



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 27, 2014 – 12:21 AM GMT

PDB ID : 2NUB
Title : Structure of Aquifex aeolicus Argonuate
Authors : Rashid, U.J.; Paterok, D.; Koglin, A.; Gohlke, H.; Piehler, J.; Chen, J.C.-H.
Deposited on : 2006-11-09
Resolution : 3.20 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

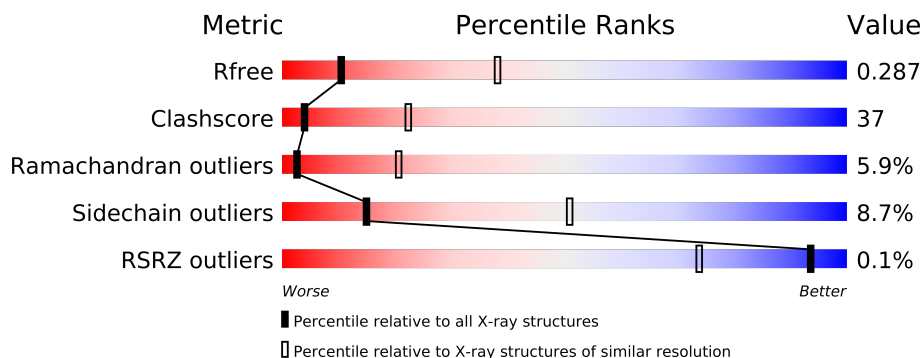
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 3.20 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}	66092	1824 (3.30-3.10)
Clashscore	79885	1078 (3.26-3.14)
Ramachandran outliers	78287	1059 (3.26-3.14)
Sidechain outliers	78261	1058 (3.26-3.14)
RSRZ outliers	66119	1825 (3.30-3.10)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	706	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5814 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Argonaute.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	690	Total	C	N	O	S	0	0	0
			5734	3743	971	1008	12			

- Molecule 2 is water.

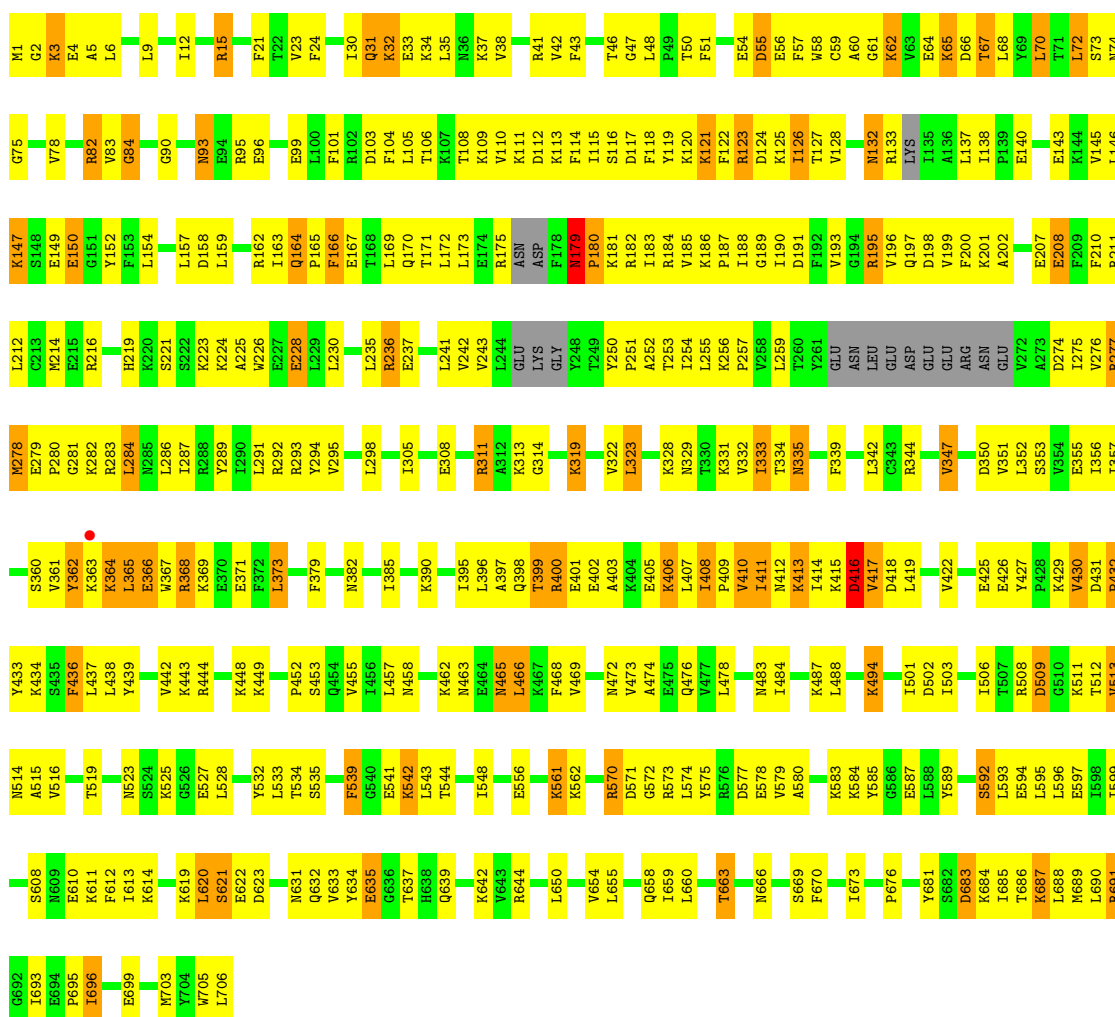
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	80	Total	O	0	0
			80	80		

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 errors 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: Argonaute

Chain A: 



4 Data and refinement statistics

Property	Value	Source
Space group	I 4 2 2	Depositor
Cell constants a, b, c, α , β , γ	125.00Å 125.00Å 253.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	72.50 – 3.20 72.50 – 2.80	Depositor EDS
% Data completeness (in resolution range)	100.0 (72.50-3.20) 97.6 (72.50-2.80)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	0.14	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.39 (at 2.82Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.234 , 0.311 0.218 , 0.287	Depositor DCC
R_{free} test set	1675 reflections (9.83%)	DCC
Wilson B-factor (Å ²)	77.2	Xtriage
Anisotropy	0.087	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 52.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 24598 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	5814	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.71% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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	0.45	0/5844	0.69	1/7840 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	417	VAL	N-CA-C	-6.57	93.27	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5734	0	6017	440	0
2	A	80	0	0	1	0
All	All	5814	0	6017	440	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 37.

