0.72
1:A:481:SER:HB3	1:A:483:ARG:HH12	1.53	0.72
1:B:260:THR:HG22	1:B:265:LYS:HB2	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:136:LYS:HB2	1:B:139:LYS:NZ	2.05	0.71
1:A:463:ASP:O	1:A:467:LYS:HG2	1.90	0.71
1:B:617:GLY:HA2	1:B:620:MET:HE3	1.72	0.71
1:A:611:MET:HB2	1:A:612:PRO:HD2	1.73	0.71
1:B:28:GLU:H	1:B:28:GLU:CD	1.99	0.70
1:A:211:ARG:O	1:A:215:ILE:HG22	1.92	0.70
1:B:528:ILE:HD11	1:B:566:LEU:HG	1.74	0.70
1:B:34:THR:HB	1:B:70:ALA:HB1	1.72	0.70
1:A:354:ARG:NH2	1:A:365:GLU:OE1	2.17	0.70
1:B:319:ASP:HB3	1:B:322:VAL:HG22	1.74	0.70
1:B:316:VAL:HG23	1:B:433:GLU:HG2	1.74	0.70
1:B:280:SER:OG	1:B:281:PRO:HD2	1.91	0.69
1:B:487:LYS:HG3	1:B:597:ASP:O	1.92	0.69
1:A:615:TYR:OH	1:A:665:ARG:NH1	2.24	0.69
1:B:113:GLU:O	1:B:116:THR:OG1	2.08	0.69
1:A:506:TYR:HE1	1:A:571:TYR:CA	2.05	0.69
1:B:219:ALA:HA	1:B:225:LEU:HD21	1.75	0.69
1:B:415:LYS:HZ3	1:B:474:ASN:CB	2.06	0.69
1:B:85:HIS:NE2	1:B:88:LEU:HD23	2.07	0.69
1:A:506:TYR:HH	1:A:570:SER:HG	1.33	0.69
1:B:171:GLU:O	1:B:173:GLU:HG3	1.92	0.69
1:B:18:HIS:ND1	1:B:19:ILE:N	2.41	0.68
1:B:381:LYS:HG3	1:B:382:ASP:H	1.57	0.68
1:A:546:LYS:O	1:A:549:MET:N	2.27	0.68
1:B:646:VAL:HG11	1:B:651:MET:HE3	1.74	0.68
1:A:408:ILE:HG22	1:A:458:LEU:HD11	1.75	0.68
1:A:534:PRO:HD3	1:A:571:TYR:CD2	2.29	0.68
1:B:244:ILE:O	1:B:248:THR:OG1	2.04	0.68
1:B:463:ASP:OD1	1:B:464:ARG:N	2.27	0.68
1:B:354:ARG:NE	1:B:365:GLU:OE1	2.26	0.68
1:B:656:THR:HG23	1:B:659:ARG:NH2	2.09	0.68
1:A:80:ILE:HD13	1:A:98:VAL:HG12	1.75	0.68
1:A:202:ASP:OD1	1:A:202:ASP:N	2.22	0.67
1:A:616:MET:HE2	1:A:620:MET:HE1	1.76	0.67
1:B:136:LYS:O	1:B:139:LYS:HG2	1.95	0.67
1:B:487:LYS:NZ	1:B:677:GLU:OE2	2.15	0.67
1:A:431:GLN:N	1:A:431:GLN:OE1	2.28	0.66
1:B:208:GLU:O	1:B:211:ARG:N	2.28	0.66
1:A:604:MET:HE2	1:A:676:ALA:HB3	1.78	0.66
1:B:175:ILE:HD11	1:B:269:LEU:CD1	2.25	0.66
1:B:3:ARG:HB3	1:B:370:TYR:CD1	2.31	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:24:THR:O	1:B:28:GLU:OE1	2.14	0.66
1:B:20:ASP:N	1:B:20:ASP:OD1	2.27	0.66
1:A:186:TYR:CD2	1:A:265:LYS:HG2	2.31	0.65
1:B:181:MET:HE1	1:B:207:ALA:O	1.96	0.65
1:B:354:ARG:NH2	1:B:365:GLU:OE1	2.29	0.65
1:A:350:GLU:OE2	1:A:381:LYS:HG3	1.95	0.65
1:B:208:GLU:CD	1:B:208:GLU:N	2.44	0.65
1:A:577:SER:HB2	1:A:580:ALA:H	1.60	0.65
1:B:211:ARG:O	1:B:215:ILE:HG13	1.97	0.65
1:B:549:MET:HE3	1:B:559:LEU:HD23	1.79	0.65
1:A:538:ILE:HB	1:A:539:PRO:HD3	1.79	0.65
1:B:207:ALA:N	1:B:208:GLU:OE1	2.30	0.64
1:B:115:GLN:O	1:B:118:THR:OG1	2.14	0.64
1:B:245:ARG:NH1	1:B:276:ASP:O	2.29	0.64
1:B:337:SER:HA	1:B:352:VAL:CG2	2.28	0.64
1:B:393:LYS:O	1:B:394:ASN:HB2	1.95	0.64
1:A:633:MET:HG3	1:A:634:GLU:N	2.08	0.64
1:A:354:ARG:HH21	1:A:365:GLU:CD	2.04	0.64
1:B:175:ILE:HD11	1:B:269:LEU:HD12	1.79	0.64
1:B:422:LYS:HD3	1:B:470:ASN:O	1.97	0.64
1:B:659:ARG:HG3	1:B:664:GLY:HA2	1.81	0.63
1:A:622:ASP:OD1	1:A:626:ARG:NH2	2.31	0.63
1:B:221:THR:HG21	1:B:252:GLU:OE1	1.98	0.63
1:A:204:LEU:O	1:A:208:GLU:HG2	1.98	0.63
1:B:684:GLU:HG2	1:B:685:ASP:N	2.13	0.63
1:B:619:ILE:O	1:B:622:ASP:N	2.32	0.63
1:B:94:ARG:O	1:B:97:ARG:N	2.30	0.62
1:B:107:ASP:OD1	1:B:139:LYS:CE	2.47	0.62
1:B:214:LEU:O	1:B:218:VAL:HG23	1.98	0.62
1:B:238:SER:O	1:B:242:GLU:OE1	2.17	0.62
1:A:611:MET:HG3	1:A:619:ILE:HD11	1.82	0.62
