



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 06:20 AM UTC

PDB ID : 3SLU / pdb_00003slu
Title : Crystal structure of NMB0315
Authors : Shen, Y.; Wang, X.; Yang, X.; Xu, H.
Deposited on : 2011-06-26
Resolution : 2.41 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

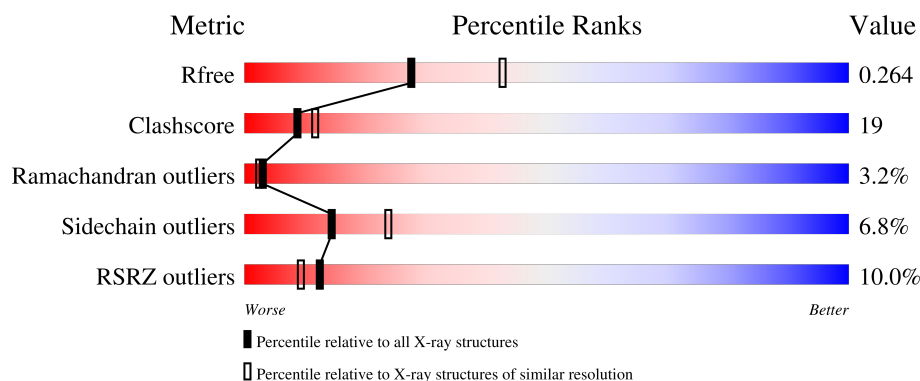
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.41 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	6062 (2.44-2.40)
Clashscore	190562	6562 (2.44-2.40)
Ramachandran outliers	187476	6481 (2.44-2.40)
Sidechain outliers	187428	6482 (2.44-2.40)
RSRZ outliers	180081	6066 (2.44-2.40)

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	371	14% 60% 30% • • 5%
1	B	371	5% 66% 27% • •

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5442 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 M23 peptidase domain protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	351	Total	C	N	O	S	0	0	0
			2646	1663	484	495	4			
1	B	358	Total	C	N	O	S	0	0	0
			2718	1704	501	509	4			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	50	GLY	-	expression tag	UNP E0N688
A	51	PRO	-	expression tag	UNP E0N688
A	52	GLY	-	expression tag	UNP E0N688
A	53	SER	-	expression tag	UNP E0N688
B	50	GLY	-	expression tag	UNP E0N688
B	51	PRO	-	expression tag	UNP E0N688
B	52	GLY	-	expression tag	UNP E0N688
B	53	SER	-	expression tag	UNP E0N688

- Molecule 2 is NICKEL (II) ION (CCD ID: NI) (formula: Ni).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Ni	0	0
			1	1		
2	B	1	Total	Ni	0	0
			1	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	25	Total	O	0	0
			25	25		
3	B	51	Total	O	0	0
			51	51		

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	195.68Å 75.50Å 81.64Å 90.00° 94.66° 90.00°	Depositor
Resolution (Å)	37.75 – 2.41 37.75 – 2.41	Depositor EDS
% Data completeness (in resolution range)	82.7 (37.75-2.41) 82.9 (37.75-2.41)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.68 (at 2.42Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.255 , 0.264 0.255 , 0.264	Depositor DCC
R_{free} test set	1916 reflections (4.14%)	wwPDB-VP
Wilson B-factor (Å ²)	52.6	Xtriage
Anisotropy	0.889	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 53.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	5442	wwPDB-VP
Average B, all atoms (Å ²)	84.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.34% 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

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

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	0.44	0/2698	0.78	0/3651
1	B	0.46	0/2772	0.80	0/3750
All	All	0.45	0/5470	0.79	0/7401

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	2646	0	2572	113	0
1	B	2718	0	2658	92	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	25	0	0	1	0
3	B	51	0	0	1	0
All	All	5442	0	5230	198	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 19.