All (440) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:277:ARG:H	1:A:277:ARG:HD3	1.11	1.08

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:596:LEU:HD11	1:A:655:LEU:HD13	1.37	1.03
1:A:512:THR:HG22	1:A:513:VAL:H	1.25	0.99
1:A:30:ILE:HB	1:A:35:LEU:HD11	1.45	0.98
1:A:313:LYS:HE3	1:A:619:LYS:HB2	1.45	0.96
1:A:12:ILE:HG13	1:A:305:ILE:HG12	1.51	0.92
1:A:123:ARG:HA	1:A:126:ILE:HD12	1.50	0.91
1:A:179:ASN:HB3	1:A:180:PRO:HA	1.52	0.89
1:A:166:PHE:HD2	1:A:166:PHE:H	1.19	0.88
1:A:32:LYS:HA	1:A:35:LEU:HD12	1.56	0.88
1:A:31:GLN:H	1:A:34:LYS:NZ	1.71	0.87
1:A:159:LEU:HD22	1:A:287:ILE:HG22	1.57	0.87
1:A:93:ASN:ND2	1:A:96:GLU:H	1.72	0.86
1:A:167:GLU:OE1	1:A:171:THR:HB	1.75	0.86
1:A:31:GLN:HB3	1:A:34:LYS:HG2	1.57	0.85
1:A:159:LEU:HD11	1:A:286:LEU:HD23	1.58	0.84
1:A:179:ASN:HB3	1:A:180:PRO:CA	2.08	0.84
1:A:291:LEU:HD11	1:A:305:ILE:HG21	1.60	0.83
1:A:108:THR:HG22	1:A:110:VAL:H	1.42	0.83
1:A:38:VAL:HG13	1:A:70:LEU:HD11	1.60	0.83
1:A:187:PRO:HB2	1:A:190:ILE:HB	1.61	0.82
1:A:356:ILE:HD13	1:A:373:LEU:HD21	1.62	0.81
1:A:93:ASN:HD21	1:A:96:GLU:H	1.29	0.81
1:A:476:GLN:HE21	1:A:476:GLN:HA	1.46	0.80
1:A:291:LEU:O	1:A:295:VAL:HG23	1.83	0.79
1:A:333:ILE:HD11	1:A:339:PHE:HA	1.64	0.78
1:A:138:ILE:HG21	1:A:162:ARG:HH21	1.48	0.78
1:A:6:LEU:HD11	1:A:311:ARG:HH21	1.50	0.77
1:A:277:ARG:HD3	1:A:277:ARG:N	1.95	0.77
1:A:364:LYS:N	1:A:364:LYS:HE3	2.00	0.77
1:A:95:ARG:O	1:A:99:GLU:HG3	1.85	0.77
1:A:512:THR:HG22	1:A:513:VAL:N	1.99	0.76
1:A:659:ILE:HG23	1:A:676:PRO:HG3	1.64	0.76
1:A:361:VAL:HG13	1:A:425:GLU:HG2	1.65	0.76
1:A:276:VAL:HG22	1:A:278:MET:H	1.50	0.75
1:A:367:TRP:O	1:A:371:GLU:HG2	1.86	0.75
1:A:476:GLN:NE2	1:A:476:GLN:HA	2.02	0.75
1:A:166:PHE:HD2	1:A:166:PHE:N	1.85	0.75
1:A:399:THR:HG23	1:A:400:ARG:H	1.52	0.75
1:A:181:LYS:O	1:A:196:VAL:HB	1.87	0.74
1:A:411:ILE:HA	1:A:449:LYS:HE2	1.69	0.74
1:A:277:ARG:CD	1:A:277:ARG:H	1.93	0.74
1:A:406:LYS:CB	1:A:406:LYS:HZ2	2.01	0.74