1:B:648:LEU:O	1:B:651:MET:N	2.31	0.62
1:B:122:GLN:NE2	2:B:2002:HOH:O	2.14	0.62
1:B:136:LYS:HB2	1:B:139:LYS:HZ3	1.63	0.62
1:B:238:SER:O	1:B:242:GLU:CD	2.43	0.62
1:B:605:MET:HE3	1:B:670:MET:HG2	1.82	0.62
1:B:340:TYR:CE1	1:B:351:ARG:HD3	2.35	0.61
1:A:96:LEU:HD23	1:A:128:VAL:HG21	1.80	0.61
1:B:101:GLY:HA2	1:B:128:VAL:HG12	1.82	0.61
1:B:487:LYS:HG3	1:B:597:ASP:OD1	2.00	0.61
1:B:237:VAL:HG23	1:B:238:SER:H	1.64	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:337:SER:HA	1:B:352:VAL:HG21	1.81	0.61
1:A:16:MET:HG3	1:A:104:THR:HG22	1.82	0.61
1:A:433:GLU:N	1:A:433:GLU:OE1	2.33	0.61
1:B:237:VAL:O	1:B:240:LEU:N	2.32	0.61
1:A:147:SER:O	1:A:150:THR:OG1	2.18	0.61
1:A:534:PRO:HG2	1:A:537:TYR:CD2	2.36	0.61
1:B:681:SER:O	1:B:684:GLU:CD	2.44	0.61
1:A:274:VAL:HG13	1:A:278:LEU:HD12	1.82	0.61
1:A:194:ILE:HD12	1:A:194:ILE:O	2.00	0.60
1:B:208:GLU:O	1:B:212:ALA:N	2.33	0.60
1:B:337:SER:OG	1:B:353:GLY:O	2.18	0.60
1:B:547:ASP:OD1	1:B:548:ALA:N	2.31	0.60
1:A:181:MET:HE2	1:A:211:ARG:HD3	1.83	0.60
1:B:242:GLU:O	1:B:246:GLN:N	2.30	0.60
1:A:182:LYS:HD3	1:A:196:GLU:CD	2.26	0.60
1:B:355:LEU:HD12	1:B:367:ASP:O	2.01	0.60
1:B:100:ASP:O	1:B:128:VAL:HG13	2.02	0.60
1:B:130:ARG:HG3	1:B:130:ARG:HH11	1.67	0.60
1:A:616:MET:CE	1:A:633:MET:HE1	2.31	0.60
1:B:311:ALA:HB3	1:B:389:LEU:HB2	1.84	0.60
1:A:270:MET:HG3	1:A:271:LEU:N	2.16	0.60
1:B:242:GLU:O	1:B:245:ARG:N	2.35	0.60
1:B:651:MET:HA	1:B:651:MET:CE	2.30	0.60
1:B:185:LYS:HB3	1:B:195:GLU:OE2	2.01	0.59
1:B:474:ASN:OD1	1:B:474:ASN:O	2.20	0.59
1:B:534:PRO:HG2	1:B:537:TYR:HD2	1.68	0.59
1:A:284:VAL:HG22	1:A:285:LYS:N	2.16	0.59
1:A:304:ASP:OD1	1:A:306:SER:N	2.35	0.59
1:B:113:GLU:OE2	1:B:114:PRO:HD2	2.03	0.59
1:A:691:LYS:HE3	1:A:691:LYS:HA	1.85	0.59
1:B:96:LEU:HB3	1:B:126:TYR:HD2	1.68	0.59
1:A:463:ASP:OD1	1:A:467:LYS:NZ	2.29	0.59
1:B:481:SER:OG	1:B:483:ARG:NH1	2.36	0.58
1:B:388:THR:HG23	1:B:398:LEU:HD12	1.84	0.58
1:A:99:LEU:HD12	1:A:99:LEU:O	2.03	0.58
1:A:441:THR:O	1:A:442:ASP:C	2.46	0.58
1:B:236:SER:OG	1:B:237:VAL:N	2.36	0.58
1:A:319:ASP:CG	1:A:320:PRO:HD2	2.29	0.58
1:A:467:LYS:HG3	1:A:468:GLU:H	1.69	0.58
1:A:212:ALA:O	1:A:215:ILE:HG23	2.04	0.58
1:A:412:VAL:O	1:A:448:VAL:HG12	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:342:LYS:NZ	1:B:392:GLU:O	2.27	0.58
1:A:26:THR:O	1:A:30:ILE:HG13	2.03	0.58
1:A:424:THR:O	1:A:428:VAL:HG23	2.04	0.58
1:A:436:THR:HG21	1:A:453:MET:HE2	1.86	0.58
1:A:73:GLU:O	1:A:75:HIS:ND1	2.35	0.57
1:B:276:ASP:HB3	1:B:277:TYR:CE1	2.40	0.57
1:B:354:ARG:CZ	1:B:365:GLU:OE1	2.53	0.57
1:B:305:ASP:OD1	1:B:305:ASP:N	2.37	0.57
1:B:9:LYS:HA	1:B:75:HIS:CD2	2.39	0.57
1:B:267:VAL:N	1:B:268:GLN:OE1	2.36	0.57
1:B:18:HIS:CE1	1:B:20:ASP:OD1	2.57	0.57
1:B:596:CYS:O	1:B:597:ASP:OD1	2.23	0.57
1:A:488:SER:O	1:A:515:PRO:HD3	2.05	0.57
1:B:103:VAL:HG11	1:B:270:MET:HE1	1.86	0.57
1:B:355:LEU:HD13	1:B:369:VAL:HG23	1.85	0.57
1:B:505:GLN:N	1:B:575:ASP:HB3	2.20	0.56
1:A:66:ALA:HB2	1:A:315:LYS:HE2	1.86	0.56
1:B:270:MET:HA	1:B:273:ALA:HB3	1.88	0.56
1:B:204:LEU:O	1:B:208:GLU:OE1	2.22	0.56
1:B:146:TYR:O	1:B:149:SER:HB3	2.04	0.56
1:A:361:ASN:OD1	1:A:361:ASN:N	2.37	0.56
1:B:83:PRO:CB	1:B:88:LEU:HD11	2.35	0.56
1:B:390:CYS:SG	1:B:391:GLY:N	2.78	0.56