All (198) 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:276:ARG:HH11	1:B:276:ARG:HB3	1.20	1.05
1:A:349:GLN:HE21	1:A:351:GLN:HG3	1.34	0.93
1:A:383:GLN:HB3	1:A:384:PRO:HD2	1.50	0.91
1:B:276:ARG:HB3	1:B:276:ARG:NH1	1.96	0.80
1:B:173:LEU:HD11	1:B:205:VAL:HG11	1.64	0.79
1:A:319:LYS:HB3	1:A:329:VAL:HG12	1.64	0.77
1:B:146:ARG:HB3	1:B:146:ARG:NH1	1.99	0.77
1:A:383:GLN:HB3	1:A:384:PRO:CD	2.19	0.71
1:B:160:LEU:N	1:B:160:LEU:HD23	2.07	0.70
1:A:349:GLN:NE2	1:A:351:GLN:HG3	2.05	0.68
1:B:68:VAL:HG22	1:B:77:VAL:HG21	1.76	0.68
1:B:105:ARG:HH11	1:B:133:ARG:HD3	1.59	0.67
1:A:67:ALA:HA	1:A:109:SER:HB3	1.77	0.67
1:A:105:ARG:CB	1:A:128:ASP:HB2	2.25	0.67
1:A:319:LYS:CB	1:A:329:VAL:HG12	2.26	0.65
1:B:146:ARG:HB3	1:B:146:ARG:HH11	1.61	0.65
1:A:327:ASN:ND2	1:A:366:THR:HG21	2.12	0.65
1:A:341:TYR:HB3	1:A:374:LEU:HD11	1.78	0.65
1:A:276:ARG:HH11	1:A:276:ARG:HG2	1.60	0.64
1:A:261:LEU:O	1:A:262:GLN:HB3	1.97	0.64
1:A:192:GLY:HA3	1:A:262:GLN:HA	1.80	0.63
1:B:308:VAL:HG12	1:B:360:ILE:HD11	1.80	0.63
1:A:349:GLN:HE21	1:A:351:GLN:CG	2.11	0.63
1:A:105:ARG:O	1:A:108:GLN:HG2	1.99	0.62
1:A:105:ARG:HA	1:A:128:ASP:HB2	1.80	0.62
1:A:285:MET:HE3	1:A:292:TRP:CZ2	2.35	0.61
1:A:235:ARG:NH1	1:B:60:THR:HG23	2.15	0.61
1:A:138:LEU:HD23	1:A:147:ARG:HA	1.82	0.60
1:A:283:TYR:CD2	1:A:294:LEU:HD13	2.36	0.60
1:B:380:ILE:HD11	1:B:390:VAL:HG11	1.82	0.60
1:A:105:ARG:CA	1:A:128:ASP:HB2	2.32	0.60
1:B:194:PHE:HZ	1:B:229:VAL:HG11	1.67	0.60
1:A:260:VAL:HG12	1:A:261:LEU:O	2.02	0.59
1:A:319:LYS:HA	1:A:328:ALA:O	2.02	0.59
1:A:121:ARG:HH11	1:A:121:ARG:HG2	1.68	0.59
1:B:99:ALA:C	1:B:101:LEU:H	2.11	0.59
1:A:144:ILE:HB	1:A:146:ARG:NH1	2.17	0.58
1:B:194:PHE:HB2	1:B:231:LYS:HE3	1.86	0.58
1:B:252:ASN:HA	1:B:388:VAL:CG1	2.34	0.58
1:B:334:ALA:HB1	3:B:460:HOH:O	2.04	0.58
1:A:331:ILE:HB	1:A:339:THR:HG22	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:281:PHE:CE1	1:B:296:THR:HA	2.39	0.57
1:B:401:ASP:O	1:B:403:ALA:N	2.37	0.57
1:B:127:THR:O	1:B:133:ARG:HA	2.05	0.57
1:A:380:ILE:O	1:A:382:GLY:N	2.38	0.57
1:A:340:LEU:C	1:A:340:LEU:HD23	2.31	0.56
1:B:169:ALA:O	1:B:173:LEU:HD13	2.06	0.56
1:B:388:VAL:HG12	1:B:389:SER:N	2.20	0.55
1:A:283:TYR:CE2	1:A:294:LEU:HD13	2.41	0.55
1:A:111:HIS:ND1	1:B:418:ARG:NH2	2.55	0.55
1:B:159:THR:C	1:B:160:LEU:HD23	2.32	0.55
1:B:278:SER:OG	1:B:301:ALA:HB2	2.06	0.55
1:A:162:SER:HB2	1:A:419:LEU:HB3	1.89	0.54
1:A:354:VAL:HB	1:A:358:GLU:OE2	2.07	0.54
1:B:160:LEU:HB3	1:B:419:LEU:HD21	1.90	0.54
1:B:334:ALA:O	1:B:335:ASN:HB3	2.07	0.54
1:A:105:ARG:HG3	1:A:128:ASP:HB2	1.90	0.54
1:A:322:LYS:O	1:A:325:TYR:HB2	2.08	0.54
1:B:94:LYS:HG3	1:B:95:TYR:CD2	2.43	0.53
1:A:372:PRO:O	1:A:373:HIS:HB3	2.07	0.53
1:A:69:GLN:O	1:A:72:ASP:HB2	2.09	0.53
1:A:69:GLN:HB2	1:A:70:PRO:HD2	1.91	0.52
1:B:308:VAL:HG22	1:B:374:LEU:HD22	1.91	0.52
1:A:315:VAL:HG22	1:A:353:ASN:OD1	2.09	0.52
1:A:380:ILE:HD11	1:A:390:VAL:CG1	2.40	0.52
1:B:146:ARG:HH11	1:B:146:ARG:CB	2.22	0.52