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:364:LYS:H	1:A:364:LYS:HE3	1.53	0.73
1:A:259:LEU:HD21	1:A:433:TYR:HA	1.70	0.73
1:A:31:GLN:HB3	1:A:34:LYS:CG	2.17	0.73
1:A:494:LYS:O	1:A:494:LYS:HD2	1.87	0.73
1:A:38:VAL:O	1:A:42:VAL:HG23	1.90	0.72
1:A:226:TRP:CZ3	1:A:251:PRO:HG3	2.25	0.71
1:A:180:PRO:HB2	1:A:183:ILE:HD12	1.71	0.71
1:A:23:VAL:CG2	1:A:56:GLU:HB3	2.21	0.71
1:A:431:ASP:OD2	1:A:434:LYS:HE2	1.91	0.71
1:A:659:ILE:HG23	1:A:676:PRO:CG	2.21	0.70
1:A:31:GLN:H	1:A:34:LYS:HZ3	1.39	0.70
1:A:165:PRO:C	1:A:167:GLU:H	1.95	0.70
1:A:138:ILE:HG21	1:A:162:ARG:NH2	2.07	0.69
1:A:610:GLU:O	1:A:611:LYS:HB2	1.93	0.69
1:A:122:PHE:C	1:A:124:ASP:H	1.95	0.69
1:A:24:PHE:CE2	1:A:82:ARG:HB2	2.27	0.69
1:A:280:PRO:HA	1:A:283:ARG:HB2	1.76	0.68
1:A:1:MET:SD	1:A:314:GLY:HA2	2.33	0.68
1:A:580:ALA:O	1:A:584:LYS:HB2	1.93	0.68
1:A:291:LEU:HD11	1:A:305:ILE:CG2	2.24	0.67
1:A:170:GLN:HG2	1:A:253:THR:HG22	1.76	0.67
1:A:333:ILE:HD11	1:A:339:PHE:CA	2.25	0.67
1:A:211:ARG:HH11	1:A:230:LEU:HD21	1.58	0.67
1:A:173:LEU:HD13	1:A:199:VAL:HG11	1.76	0.67
1:A:462:LYS:C	1:A:463:ASN:HD22	1.98	0.67
1:A:284:LEU:O	1:A:287:ILE:HG12	1.94	0.67
1:A:398:GLN:HA	1:A:427:TYR:HE2	1.59	0.67
1:A:93:ASN:HD22	1:A:93:ASN:C	1.96	0.67
1:A:210:PHE:O	1:A:214:MET:HB2	1.94	0.66
1:A:147:LYS:HB3	1:A:621:SER:HB3	1.76	0.66
1:A:42:VAL:O	1:A:46:THR:HB	1.96	0.66
1:A:46:THR:CG2	1:A:48:LEU:HB2	2.25	0.66
1:A:356:ILE:HD11	1:A:373:LEU:HD11	1.77	0.66
1:A:399:THR:HG23	1:A:401:GLU:H	1.61	0.66
1:A:347:VAL:HB	1:A:385:ILE:HD11	1.77	0.66
1:A:411:ILE:HG22	1:A:449:LYS:HZ3	1.61	0.66
1:A:333:ILE:CD1	1:A:339:PHE:HA	2.26	0.65
1:A:573:ARG:HH12	1:A:644:ARG:HD3	1.61	0.65
1:A:1:MET:HG2	1:A:2:GLY:H	1.60	0.65
1:A:62:LYS:CE	1:A:62:LYS:H	2.09	0.65
1:A:512:THR:CG2	1:A:513:VAL:H	2.04	0.65
1:A:190:ILE:N	1:A:190:ILE:HD12	2.12	0.64