1:B:276:ASP:HB3	1:B:277:TYR:CD1	2.41	0.56
1:B:266:GLY:H	1:B:268:GLN:HE22	1.54	0.56
1:A:98:VAL:O	1:A:329:ARG:NH1	2.39	0.55
1:B:108:ALA:HB3	1:B:139:LYS:HZ1	1.72	0.55
1:B:187:THR:CG2	1:B:193:GLU:O	2.54	0.55
1:B:616:MET:HG2	1:B:620:MET:CE	2.36	0.55
1:B:15:ILE:HG22	1:B:23:LYS:HG3	1.88	0.55
1:B:19:ILE:CD1	1:B:23:LYS:HD3	2.36	0.55
1:B:237:VAL:HG23	1:B:238:SER:N	2.22	0.55
1:A:19:ILE:HA	1:A:23:LYS:H	1.71	0.55
1:A:616:MET:HE3	1:A:633:MET:HE1	1.87	0.55
1:B:609:ILE:HD11	1:B:654:TYR:OH	2.07	0.55
1:B:634:GLU:O	1:B:640:GLN:NE2	2.39	0.55
1:B:92:VAL:O	1:B:96:LEU:HD13	2.06	0.55
1:A:610:GLU:CD	1:A:636:ARG:HH21	2.09	0.55
1:A:619:ILE:O	1:A:622:ASP:N	2.40	0.55
1:B:343:ASN:OD1	1:B:345:THR:HB	2.07	0.55
1:B:130:ARG:NH1	1:B:130:ARG:HG3	2.20	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:482:TYR:HB2	1:B:557:TYR:CD2	2.41	0.55
1:B:493:GLN:HB2	1:B:510:HIS:CE1	2.42	0.55
1:A:130:ARG:HH11	1:A:130:ARG:CG	2.11	0.55
1:B:115:GLN:C	1:B:118:THR:HG1	2.15	0.55
1:B:113:GLU:CD	1:B:114:PRO:HD2	2.32	0.55
1:B:350:GLU:OE2	1:B:382:ASP:N	2.40	0.55
1:B:611:MET:SD	1:B:619:ILE:HG13	2.47	0.55
1:A:654:TYR:O	1:A:657:SER:N	2.39	0.54
1:B:609:ILE:CD1	1:B:654:TYR:OH	2.56	0.54
1:B:88:LEU:HD22	1:B:91:GLU:HB2	1.90	0.54
1:B:289:GLY:C	1:B:299:VAL:HG12	2.33	0.54
1:A:166:ILE:HD12	1:A:174:ALA:HB3	1.88	0.54
1:B:544:GLY:CA	1:B:582:LYS:HG3	2.38	0.54
1:A:467:LYS:HG3	1:A:468:GLU:N	2.22	0.54
1:B:354:ARG:O	1:B:378:VAL:HG12	2.06	0.54
1:B:107:ASP:OD1	1:B:139:LYS:NZ	2.41	0.54
1:B:390:CYS:SG	1:B:394:ASN:HB3	2.48	0.54
1:A:611:MET:HE3	1:A:619:ILE:HD12	1.89	0.54
1:A:612:PRO:HG2	1:A:615:TYR:CD2	2.43	0.54
1:A:663:GLN:OE1	1:A:663:GLN:N	2.41	0.54
1:B:92:VAL:HG12	1:B:93:GLU:N	2.21	0.54
1:A:99:LEU:HD13	1:A:101:GLY:O	2.08	0.53
1:A:493:GLN:NE2	1:A:508:ASP:OD1	2.39	0.53
1:B:423:MET:HG3	1:B:465:MET:HE1	1.88	0.53
1:A:612:PRO:HG2	1:A:615:TYR:CE2	2.42	0.53
1:A:335:MET:HB3	1:A:369:VAL:HG23	1.91	0.53
1:A:419:ASP:OD1	1:A:420:GLN:N	2.41	0.53
1:B:106:LEU:HD13	1:B:132:VAL:HG13	1.90	0.53
1:B:691:LYS:CG	1:B:692:GLY:N	2.65	0.53
1:A:186:TYR:HD2	1:A:265:LYS:HG2	1.72	0.53
1:A:201:GLU:HA	1:A:204:LEU:HB2	1.91	0.53
1:B:394:ASN:OD1	1:B:395:ASP:N	2.41	0.53
1:A:373:ASP:OD1	1:A:374:ILE:N	2.29	0.53
1:A:486:PHE:O	1:A:515:PRO:HB3	2.09	0.53
1:B:626:ARG:HD3	1:B:651:MET:CE	2.38	0.53
1:A:350:GLU:HG3	1:A:381:LYS:HE2	1.91	0.52
1:A:163:GLN:HA	1:A:176:ILE:O	2.10	0.52
1:A:436:THR:HG22	1:A:436:THR:O	2.09	0.52
1:A:18:HIS:ND1	1:A:19:ILE:N	2.57	0.52
1:A:149:SER:O	1:A:152:HIS:HB2	2.10	0.52
1:A:186:TYR:CE2	1:A:265:LYS:HA	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:509:VAL:HG22	1:A:584:ALA:HB1	1.91	0.52
1:A:288:ILE:HD11	1:A:298:GLU:HG3	1.92	0.52
1:A:577:SER:HB2	1:A:579:MET:H	1.74	0.52
1:B:233:GLU:O	1:B:234:GLU:HB2	2.09	0.52
1:A:337:SER:OG	1:A:353:GLY:O	2.21	0.52
1:B:200:PRO:HG2	1:B:203:HIS:HE2	1.75	0.52
1:A:162:ILE:HG22	1:A:214:LEU:HD21	1.91	0.51
1:A:619:ILE:O	1:A:622:ASP:HB3	2.11	0.51
1:A:689:LYS:O	1:A:691:LYS:HD2	2.10	0.51
1:B:538:ILE:HB	1:B:539:PRO:HD3	1.92	0.51
1:A:159:ALA:HB2	1:A:254:TYR:HB2	1.93	0.51
1:A:413:GLU:HG3	1:A:413:GLU:O	2.11	0.51
1:B:269:LEU:O	1:B:272:ASP:HB2	2.10	0.51
1:A:537:TYR:HB3	1:A:581:PHE:CE2	2.45	0.51
1:B:605:MET:HG3	1:B:648:LEU:HD13	1.92	0.51
1:A:559:LEU:HD21	1:A:562:VAL:HG21	1.91	0.51
1:A:428:VAL:O	1:A:431:GLN:CD	2.51	0.51
1:A:611:MET:HG3	1:A:619:ILE:CD1	2.40	0.51
1:B:159:ALA:HB2	1:B:254:TYR:HB2	1.93	0.51
1:A:567:TYR:CD1	1:A:567:TYR:C	2.89	0.51
1:B:85:HIS:HB2	1:B:87:ASP:OD1	2.11	0.51
1:B:459:ASP:HA	1:B:462:VAL:CG1	2.40	0.51
1:B:120:TRP:HZ2	1:B:254:TYR:CE2	2.29	0.51
1:A:488:SER:HB2	1:A:596:CYS:HA	1.92	0.51
1:B:28:GLU:O	1:B:29:ARG:C	2.54	0.51
1:B:90:VAL:O	1:B:93:GLU:HG2	2.10	0.50
1:B:617:GLY:CA	1:B:620:MET:HE3	2.39	0.50
1:A:414:PRO:HB2	1:A:419:ASP:OD1	2.12	0.50
1:B:134:VAL:HG23	1:B:257:LEU:O	2.11	0.50
1:A:223:ASP:HA	1:A:226:MET:HB2	1.93	0.50
1:A:510:HIS:HB3	1:A:567:TYR:CZ	2.46	0.50
1:B:187:THR:HG21	1:B:193:GLU:O	2.11	0.50
1:B:381:LYS:HG3	1:B:382:ASP:N	2.25	0.50
1:B:491:GLN:HG2	1:B:512:GLU:HB2	1.93	0.50
1:A:399:GLU:CG	1:A:400:SER:N	2.74	0.50
1:A:605:MET:HE3	1:A:670:MET:HG2	1.93	0.50
1:B:135:ASN:OD1	1:B:136:LYS:N	2.45	0.50
1:B:136:LYS:HB2	1:B:139:LYS:HZ2	1.77	0.50
1:B:174:ALA:HB1	1:B:184:PHE:O	2.11	0.50
1:B:631:ASP:C	1:B:631:ASP:OD1	2.55	0.50
1:A:328:PHE:O	1:A:374:ILE:HG23	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:251:VAL:HG12	1:B:251:VAL:O	2.12	0.50
1:B:19:ILE:HD13	1:B:23:LYS:HB3	1.93	0.50
1:B:268:GLN:HG2	1:B:269:LEU:N	2.27	0.50
1:A:615:TYR:O	1:A:618:ASP:N	2.43	0.50
1:B:36:ARG:HG3	1:B:36:ARG:O	2.11	0.50
1:B:413:GLU:OE1	1:B:474:ASN:CG	2.54	0.50
1:A:66:ALA:HB2	1:A:315:LYS:NZ	2.27	0.49
1:B:285:LYS:HG3	1:B:285:LYS:O	2.10	0.49
1:B:343:ASN:O	1:B:347:GLY:N	2.45	0.49
1:B:658:LEU:O	1:B:662:THR:HG22	2.11	0.49
1:A:293:SER:O	1:A:295:PRO:HD3	2.13	0.49
1:A:527:ALA:HB3	1:A:566:LEU:O	2.13	0.49
1:A:89:THR:O	1:A:93:GLU:HG3	2.13	0.49
1:A:392:GLU:N	2:A:2008:HOH:O	2.43	0.49
1:A:399:GLU:CG	1:A:400:SER:H	2.26	0.49
1:B:477:ALA:O	1:B:479:MET:HG3	2.12	0.49
1:A:330:VAL:HG13	1:A:330:VAL:O	2.11	0.49
1:B:528:ILE:HD12	1:B:566:LEU:O	2.12	0.49
1:A:257:LEU:HD12	1:A:257:LEU:N	2.27	0.49
1:A:537:TYR:HB3	1:A:581:PHE:CD2	2.47	0.49
1:A:214:LEU:O	1:A:218:VAL:HG23	2.13	0.49
1:B:164:LEU:HD21	1:B:206:ARG:HG2	1.94	0.48
1:B:268:GLN:CG	1:B:269:LEU:N	2.76	0.48
1:B:308:GLU:HG3	1:B:309:PHE:H	1.78	0.48
1:B:456:LEU:HD12	1:B:456:LEU:HA	1.62	0.48
1:B:554:LEU:CD2	1:B:600:ILE:HG13	2.43	0.48
1:A:462:VAL:HG13	1:A:463:ASP:N	2.29	0.48
1:B:534:PRO:HG2	1:B:537:TYR:CD2	2.48	0.48
1:A:397:ILE:HD12	1:A:397:ILE:N	2.28	0.48
1:B:88:LEU:HD13	1:B:91:GLU:HB3	1.95	0.48
1:B:223:ASP:HA	1:B:226:MET:HB3	1.94	0.48
1:B:221:THR:HG22	1:B:221:THR:O	2.13	0.48
1:B:223:ASP:HA	1:B:226:MET:CB	2.43	0.48
1:B:291:ARG:HB3	1:B:395:ASP:HB2	1.94	0.48
1:A:66:ALA:HB2	1:A:315:LYS:CE	2.43	0.48
1:A:133:PHE:HE2	1:A:135:ASN:HD22	1.60	0.48
1:B:35:GLY:O	1:B:36:ARG:C	2.57	0.48
1:B:120:TRP:HZ2	1:B:254:TYR:CD2	2.31	0.48
1:B:19:ILE:HD11	1:B:23:LYS:HD3	1.95	0.48
1:B:177:ASP:OD2	1:B:180:GLU:HB2	2.14	0.48
1:B:662:THR:HG21	1:B:666:GLY:CA	2.40	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:358:MET:HE3	1:A:363:ARG:HH11	1.79	0.48
1:A:608:THR:O	1:A:668:TYR:HA	2.14	0.48
1:B:312:LEU:HD12	1:B:387:ASP:O	2.14	0.48
1:B:630:VAL:HA	1:B:644:ALA:HA	1.95	0.48
1:A:34:THR:HG22	1:A:72:TRP:HB2	1.95	0.47
1:A:534:PRO:HD3	1:A:571:TYR:CE2	2.48	0.47
1:B:544:GLY:O	1:B:547:ASP:OD1	2.33	0.47
1:B:208:GLU:CD	1:B:209:GLU:N	2.67	0.47