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:279:GLU:HB2	1:A:280:PRO:HD2	1.78	0.64
1:A:408:ILE:HD12	1:A:408:ILE:N	2.13	0.64
1:A:64:GLU:O	1:A:65:LYS:HG3	1.97	0.64
1:A:690:LEU:C	1:A:691:ARG:HD2	2.17	0.64
1:A:62:LYS:HE2	1:A:62:LYS:O	1.98	0.63
1:A:108:THR:CG2	1:A:110:VAL:HB	2.29	0.63
1:A:584:LYS:HD2	1:A:585:TYR:CD1	2.34	0.62
1:A:313:LYS:CE	1:A:619:LYS:HB2	2.26	0.62
1:A:23:VAL:HG23	1:A:58:TRP:CD1	2.35	0.62
1:A:406:LYS:HZ2	1:A:406:LYS:HB3	1.63	0.62
1:A:24:PHE:CE2	1:A:68:LEU:HG	2.34	0.62
1:A:368:ARG:HH11	1:A:368:ARG:HG3	1.64	0.62
1:A:46:THR:HG22	1:A:48:LEU:HB2	1.81	0.62
1:A:34:LYS:O	1:A:37:LYS:HB2	1.99	0.62
1:A:120:LYS:HE2	1:A:121:LYS:HG2	1.81	0.62
1:A:398:GLN:O	1:A:398:GLN:HG3	1.99	0.62
1:A:202:ALA:HB2	1:A:241:LEU:HG	1.82	0.62
1:A:211:ARG:NH1	1:A:230:LEU:HD21	2.14	0.61
1:A:397:ALA:HB1	1:A:402:GLU:OE2	1.99	0.61
1:A:574:LEU:HB2	1:A:597:GLU:HG2	1.82	0.61
1:A:542:LYS:O	1:A:542:LYS:HG2	1.99	0.61
1:A:395:ILE:HD11	1:A:409:PRO:HG2	1.82	0.61
1:A:65:LYS:C	1:A:67:THR:H	2.04	0.61
1:A:502:ASP:OD1	1:A:686:THR:HG21	2.00	0.61
1:A:408:ILE:HB	1:A:409:PRO:HD3	1.81	0.61
1:A:501:ILE:HD12	1:A:501:ILE:O	2.01	0.61
1:A:523:ASN:ND2	1:A:527:GLU:HB2	2.16	0.61
1:A:406:LYS:C	1:A:408:ILE:H	2.04	0.61
1:A:508:ARG:O	1:A:509:ASP:HB2	2.01	0.61
1:A:83:VAL:HG12	1:A:84:GLY:H	1.66	0.61
1:A:140:GLU:OE2	1:A:162:ARG:HB2	2.01	0.60
1:A:574:LEU:N	1:A:597:GLU:OE2	2.32	0.60
1:A:687:LYS:NZ	1:A:687:LYS:HB2	2.15	0.60
1:A:65:LYS:O	1:A:67:THR:N	2.34	0.60
1:A:595:LEU:O	1:A:596:LEU:HD12	2.02	0.60
1:A:333:ILE:HD11	1:A:339:PHE:N	2.16	0.60
1:A:323:LEU:O	1:A:323:LEU:HD12	2.02	0.60
1:A:352:LEU:HA	1:A:418:ASP:OD1	2.00	0.60
1:A:6:LEU:HD11	1:A:311:ARG:NH2	2.15	0.60
1:A:132:ASN:O	1:A:133:ARG:HB2	2.02	0.60
1:A:250:TYR:HB3	1:A:254:ILE:HD11	1.84	0.60
1:A:31:GLN:HB3	1:A:34:LYS:CD	2.32	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:621:SER:O	1:A:623:ASP:N	2.35	0.59
1:A:31:GLN:H	1:A:34:LYS:HZ2	1.51	0.59
1:A:199:VAL:HG22	1:A:242:VAL:HG22	1.85	0.59
1:A:93:ASN:HD21	1:A:96:GLU:HG3	1.66	0.59
1:A:418:ASP:O	1:A:452:PRO:HG2	2.03	0.59
1:A:54:GLU:HG3	1:A:55:ASP:OD1	2.03	0.58
1:A:506:ILE:HG13	1:A:690:LEU:HD22	1.84	0.58
1:A:198:ASP:O	1:A:243:VAL:HG22	2.02	0.58
1:A:401:GLU:O	1:A:405:GLU:N	2.35	0.58
1:A:614:LYS:NZ	1:A:663:THR:HG21	2.19	0.58
1:A:412:ASN:CG	1:A:413:LYS:H	2.02	0.58
1:A:21:PHE:HD2	1:A:58:TRP:HB3	1.67	0.58
1:A:32:LYS:HA	1:A:35:LEU:CD1	2.31	0.58
1:A:104:PHE:O	1:A:108:THR:HB	2.03	0.57
1:A:30:ILE:HG13	1:A:30:ILE:O	2.04	0.57
1:A:438:LEU:O	1:A:442:VAL:HG23	2.05	0.57
1:A:398:GLN:HA	1:A:427:TYR:CE2	2.39	0.57
1:A:523:ASN:OD1	1:A:525:LYS:N	2.36	0.57
1:A:406:LYS:HA	1:A:409:PRO:HD2	1.85	0.57
1:A:503:ILE:HD12	1:A:578:GLU:OE2	2.04	0.57
1:A:365:LEU:O	1:A:365:LEU:HD13	2.05	0.57
1:A:200:PHE:CE1	1:A:241:LEU:HB2	2.40	0.57
1:A:117:ASP:HA	1:A:120:LYS:CG	2.34	0.57
1:A:439:TYR:CD1	1:A:455:VAL:HG11	2.40	0.57
1:A:118:PHE:O	1:A:122:PHE:HB2	2.05	0.56
1:A:476:GLN:CA	1:A:476:GLN:HE21	2.09	0.56
1:A:333:ILE:O	1:A:333:ILE:CG1	2.52	0.56
1:A:23:VAL:HG21	1:A:56:GLU:HB3	1.87	0.56
1:A:654:VAL:O	1:A:658:GLN:HG3	2.05	0.56
1:A:279:GLU:CB	1:A:280:PRO:HD2	2.35	0.56
1:A:83:VAL:HG12	1:A:84:GLY:N	2.21	0.56
1:A:31:GLN:O	1:A:33:GLU:N	2.39	0.56
1:A:122:PHE:C	1:A:124:ASP:N	2.59	0.56
1:A:570:ARG:HG3	1:A:574:LEU:HG	1.86	0.56
1:A:361:VAL:O	1:A:364:LYS:HG3	2.05	0.56
1:A:360:SER:HB3	1:A:364:LYS:HD3	1.88	0.56
1:A:426:GLU:OE2	1:A:457:LEU:HD13	2.06	0.56
1:A:119:TYR:O	1:A:123:ARG:HB3	2.06	0.56
1:A:400:ARG:HA	1:A:402:GLU:OE1	2.05	0.55
1:A:73:SER:C	1:A:75:GLY:H	2.08	0.55
1:A:506:ILE:HD11	1:A:690:LEU:HD22	1.88	0.55
1:A:119:TYR:O	1:A:123:ARG:N	2.39	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:407:LEU:O	1:A:411:ILE:HG12	2.07	0.55
1:A:184:ARG:HE	1:A:193:VAL:HG11	1.71	0.55
1:A:429:LYS:O	1:A:430:VAL:HG23	2.06	0.55
1:A:82:ARG:O	1:A:82:ARG:HD3	2.07	0.55
1:A:463:ASN:N	1:A:463:ASN:HD22	2.03	0.55
1:A:705:TRP:O	1:A:706:LEU:C	2.43	0.55
1:A:400:ARG:HH11	1:A:400:ARG:HG2	1.71	0.54
1:A:328:LYS:HE3	1:A:342:LEU:HB3	1.90	0.54
1:A:277:ARG:HB2	2:A:733:HOH:O	2.07	0.54
1:A:506:ILE:CD1	1:A:690:LEU:HD22	2.36	0.54
1:A:506:ILE:CG1	1:A:690:LEU:HD22	2.37	0.54
1:A:443:LYS:NZ	1:A:453:SER:O	2.41	0.54
1:A:431:ASP:HB3	1:A:434:LYS:O	2.07	0.54
1:A:30:ILE:C	1:A:32:LYS:H	2.09	0.54
1:A:633:VAL:O	1:A:633:VAL:HG12	2.07	0.54
1:A:429:LYS:O	1:A:430:VAL:CB	2.56	0.54
1:A:533:LEU:HD21	1:A:689:MET:HG3	1.89	0.54
1:A:511:LYS:HG2	1:A:541:GLU:HG2	1.90	0.54
1:A:166:PHE:CD2	1:A:166:PHE:N	2.56	0.53
1:A:411:ILE:HG22	1:A:449:LYS:NZ	2.23	0.53
1:A:579:VAL:O	1:A:583:LYS:HG3	2.08	0.53
1:A:406:LYS:HZ2	1:A:406:LYS:HB2	1.73	0.53
1:A:402:GLU:O	1:A:406:LYS:N	2.41	0.53
1:A:574:LEU:HB2	1:A:597:GLU:CG	2.39	0.53
1:A:195:ARG:HH11	1:A:195:ARG:HG3	1.73	0.53
1:A:515:ALA:HB3	1:A:543:LEU:HD11	1.89	0.53
1:A:31:GLN:HB3	1:A:34:LYS:HD3	1.91	0.53
1:A:333:ILE:O	1:A:333:ILE:HG12	2.08	0.53
1:A:660:LEU:O	1:A:663:THR:HB	2.08	0.53
1:A:666:ASN:ND2	1:A:673:ILE:HG21	2.23	0.53
1:A:105:LEU:HD13	1:A:111:LYS:HD2	1.89	0.53
1:A:406:LYS:C	1:A:408:ILE:N	2.60	0.53
1:A:690:LEU:O	1:A:691:ARG:HD2	2.08	0.53
1:A:350:ASP:OD1	1:A:351:VAL:HG23	2.09	0.53
1:A:473:VAL:O	1:A:476:GLN:N	2.42	0.53
1:A:686:THR:CG2	1:A:687:LYS:N	2.72	0.53
1:A:123:ARG:CA	1:A:126:ILE:HD12	2.32	0.53
1:A:408:ILE:O	1:A:412:ASN:HB2	2.09	0.52
1:A:332:VAL:O	1:A:334:THR:HG23	2.08	0.52
1:A:46:THR:HG22	1:A:48:LEU:H	1.74	0.52
1:A:544:THR:HG23	1:A:548:ILE:HD13	1.91	0.52
1:A:410:VAL:C	1:A:412:ASN:H	2.12	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:478:LEU:HB3	1:A:483:ASN:O	2.10	0.52
1:A:283:ARG:O	1:A:287:ILE:HG23	2.09	0.52
1:A:403:ALA:HB2	1:A:436:PHE:CZ	2.45	0.52
1:A:62:LYS:H	1:A:62:LYS:CD	2.22	0.52
1:A:128:VAL:CG2	1:A:275:ILE:HG13	2.40	0.52
1:A:93:ASN:ND2	1:A:96:GLU:HG3	2.24	0.52
1:A:114:PHE:HA	1:A:293:ARG:NH1	2.24	0.52
1:A:501:ILE:C	1:A:501:ILE:HD12	2.30	0.52
1:A:610:GLU:HB3	1:A:613:ILE:HG23	1.92	0.52
1:A:686:THR:HG23	1:A:687:LYS:N	2.24	0.52
1:A:73:SER:C	1:A:75:GLY:N	2.63	0.52
1:A:407:LEU:C	1:A:408:ILE:HD12	2.31	0.51
1:A:399:THR:CG2	1:A:400:ARG:H	2.17	0.51
1:A:164:GLN:HB3	1:A:257:PRO:O	2.10	0.51
1:A:280:PRO:O	1:A:281:GLY:C	2.47	0.51
1:A:93:ASN:ND2	1:A:93:ASN:C	2.64	0.51
1:A:46:THR:HG22	1:A:48:LEU:N	2.26	0.51
1:A:399:THR:HG23	1:A:400:ARG:N	2.22	0.51
1:A:126:ILE:O	1:A:137:LEU:HB2	2.10	0.51
1:A:187:PRO:CB	1:A:190:ILE:HD13	2.40	0.51
1:A:398:GLN:CG	1:A:398:GLN:O	2.59	0.51
1:A:429:LYS:O	1:A:430:VAL:HB	2.11	0.51
1:A:120:LYS:HG3	1:A:121:LYS:H	1.75	0.51
1:A:145:VAL:C	1:A:146:LEU:HD23	2.30	0.51
1:A:202:ALA:HA	1:A:241:LEU:HD12	1.92	0.51
1:A:444:ARG:O	1:A:448:LYS:HG3	2.11	0.51
1:A:159:LEU:HD22	1:A:287:ILE:CG2	2.37	0.51
1:A:167:GLU:CD	1:A:171:THR:HB	2.30	0.51
1:A:369:LYS:HE2	1:A:458:ASN:OD1	2.11	0.51
1:A:108:THR:HG22	1:A:110:VAL:HB	1.92	0.50
1:A:501:ILE:HG22	1:A:519:THR:HG23	1.93	0.50
1:A:110:VAL:HG13	1:A:111:LYS:N	2.26	0.50
1:A:364:LYS:H	1:A:364:LYS:CE	2.23	0.50
1:A:187:PRO:HA	1:A:255:LEU:HD23	1.93	0.50
1:A:511:LYS:CG	1:A:541:GLU:HG2	2.40	0.50
1:A:412:ASN:O	1:A:414:ILE:N	2.44	0.50
1:A:532:TYR:HD1	1:A:699:GLU:HB3	1.75	0.50
1:A:259:LEU:CD2	1:A:433:TYR:HA	2.41	0.50
1:A:93:ASN:HD21	1:A:96:GLU:N	2.03	0.50
1:A:132:ASN:O	1:A:133:ARG:CB	2.60	0.50
1:A:41:ARG:HD2	1:A:72:LEU:HA	1.93	0.50
1:A:400:ARG:NH1	1:A:400:ARG:HG2	2.27	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:24:PHE:HE2	1:A:68:LEU:HG	1.75	0.50
1:A:528:LEU:HD22	1:A:703:MET:HG3	1.92	0.49
1:A:126:ILE:CD1	1:A:127:THR:HG23	2.42	0.49
1:A:189:GLY:C	1:A:190:ILE:HD12	2.32	0.49
1:A:62:LYS:HE2	1:A:62:LYS:H	1.76	0.49
1:A:187:PRO:HB2	1:A:190:ILE:HD13	1.94	0.49
1:A:683:ASP:HA	1:A:686:THR:HG22	1.94	0.49
1:A:689:MET:HB3	1:A:696:ILE:HD11	1.95	0.49
1:A:5:ALA:CB	1:A:608:SER:HB2	2.42	0.49