1:A:32:TYR:CD1	1:A:32:TYR:C	2.93	0.47
1:A:72:TRP:HH2	1:A:268:GLN:HG2	1.79	0.47
1:A:178:LEU:O	1:A:211:ARG:HD2	2.15	0.47
1:B:28:GLU:O	1:B:31:LEU:CA	2.62	0.47
1:A:88:LEU:O	1:A:92:VAL:HG23	2.15	0.47
1:A:186:TYR:HE2	1:A:265:LYS:HA	1.79	0.47
1:A:493:GLN:HG2	1:A:494:GLY:N	2.29	0.47
1:A:631:ASP:OD1	1:A:631:ASP:C	2.57	0.47
1:A:667:THR:CG2	1:A:668:TYR:N	2.77	0.47
1:B:174:ALA:CB	1:B:185:LYS:HA	2.45	0.47
1:B:268:GLN:CD	1:B:269:LEU:H	2.23	0.47
1:B:420:GLN:O	1:B:424:THR:HG22	2.14	0.47
1:B:484:GLU:CD	1:B:554:LEU:HB3	2.39	0.47
1:A:103:VAL:HG21	1:A:270:MET:HE1	1.97	0.47
1:A:181:MET:HG2	1:A:211:ARG:HH11	1.79	0.47
1:A:253:PHE:CD1	1:A:254:TYR:N	2.82	0.47
1:A:330:VAL:HG13	1:A:371:SER:HA	1.96	0.47
1:A:390:CYS:SG	1:A:391:GLY:N	2.87	0.47
1:A:581:PHE:O	1:A:582:LYS:C	2.58	0.47
1:A:638:ASN:OD1	1:A:638:ASN:C	2.56	0.47
1:B:25:THR:O	1:B:29:ARG:HG2	2.14	0.47
1:B:113:GLU:HG3	1:B:114:PRO:HD2	1.96	0.47
1:B:411:SER:HA	1:B:449:ILE:HD13	1.96	0.47
1:B:413:GLU:HB3	1:B:474:ASN:CG	2.39	0.47
1:B:426:ALA:HB2	1:B:469:PHE:CD2	2.50	0.47
1:A:412:VAL:HG22	1:A:448:VAL:CG1	2.45	0.47
1:A:577:SER:HB2	1:A:579:MET:N	2.30	0.47
1:B:423:MET:HG3	1:B:465:MET:CE	2.44	0.47
1:A:358:MET:HE3	1:A:363:ARG:NH1	2.30	0.47
1:B:222:SER:CB	1:B:225:LEU:HD23	2.30	0.47
1:A:635:PRO:HB3	1:A:640:GLN:OE1	2.16	0.46
1:B:113:GLU:CG	1:B:114:PRO:HD2	2.45	0.46
1:B:146:TYR:CD1	1:B:146:TYR:C	2.92	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:604:MET:HE2	1:A:676:ALA:CB	2.45	0.46
1:B:28:GLU:O	1:B:31:LEU:HB2	2.16	0.46
1:B:88:LEU:HD13	1:B:92:VAL:H	1.80	0.46
1:B:349:ARG:CZ	1:B:392:GLU:OE1	2.63	0.46
1:A:480:VAL:N	2:A:2011:HOH:O	2.33	0.46
1:B:340:TYR:CD2	1:B:349:ARG:NH2	2.81	0.46
1:B:429:LYS:O	1:B:432:GLU:HB2	2.15	0.46
1:B:612:PRO:O	1:B:615:TYR:HD2	1.99	0.46
1:A:29:ARG:NH1	1:A:264:ASN:OD1	2.49	0.46
1:A:350:GLU:OE2	1:A:382:ASP:N	2.45	0.46
1:A:611:MET:HE1	1:A:642:VAL:CG2	2.39	0.46
1:B:130:ARG:HH11	1:B:130:ARG:CG	2.28	0.46
1:B:619:ILE:O	1:B:622:ASP:HB3	2.15	0.46
1:A:236:SER:OG	1:A:239:GLU:HB2	2.15	0.46
1:A:291:ARG:NH1	1:A:395:ASP:OD1	2.48	0.46
1:A:350:GLU:HG2	1:A:380:LEU:HD22	1.97	0.46
1:B:204:LEU:HD23	1:B:208:GLU:HG3	1.98	0.46
1:B:330:VAL:HG23	1:B:330:VAL:O	2.16	0.46
1:A:144:PHE:O	1:A:148:VAL:HG23	2.15	0.46
1:B:101:GLY:HA2	1:B:128:VAL:CG1	2.45	0.46
1:B:308:GLU:O	1:B:332:SER:OG	2.34	0.46
1:A:250:ASN:C	1:A:251:VAL:HG23	2.40	0.46
1:B:132:VAL:HB	1:B:256:VAL:HG22	1.98	0.46
1:B:154:ARG:HG3	1:B:636:ARG:HD2	1.98	0.46
1:B:195:GLU:HG2	1:B:197:ILE:HG23	1.97	0.46
1:B:415:LYS:HZ3	1:B:474:ASN:N	2.13	0.46
1:B:138:ASP:HA	1:B:169:GLU:O	2.16	0.46
1:A:406:PRO:HG3	1:A:438:HIS:CD2	2.52	0.45
1:B:90:VAL:HA	1:B:93:GLU:OE2	2.16	0.45
1:B:257:LEU:N	1:B:257:LEU:HD12	2.31	0.45
1:B:480:VAL:HG23	1:B:482:TYR:CE2	2.51	0.45
1:B:616:MET:O	1:B:618:ASP:N	2.49	0.45
1:A:572:HIS:CD2	1:A:573:ASP:H	2.34	0.45
1:B:85:HIS:NE2	1:B:88:LEU:CD2	2.77	0.45
1:B:260:THR:HG23	1:B:260:THR:O	2.17	0.45
1:A:136:LYS:O	1:A:139:LYS:HG2	2.16	0.45
1:A:537:TYR:CB	1:A:581:PHE:HE2	2.29	0.45
1:B:605:MET:CE	1:B:670:MET:HG2	2.44	0.45
1:A:96:LEU:CD2	1:A:128:VAL:HG21	2.46	0.45
1:A:419:ASP:O	1:A:422:LYS:N	2.49	0.45
1:A:480:VAL:HG22	2:A:2011:HOH:O	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:634:GLU:HG2	1:A:635:PRO:O	2.16	0.45