1:A:278:MET:HB2	1:A:282:LYS:NZ	2.28	0.49
1:A:403:ALA:HB2	1:A:436:PHE:HZ	1.78	0.49
1:A:463:ASN:N	1:A:463:ASN:ND2	2.61	0.49
1:A:12:ILE:HD11	1:A:101:PHE:CE2	2.47	0.49
1:A:137:LEU:HD12	1:A:163:ILE:HG13	1.95	0.49
1:A:173:LEU:CD1	1:A:199:VAL:HG11	2.41	0.49
1:A:355:GLU:CD	1:A:414:ILE:HD13	2.33	0.48
1:A:610:GLU:HB3	1:A:613:ILE:CG2	2.43	0.48
1:A:693:ILE:O	1:A:695:PRO:HD3	2.13	0.48
1:A:681:TYR:CE2	1:A:684:LYS:HD3	2.48	0.48
1:A:111:LYS:HG2	1:A:294:TYR:OH	2.13	0.48
1:A:157:LEU:HD12	1:A:158:ASP:N	2.28	0.48
1:A:187:PRO:HA	1:A:254:ILE:O	2.13	0.48
1:A:329:ASN:OD1	1:A:331:LYS:HB3	2.13	0.48
1:A:599:ILE:N	1:A:599:ILE:HD12	2.29	0.48
1:A:276:VAL:HG13	1:A:278:MET:HG2	1.94	0.48
1:A:106:THR:O	1:A:109:LYS:HD2	2.13	0.48
1:A:612:PHE:HA	1:A:631:ASN:OD1	2.14	0.48
1:A:114:PHE:HD2	1:A:115:ILE:HD12	1.78	0.48
1:A:430:VAL:O	1:A:432:PRO:HD3	2.13	0.48
1:A:183:ILE:O	1:A:185:VAL:HG13	2.14	0.48
1:A:58:TRP:N	1:A:58:TRP:CD1	2.82	0.48
1:A:408:ILE:O	1:A:409:PRO:C	2.52	0.47
1:A:3:LYS:O	1:A:3:LYS:HG2	2.14	0.47
1:A:319:LYS:HD2	1:A:319:LYS:N	2.30	0.47
1:A:539:PHE:C	1:A:539:PHE:CD2	2.86	0.47
1:A:362:TYR:O	1:A:364:LYS:HE2	2.15	0.47
1:A:30:ILE:HG22	1:A:35:LEU:HD21	1.95	0.47
1:A:406:LYS:CA	1:A:409:PRO:HD2	2.43	0.47
1:A:122:PHE:O	1:A:124:ASP:N	2.47	0.47
1:A:400:ARG:HA	1:A:400:ARG:HD3	1.43	0.47
1:A:506:ILE:HG12	1:A:690:LEU:HD13	1.96	0.47
1:A:637:THR:HG23	1:A:637:THR:O	2.15	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:162:ARG:C	1:A:163:ILE:HD12	2.35	0.47
1:A:659:ILE:CG2	1:A:676:PRO:HG3	2.41	0.47
1:A:313:LYS:CE	1:A:619:LYS:H	2.27	0.47
1:A:397:ALA:HB3	1:A:402:GLU:HG3	1.96	0.47
1:A:117:ASP:OD1	1:A:120:LYS:HD3	2.14	0.47
1:A:31:GLN:CB	1:A:34:LYS:HD3	2.45	0.46
1:A:687:LYS:HB2	1:A:687:LYS:HZ2	1.79	0.46
1:A:614:LYS:HZ2	1:A:663:THR:HG21	1.79	0.46
1:A:368:ARG:NH1	1:A:368:ARG:HG3	2.30	0.46
1:A:225:ALA:O	1:A:228:GLU:HB2	2.15	0.46
1:A:669:SER:O	1:A:670:PHE:CD1	2.68	0.46
1:A:15:ARG:HE	1:A:15:ARG:HB2	1.35	0.46
1:A:360:SER:OG	1:A:369:LYS:NZ	2.49	0.46
1:A:408:ILE:N	1:A:408:ILE:CD1	2.78	0.46
1:A:200:PHE:HE2	1:A:243:VAL:HG13	1.81	0.46
1:A:685:ILE:HD11	1:A:705:TRP:HB3	1.97	0.46
1:A:511:LYS:HD3	1:A:541:GLU:HG2	1.96	0.46
1:A:179:ASN:OD1	1:A:434:LYS:HD3	2.15	0.46
1:A:397:ALA:HB1	1:A:401:GLU:HG2	1.97	0.46
1:A:684:LYS:O	1:A:688:LEU:HB2	2.16	0.46
1:A:599:ILE:HB	1:A:642:LYS:HB3	1.97	0.46
1:A:466:LEU:O	1:A:466:LEU:HG	2.15	0.46
1:A:592:SER:O	1:A:593:LEU:HD12	2.15	0.46
1:A:402:GLU:O	1:A:406:LYS:HB2	2.16	0.46
1:A:406:LYS:O	1:A:408:ILE:N	2.49	0.45
1:A:230:LEU:O	1:A:236:ARG:NH2	2.49	0.45
1:A:683:ASP:O	1:A:687:LYS:CB	2.65	0.45
1:A:357:ILE:HB	1:A:422:VAL:HG22	1.98	0.45
1:A:406:LYS:NZ	1:A:406:LYS:HB2	2.30	0.45
1:A:43:PHE:O	1:A:47:GLY:N	2.46	0.45
1:A:9:LEU:HD13	1:A:154:LEU:HD13	1.99	0.45
1:A:465:ASN:O	1:A:469:VAL:HG23	2.15	0.45
1:A:59:CYS:O	1:A:61:GLY:N	2.45	0.45
1:A:46:THR:HG22	1:A:48:LEU:CB	2.45	0.45
1:A:429:LYS:O	1:A:430:VAL:CG2	2.65	0.45
1:A:561:LYS:O	1:A:562:LYS:C	2.55	0.45
1:A:64:GLU:HA	1:A:82:ARG:HH12	1.82	0.45
1:A:683:ASP:O	1:A:687:LYS:HB2	2.17	0.45
1:A:410:VAL:O	1:A:412:ASN:N	2.50	0.45
1:A:1:MET:HG2	1:A:2:GLY:N	2.30	0.45
1:A:419:LEU:HD12	1:A:452:PRO:O	2.16	0.45
1:A:639:GLN:O	1:A:639:GLN:HG3	2.17	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:159:LEU:O	1:A:283:ARG:NH1	2.50	0.45
1:A:344:ARG:HA	1:A:344:ARG:HD3	1.83	0.45
1:A:356:ILE:CD1	1:A:373:LEU:HD11	2.46	0.45
1:A:396:LEU:O	1:A:397:ALA:HB2	2.17	0.45
1:A:408:ILE:O	1:A:412:ASN:CB	2.65	0.45
1:A:411:ILE:HB	1:A:449:LYS:HZ1	1.82	0.45
1:A:62:LYS:HE2	1:A:62:LYS:N	2.32	0.45
1:A:403:ALA:CB	1:A:436:PHE:HZ	2.30	0.44
1:A:149:GLU:CD	1:A:619:LYS:HD3	2.38	0.44
1:A:104:PHE:HB3	1:A:298:LEU:CD2	2.47	0.44
1:A:162:ARG:NH1	1:A:186:LYS:NZ	2.66	0.44
1:A:277:ARG:HH11	1:A:277:ARG:HG3	1.81	0.44
1:A:108:THR:O	1:A:109:LYS:HB2	2.18	0.44
1:A:293:ARG:O	1:A:294:TYR:C	2.55	0.44
1:A:179:ASN:HB3	1:A:180:PRO:C	2.38	0.44
1:A:403:ALA:O	1:A:407:LEU:HB2	2.18	0.44
1:A:406:LYS:NZ	1:A:438:LEU:HD22	2.32	0.44
1:A:577:ASP:OD1	1:A:577:ASP:N	2.44	0.44
1:A:235:LEU:O	1:A:237:GLU:N	2.50	0.44
1:A:172:LEU:CD2	1:A:175:ARG:HH11	2.30	0.44
1:A:556:GLU:OE2	1:A:589:TYR:HE2	2.00	0.44
1:A:473:VAL:O	1:A:474:ALA:C	2.56	0.44
1:A:170:GLN:HB2	1:A:252:ALA:C	2.38	0.44
1:A:3:LYS:HD2	1:A:610:GLU:HA	1.99	0.43
1:A:113:LYS:O	1:A:116:SER:HB3	2.17	0.43
1:A:126:ILE:HB	1:A:137:LEU:HB3	2.01	0.43
1:A:282:LYS:O	1:A:286:LEU:N	2.49	0.43
1:A:104:PHE:HB3	1:A:298:LEU:HD21	2.00	0.43
1:A:632:GLN:HG3	1:A:632:GLN:O	2.19	0.43
1:A:484:ILE:HG13	1:A:484:ILE:O	2.17	0.43
1:A:123:ARG:HA	1:A:126:ILE:HG23	2.00	0.43
1:A:105:LEU:HD11	1:A:143:GLU:HG2	1.99	0.43
1:A:468:PHE:O	1:A:472:ASN:HB2	2.18	0.43
1:A:313:LYS:HE2	1:A:619:LYS:H	1.83	0.43
1:A:163:ILE:HD12	1:A:163:ILE:N	2.34	0.43
1:A:169:LEU:HD21	1:A:242:VAL:HG21	1.99	0.43
1:A:332:VAL:O	1:A:334:THR:N	2.51	0.43
1:A:594:GLU:OE1	1:A:650:LEU:HG	2.18	0.43
1:A:216:ARG:NH1	1:A:509:ASP:OD2	2.52	0.43
1:A:184:ARG:HE	1:A:193:VAL:CG1	2.31	0.43
1:A:150:GLU:HG3	1:A:152:TYR:HE2	1.83	0.43
1:A:683:ASP:CA	1:A:686:THR:HG22	2.48	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:274:ASP:O	1:A:275:ILE:HD13	2.18	0.43
1:A:179:ASN:CB	1:A:180:PRO:CA	2.88	0.43
1:A:406:LYS:C	1:A:409:PRO:HD2	2.39	0.43
1:A:415:LYS:O	1:A:416:ASP:O	2.37	0.43
1:A:111:LYS:O	1:A:115:ILE:HD13	2.18	0.43
1:A:523:ASN:OD1	1:A:523:ASN:C	2.58	0.42
1:A:511:LYS:CD	1:A:541:GLU:HG2	2.49	0.42
1:A:322:VAL:HG12	1:A:488:LEU:HD23	2.00	0.42
1:A:353:SER:HB2	1:A:390:LYS:HD3	2.01	0.42
1:A:50:THR:HG22	1:A:51:PHE:N	2.34	0.42
1:A:70:LEU:HG	1:A:78:VAL:HG13	2.02	0.42
1:A:145:VAL:O	1:A:146:LEU:HD23	2.19	0.42
1:A:620:LEU:HD12	1:A:620:LEU:HA	1.76	0.42
1:A:379:PHE:HE2	1:A:474:ALA:CB	2.32	0.42
1:A:23:VAL:HA	1:A:57:PHE:O	2.20	0.42
1:A:120:LYS:CE	1:A:121:LYS:HE3	2.50	0.42
1:A:200:PHE:HD1	1:A:201:LYS:O	2.03	0.42
1:A:83:VAL:O	1:A:84:GLY:O	2.38	0.42
1:A:30:ILE:O	1:A:32:LYS:HG3	2.19	0.42
1:A:120:LYS:C	1:A:122:PHE:H	2.22	0.42
1:A:487:LYS:HE2	1:A:525:LYS:CB	2.50	0.42
1:A:32:LYS:O	1:A:35:LEU:HB2	2.20	0.42
1:A:108:THR:HG22	1:A:110:VAL:N	2.22	0.42
1:A:190:ILE:HG13	1:A:219:HIS:CG	2.55	0.41
1:A:65:LYS:C	1:A:67:THR:N	2.72	0.41
1:A:570:ARG:HH21	1:A:578:GLU:CD	2.22	0.41
1:A:501:ILE:CG2	1:A:519:THR:HG23	2.50	0.41
1:A:523:ASN:HD21	1:A:527:GLU:HB2	1.83	0.41
1:A:167:GLU:O	1:A:256:LYS:HG2	2.21	0.41
1:A:105:LEU:HD13	1:A:111:LYS:CD	2.49	0.41
1:A:197:GLN:HB2	1:A:243:VAL:O	2.19	0.41
1:A:683:ASP:HA	1:A:686:THR:CG2	2.51	0.41
1:A:335:ASN:C	1:A:335:ASN:ND2	2.73	0.41
1:A:103:ASP:O	1:A:106:THR:N	2.45	0.41
1:A:169:LEU:CD2	1:A:242:VAL:HG21	2.51	0.41
1:A:487:LYS:HD2	1:A:527:GLU:HG3	2.01	0.41
1:A:128:VAL:HG21	1:A:275:ILE:HG13	2.02	0.41
1:A:366:GLU:OE2	1:A:366:GLU:N	2.52	0.41
1:A:544:THR:O	1:A:548:ILE:HD13	2.21	0.41
1:A:224:LYS:O	1:A:228:GLU:HG2	2.20	0.41
1:A:399:THR:OG1	1:A:400:ARG:N	2.51	0.41
1:A:532:TYR:CE2	1:A:534:THR:HG21	2.56	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:37:LYS:HD3	1:A:37:LYS:HA	1.99	0.41
1:A:226:TRP:CE3	1:A:226:TRP:HA	2.56	0.41
1:A:207:GLU:HG3	1:A:208:GLU:N	2.35	0.41
1:A:412:ASN:CG	1:A:413:LYS:N	2.71	0.41
1:A:413:LYS:HG2	1:A:413:LYS:O	2.19	0.41
1:A:195:ARG:CG	1:A:195:ARG:HH11	2.33	0.41
1:A:575:TYR:CD1	1:A:575:TYR:N	2.89	0.41
1:A:30:ILE:C	1:A:32:LYS:N	2.74	0.40
1:A:208:GLU:HG2	1:A:208:GLU:H	1.36	0.40
1:A:516:VAL:HG22	1:A:535:SER:HB3	2.03	0.40
1:A:180:PRO:O	1:A:183:ILE:HG13	2.21	0.40
1:A:38:VAL:HG22	1:A:72:LEU:HD21	2.03	0.40
1:A:487:LYS:HE2	1:A:525:LYS:HB3	2.02	0.40
1:A:353:SER:CB	1:A:390:LYS:HD3	2.51	0.40
1:A:190:ILE:HG22	1:A:191:ASP:N	2.37	0.40
1:A:289:TYR:O	1:A:292:ARG:N	2.54	0.40
1:A:74:ASN:OD1	1:A:74:ASN:O	2.39	0.40
1:A:413:LYS:O	1:A:415:LYS:N	2.54	0.40
1:A:584:LYS:O	1:A:587:GLU:HB3	2.20	0.40