1:B:440:HIS:O	1:B:448:VAL:HG23	2.15	0.45
1:B:554:LEU:HD23	1:B:600:ILE:HG13	1.97	0.45
1:A:270:MET:O	1:A:273:ALA:N	2.49	0.45
1:A:643:ASN:C	1:A:643:ASN:OD1	2.60	0.45
1:B:228:LYS:HA	1:B:233:GLU:OE2	2.17	0.45
1:B:268:GLN:CG	1:B:269:LEU:H	2.30	0.45
1:B:605:MET:SD	1:B:672:PHE:HA	2.56	0.45
1:B:450:ILE:HD11	1:B:461:LEU:HD13	1.99	0.45
1:A:270:MET:HG3	1:A:271:LEU:H	1.80	0.45
1:B:215:ILE:HG13	1:B:215:ILE:H	1.62	0.45
1:A:109:GLN:HG3	1:A:110:SER:N	2.31	0.45
1:A:269:LEU:O	1:A:272:ASP:HB2	2.16	0.45
1:A:412:VAL:HG22	1:A:448:VAL:HG11	1.99	0.45
1:B:200:PRO:HG2	1:B:203:HIS:NE2	2.32	0.45
1:B:225:LEU:HG	1:B:226:MET:N	2.31	0.45
1:A:194:ILE:HG13	2:A:2006:HOH:O	2.17	0.45
1:A:616:MET:CE	1:A:620:MET:HE1	2.45	0.45
1:B:85:HIS:CD2	1:B:88:LEU:HG	2.51	0.45
1:A:338:GLY:HA2	1:A:351:ARG:HH12	1.82	0.45
1:A:633:MET:CG	1:A:634:GLU:N	2.79	0.45
1:B:88:LEU:CD1	1:B:91:GLU:HB3	2.47	0.45
1:B:164:LEU:HB3	1:B:176:ILE:HG13	1.99	0.45
1:B:242:GLU:O	1:B:243:ALA:C	2.58	0.45
1:B:545:LEU:O	1:B:549:MET:HG3	2.17	0.45
1:B:597:ASP:O	1:B:597:ASP:OD1	2.35	0.45
1:A:19:ILE:C	1:A:21:ALA:N	2.72	0.44
1:B:234:GLU:C	1:B:235:ILE:HD13	2.42	0.44
1:A:463:ASP:O	1:A:467:LYS:NZ	2.45	0.44
1:B:162:ILE:HG13	1:B:163:GLN:HG3	1.99	0.44
1:A:19:ILE:HD13	1:A:24:THR:H	1.83	0.44
1:A:291:ARG:HD2	1:A:297:GLU:OE1	2.18	0.44
1:A:633:MET:SD	1:A:640:GLN:HG3	2.57	0.44
1:A:132:VAL:HB	1:A:256:VAL:HG13	1.99	0.44
1:B:341:VAL:HG23	1:B:350:GLU:HB2	2.00	0.44
1:A:18:HIS:ND1	1:A:18:HIS:C	2.75	0.44
1:B:88:LEU:HD12	1:B:88:LEU:C	2.40	0.44
1:B:287:ILE:HD12	1:B:398:LEU:HD22	2.00	0.44
1:A:325:LEU:HD12	1:A:325:LEU:HA	1.89	0.44
1:A:605:MET:HA	1:A:671:TYR:O	2.17	0.44
1:B:19:ILE:HG22	1:B:19:ILE:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:411:SER:HA	1:B:449:ILE:CD1	2.48	0.44
1:B:463:ASP:OD1	1:B:463:ASP:C	2.59	0.44
1:A:177:ASP:OD2	1:A:180:GLU:HB2	2.17	0.44
1:A:493:GLN:HB2	1:A:510:HIS:CE1	2.53	0.44
1:B:89:THR:O	1:B:93:GLU:HB3	2.18	0.44
1:B:209:GLU:HA	1:B:212:ALA:HB3	2.00	0.44
1:B:616:MET:HG2	1:B:620:MET:HE2	1.99	0.44
1:A:298:GLU:OE1	1:A:298:GLU:HA	2.18	0.44
1:A:354:ARG:HB3	1:A:365:GLU:OE2	2.18	0.44
1:B:34:THR:CB	1:B:70:ALA:HB1	2.47	0.43
1:B:266:GLY:C	1:B:268:GLN:OE1	2.61	0.43
1:B:291:ARG:HD3	1:B:395:ASP:OD2	2.17	0.43
1:B:418:ALA:O	1:B:422:LYS:HG3	2.18	0.43
1:B:419:ASP:OD2	1:B:472:GLU:HG3	2.18	0.43
1:B:485:THR:HG22	1:B:601:LEU:HD11	1.99	0.43
1:A:415:LYS:NZ	1:A:474:ASN:OD1	2.50	0.43
1:A:381:LYS:HG3	1:A:382:ASP:H	1.82	0.43
1:B:136:LYS:CB	1:B:139:LYS:HZ3	2.30	0.43
1:B:69:THR:HG22	1:B:76:ARG:NH1	2.33	0.43
1:B:292:ALA:H	1:B:395:ASP:HB2	1.83	0.43
1:B:339:SER:O	1:B:352:VAL:HG13	2.18	0.43
1:B:354:ARG:HB2	1:B:378:VAL:HG11	1.99	0.43
1:B:668:TYR:CD1	1:B:668:TYR:C	2.96	0.43
1:A:135:ASN:HD21	1:A:261:ALA:HB2	1.82	0.43
1:B:616:MET:O	1:B:619:ILE:N	2.44	0.43
1:A:292:ALA:HB2	1:A:397:ILE:HD11	2.00	0.43
1:A:633:MET:HG2	1:B:633:MET:HB3	2.01	0.43
1:B:547:ASP:OD1	1:B:547:ASP:N	2.51	0.43
1:A:668:TYR:CD1	1:A:668:TYR:C	2.96	0.43
1:B:541:VAL:HG13	1:B:585:ALA:HB2	2.01	0.43
1:A:5:PHE:CD2	1:A:76:ARG:HB2	2.53	0.43
1:A:496:PHE:CZ	1:A:583:ILE:HD12	2.54	0.43
1:B:579:MET:HE2	1:B:579:MET:HB3	1.86	0.43
1:A:441:THR:O	1:A:441:THR:HG22	2.18	0.43