There are no symmetry-related clashes.

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	680/706 (96%)	526 (77%)	114 (17%)	40 (6%)	2 20

All (40) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	32	LYS
1	A	132	ASN
1	A	399	THR
1	A	416	ASP

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Mol	Chain	Res	Type
1	A	430	VAL
1	A	513	VAL
1	A	571	ASP
1	A	621	SER
1	A	622	GLU
1	A	4	GLU
1	A	65	LYS
1	A	66	ASP
1	A	67	THR
1	A	72	LEU
1	A	84	GLY
1	A	90	GLY
1	A	121	LYS
1	A	125	LYS
1	A	182	ARG
1	A	188	ILE
1	A	212	LEU
1	A	236	ARG
1	A	278	MET
1	A	410	VAL
1	A	411	ILE
1	A	413	LYS
1	A	572	GLY
1	A	179	ASN
1	A	31	GLN
1	A	223	LYS
1	A	60	ALA
1	A	123	ARG
1	A	150	GLU
1	A	221	SER
1	A	228	GLU
1	A	362	TYR
1	A	408	ILE
1	A	432	PRO
1	A	635	GLU
1	A	180	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 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	631/647 (98%)	576 (91%)	55 (9%)	15 51

All (55) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LYS
1	A	15	ARG
1	A	55	ASP
1	A	62	LYS
1	A	70	LEU
1	A	82	ARG
1	A	93	ASN
1	A	112	ASP
1	A	126	ILE
1	A	147	LYS
1	A	164	GLN
1	A	166	PHE
1	A	179	ASN
1	A	195	ARG
1	A	208	GLU
1	A	277	ARG
1	A	284	LEU
1	A	308	GLU
1	A	311	ARG
1	A	319	LYS
1	A	323	LEU
1	A	333	ILE
1	A	335	ASN
1	A	347	VAL
1	A	363	LYS
1	A	364	LYS
1	A	365	LEU
1	A	366	GLU
1	A	368	ARG
1	A	373	LEU
1	A	382	ASN
1	A	400	ARG
1	A	406	LYS
1	A	416	ASP
1	A	417	VAL
1	A	436	PHE
1	A	437	LEU
1	A	465	ASN

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Mol	Chain	Res	Type
1	A	466	LEU
1	A	494	LYS
1	A	509	ASP
1	A	514	ASN
1	A	539	PHE
1	A	542	LYS
1	A	561	LYS
1	A	570	ARG
1	A	592	SER
1	A	620	LEU
1	A	634	TYR
1	A	635	GLU
1	A	663	THR
1	A	683	ASP
1	A	687	LYS
1	A	691	ARG
1	A	696	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	93	ASN
1	A	98	GLN
1	A	164	GLN
1	A	335	ASN
1	A	382	ASN
1	A	463	ASN
1	A	472	ASN
1	A	476	GLN
1	A	639	GLN
1	A	671	GLN

5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates 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

6.1 Protein, DNA and RNA chains

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	690/706 (97%)	-0.18	1 (0%)	93 74	16, 56, 131, 179	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	363	LYS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.