1:B:88:LEU:HD13	1:B:91:GLU:CB	2.48	0.43
1:A:421:ASP:O	1:A:424:THR:OG1	2.35	0.42
1:A:602:GLU:CD	1:A:627:ARG:HH22	2.26	0.42
1:A:622:ASP:CG	1:A:626:ARG:HH21	2.27	0.42
1:B:113:GLU:O	1:B:114:PRO:C	2.62	0.42
1:B:174:ALA:HB2	1:B:185:LYS:HA	2.00	0.42
1:B:356:LEU:HD23	1:B:365:GLU:HA	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:689:LYS:HE2	1:B:689:LYS:HB3	1.85	0.42
1:A:317:MET:HE2	1:A:317:MET:HB2	1.74	0.42
1:A:458:LEU:O	1:A:462:VAL:HG12	2.20	0.42
1:B:24:THR:O	1:B:28:GLU:CD	2.62	0.42
1:A:415:LYS:HB2	1:A:472:GLU:OE1	2.19	0.42
1:A:522:PHE:CD2	1:A:549:MET:HE1	2.54	0.42
1:B:3:ARG:HB3	1:B:370:TYR:CE1	2.54	0.42
1:B:338:GLY:H	1:B:352:VAL:HG22	1.84	0.42
1:B:410:LEU:HD23	1:B:478:PRO:HA	2.01	0.42
1:B:622:ASP:O	1:B:626:ARG:HG3	2.20	0.42
1:A:399:GLU:HG2	1:A:400:SER:N	2.35	0.42
1:B:270:MET:HG3	1:B:271:LEU:N	2.34	0.42
1:B:442:ASP:OD1	1:B:447:GLN:O	2.37	0.42
1:A:354:ARG:H	1:A:354:ARG:HG3	1.35	0.42
1:A:510:HIS:HB3	1:A:567:TYR:CE1	2.54	0.42
1:A:529:VAL:HG23	1:A:530:GLY:H	1.84	0.42
1:A:436:THR:HG21	1:A:453:MET:SD	2.60	0.42
1:A:89:THR:HG22	1:A:93:GLU:OE2	2.20	0.42
1:B:31:LEU:HD22	1:B:68:THR:HG21	2.01	0.42
1:B:678:VAL:HG13	1:B:679:PRO:HD2	2.00	0.42
1:A:117:GLU:HG3	1:A:155:LEU:HD11	2.02	0.42
1:A:157:ALA:HB1	1:A:254:TYR:CD2	2.54	0.42
1:A:536:GLU:HG3	1:A:537:TYR:CD1	2.55	0.42
1:A:616:MET:HE2	1:A:620:MET:CE	2.47	0.42
1:B:622:ASP:OD2	1:B:654:TYR:HE1	2.02	0.42
1:A:346:LYS:O	1:A:348:LYS:HG3	2.20	0.41
1:A:112:VAL:CG1	1:A:150:THR:HB	2.46	0.41
1:B:267:VAL:C	1:B:268:GLN:OE1	2.58	0.41
1:A:188:ASN:ND2	1:A:192:THR:OG1	2.53	0.41
1:A:199:ILE:H	1:A:199:ILE:HG13	1.52	0.41
1:B:16:MET:HE2	1:B:104:THR:HG23	2.01	0.41
1:B:646:VAL:HG13	1:B:647:PRO:HD2	2.02	0.41
1:A:493:GLN:HB2	1:A:510:HIS:ND1	2.35	0.41
1:B:83:PRO:CG	1:B:88:LEU:HD11	2.50	0.41
1:B:88:LEU:CD1	1:B:92:VAL:H	2.32	0.41
1:B:466:LYS:O	1:B:470:ASN:HA	2.20	0.41
1:A:160:ALA:HA	1:A:161:PRO:HD3	1.97	0.41
1:A:358:MET:CE	1:A:363:ARG:HH11	2.32	0.41
1:B:144:PHE:CD2	1:B:165:PRO:HG3	2.55	0.41
1:B:203:HIS:C	1:B:205:ASP:N	2.78	0.41
1:B:304:ASP:OD1	1:B:306:SER:N	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:413:GLU:OE1	1:B:474:ASN:ND2	2.53	0.41
1:B:319:ASP:CB	1:B:322:VAL:HG22	2.48	0.41
1:B:510:HIS:C	1:B:511:ILE:HG13	2.46	0.41
1:A:269:LEU:HD13	1:A:269:LEU:HA	1.80	0.41
1:A:484:GLU:OE2	1:A:555:ALA:N	2.49	0.41
1:A:546:LYS:HG3	1:A:547:ASP:N	2.36	0.41
1:B:345:THR:OG1	1:B:388:THR:N	2.46	0.41
1:A:381:LYS:HE3	1:A:382:ASP:OD2	2.21	0.41
1:B:616:MET:HE3	1:B:616:MET:HB2	1.81	0.41
1:A:203:HIS:HA	1:A:206:ARG:HD3	2.03	0.41
1:A:304:ASP:O	1:A:333:GLY:N	2.50	0.41
1:A:338:GLY:HA2	1:A:351:ARG:NH1	2.35	0.41
1:B:29:ARG:HE	1:B:29:ARG:HA	1.86	0.41
1:B:230:LEU:H	1:B:230:LEU:HD12	1.85	0.41
1:B:456:LEU:O	1:B:459:ASP:N	2.54	0.41
1:B:511:ILE:HG23	1:B:565:LYS:O	2.21	0.41
1:A:99:LEU:HD12	1:A:99:LEU:C	2.46	0.41
1:A:413:GLU:HA	1:A:414:PRO:HD2	1.79	0.41
1:B:218:VAL:C	1:B:220:GLU:N	2.78	0.41
1:A:120:TRP:HZ2	1:A:254:TYR:CE2	2.38	0.40
1:B:434:ASP:HA	1:B:435:PRO:HD2	1.91	0.40
1:A:335:MET:HG3	1:A:336:THR:N	2.36	0.40
1:B:547:ASP:CG	1:B:548:ALA:H	2.24	0.40
1:B:686:ILE:HG22	1:B:690:ASN:ND2	2.36	0.40
1:A:260:THR:HG23	1:A:263:LYS:HB2	2.04	0.40
1:A:426:ALA:O	1:A:430:LEU:HG	2.22	0.40
1:A:528:ILE:HG13	1:A:533:VAL:HB	2.03	0.40
1:B:213:SER:O	1:B:216:GLU:OE1	2.39	0.40
1:B:218:VAL:C	1:B:220:GLU:H	2.29	0.40
1:B:635:PRO:HA	1:B:640:GLN:OE1	2.21	0.40
1:A:171:GLU:O	1:A:172:PHE:C	2.65	0.40
1:A:300:ILE:CG2	1:A:302:LYS:HG2	2.51	0.40
1:B:178:LEU:HD11	1:B:210:ALA:HB1	2.03	0.40
1:B:533:VAL:O	1:B:534:PRO:C	2.63	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:169:GLU:OE2	1:A:340:TYR:OH[1_455]	2.18	0.02

5.3 Torsion angles

5.3.1 Protein backbone

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	639/693 (92%)	592 (93%)	46 (7%)	1 (0%)	43	66
1	B	639/693 (92%)	583 (91%)	53 (8%)	3 (0%)	24	49
All	All	1278/1386 (92%)	1175 (92%)	99 (8%)	4 (0%)	36	59

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	691	LYS
1	B	394	ASN
1	B	251	VAL
1	A	251	VAL

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 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	543/579 (94%)	498 (92%)	45 (8%)	10	27
1	B	543/579 (94%)	491 (90%)	52 (10%)	8	22
All	All	1086/1158 (94%)	989 (91%)	97 (9%)	9	24

All (97) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	HIS
1	A	34	THR

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Mol	Chain	Res	Type
1	A	96	LEU
1	A	109	GLN
1	A	113	GLU
1	A	118	THR
1	A	130	ARG
1	A	150	THR
1	A	173	GLU
1	A	194	ILE
1	A	199	ILE
1	A	201	GLU
1	A	202	ASP
1	A	204	LEU
1	A	213	SER
1	A	215	ILE
1	A	234	GLU
1	A	251	VAL
1	A	256	VAL
1	A	268	GLN
1	A	269	LEU
1	A	288	ILE
1	A	298	GLU
1	A	302	LYS
1	A	317	MET
1	A	329	ARG
1	A	336	THR
1	A	354	ARG
1	A	361	ASN
1	A	369	VAL
1	A	378	VAL
1	A	396	ILE
1	A	408	ILE
1	A	412	VAL
1	A	416	SER
1	A	529	VAL
1	A	532	VAL
1	A	559	LEU
1	A	577	SER
1	A	579	MET
1	A	611	MET
1	A	631	ASP
1	A	633	MET
1	A	667	THR

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Mol	Chain	Res	Type
1	A	690	ASN
1	B	8	GLU
1	B	20	ASP
1	B	28	GLU
1	B	29	ARG
1	B	86	VAL
1	B	87	ASP
1	B	92	VAL
1	B	112	VAL
1	B	116	THR
1	B	130	ARG
1	B	176	ILE
1	B	187	THR
1	B	192	THR
1	B	195	GLU
1	B	203	HIS
1	B	208	GLU
1	B	215	ILE
1	B	220	GLU
1	B	225	LEU
1	B	233	GLU
1	B	235	ILE
1	B	242	GLU
1	B	249	THR
1	B	268	GLN
1	B	274	VAL
1	B	293	SER
1	B	294	ASN
1	B	305	ASP
1	B	306	SER
1	B	325	LEU
1	B	332	SER
1	B	348	LYS
1	B	352	VAL
1	B	361	ASN
1	B	363	ARG
1	B	380	LEU
1	B	393	LYS
1	B	395	ASP
1	B	453	MET
1	B	463	ASP
1	B	475	VAL

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Mol	Chain	Res	Type
1	B	487	LYS
1	B	492	VAL
1	B	528	ILE
1	B	574	VAL
1	B	579	MET
1	B	611	MET
1	B	624	THR
1	B	630	VAL
1	B	649	SER
1	B	662	THR
1	B	684	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	163	GLN
1	A	526	ASN
1	A	661	ASN
1	B	75	HIS
1	B	78	ASN
1	B	357	GLN
1	B	425	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	649/693 (93%)	-0.11	5 (0%) 82 78	41, 81, 128, 172	0
1	B	649/693 (93%)	0.10	8 (1%) 76 71	43, 97, 157, 227	0
All	All	1298/1386 (93%)	-0.00	13 (1%) 79 74	41, 89, 145, 227	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	641	VAL	4.2
1	B	18	HIS	2.8
1	A	284	VAL	2.7
1	B	142	ALA	2.6
1	A	2	ALA	2.6
1	A	384	GLY	2.1
1	B	642	VAL	2.1
1	B	160	ALA	2.1
1	A	506	TYR	2.1
1	B	251	VAL	2.0
1	A	18	HIS	2.0
1	B	404	PRO	2.0
1	B	7	LEU	2.0

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 oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.