1:A:401:ASP:O	1:A:402:LYS:C	2.53	0.52
1:B:276:ARG:HH11	1:B:276:ARG:CB	2.06	0.52
1:A:243:SER:OG	1:A:244:ASP:N	2.43	0.51
1:B:67:ALA:HA	1:B:109:SER:HB3	1.91	0.51
1:A:418:ARG:NH2	1:B:111:HIS:ND1	2.58	0.51
1:B:128:ASP:HA	1:B:133:ARG:HG2	1.93	0.51
1:B:272:LEU:HD23	1:B:272:LEU:N	2.25	0.51
1:B:340:LEU:HB3	1:B:377:GLU:HB3	1.93	0.51
1:B:289:LEU:O	1:B:290:HIS:HB2	2.12	0.50
1:A:278:SER:OG	1:A:299:ASP:HB3	2.12	0.50
1:A:341:TYR:CD2	1:A:341:TYR:N	2.79	0.50
1:A:123:VAL:HG13	1:A:138:LEU:HB2	1.91	0.50
1:A:255:ASP:HB2	1:A:256:GLU:OE2	2.12	0.50
1:A:381:ASN:ND2	3:A:434:HOH:O	2.40	0.50
1:A:115:GLY:HA3	1:A:121:ARG:CZ	2.41	0.50
1:A:78:LEU:HG	1:A:83:MET:SD	2.52	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:141:LYS:O	1:B:143:GLY:N	2.45	0.49
1:A:108:GLN:HG3	1:A:109:SER:N	2.25	0.49
1:B:332:ARG:HG3	1:B:332:ARG:HH11	1.77	0.49
1:A:72:ASP:OD2	1:A:77:VAL:HG22	2.12	0.49
1:A:132:GLU:OE1	1:A:293:ARG:HG3	2.13	0.49
1:A:180:VAL:HA	1:A:183:ARG:NH2	2.28	0.49
1:B:58:VAL:HG13	1:B:58:VAL:O	2.13	0.48
1:B:328:ALA:HA	1:B:341:TYR:O	2.14	0.48
1:B:160:LEU:CB	1:B:419:LEU:HD21	2.43	0.48
1:A:399:GLN:C	1:A:401:ASP:H	2.20	0.48
1:A:420:ARG:HB3	1:B:62:TYR:HE1	1.79	0.48
1:B:298:ILE:CD1	1:B:387:PRO:HG2	2.43	0.48
1:A:358:GLU:H	1:A:358:GLU:CD	2.21	0.48
1:B:205:VAL:O	1:B:205:VAL:HG13	2.14	0.48
1:A:169:ALA:HB2	1:A:199:LEU:HB2	1.96	0.48
1:A:327:ASN:HD22	1:A:366:THR:HG21	1.77	0.48
1:B:102:ARG:HH11	1:B:102:ARG:HB3	1.78	0.48
1:B:327:ASN:HB2	1:B:344:LEU:O	2.14	0.48
1:A:349:GLN:NE2	1:A:351:GLN:CG	2.73	0.47
1:B:94:LYS:HE2	1:B:95:TYR:CZ	2.49	0.47
1:B:285:MET:HB2	1:B:292:TRP:CE2	2.49	0.47
1:A:156:VAL:HG22	1:A:212:LEU:HG	1.95	0.47
1:A:296:THR:HB	1:A:384:PRO:CG	2.43	0.47
1:A:338:GLU:HG3	1:A:379:ARG:HB2	1.96	0.47
1:A:181:GLU:H	1:A:181:GLU:HG3	1.46	0.47
1:A:237:GLN:OE1	1:A:256:GLU:HB3	2.14	0.47
1:A:123:VAL:HG12	1:A:145:TRP:CZ3	2.50	0.47
1:A:144:ILE:HB	1:A:146:ARG:HH12	1.79	0.47
1:A:159:THR:OG1	1:A:211:SER:HB2	2.15	0.47
1:A:105:ARG:CG	1:A:128:ASP:HB2	2.45	0.47
1:A:296:THR:O	1:A:377:GLU:HG3	2.15	0.47
1:B:72:ASP:OD1	1:B:80:ARG:NH2	2.38	0.47
1:A:302:ALA:O	1:A:363:VAL:HG11	2.14	0.47
1:A:285:MET:HE3	1:A:292:TRP:HZ2	1.76	0.47
1:A:332:ARG:C	1:A:334:ALA:H	2.23	0.47
1:A:401:ASP:O	1:A:404:ALA:N	2.47	0.46
1:B:401:ASP:O	1:B:402:LYS:C	2.58	0.46
1:A:235:ARG:HH11	1:B:60:THR:HG23	1.79	0.46
1:B:98:GLU:CB	1:B:101:LEU:HD12	2.46	0.46
1:B:182:ILE:HD13	1:B:221:ALA:HB1	1.98	0.46
1:A:94:LYS:N	1:A:94:LYS:HD3	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:363:VAL:HG12	1:B:364:GLY:N	2.30	0.45
1:A:283:TYR:CE1	1:A:294:LEU:HB2	2.52	0.45
1:A:330:MET:HA	1:A:339:THR:O	2.16	0.45
1:B:154:MET:HE3	1:B:212:LEU:HD23	1.98	0.45
1:A:318:PHE:CG	1:A:319:LYS:N	2.85	0.45
1:A:160:LEU:HB3	1:A:419:LEU:HD21	1.98	0.45
1:A:212:LEU:HD12	1:A:212:LEU:N	2.32	0.45
1:B:283:TYR:CE1	1:B:294:LEU:HB2	2.50	0.45
1:B:102:ARG:HH11	1:B:102:ARG:CB	2.30	0.45
1:B:285:MET:HE3	1:B:290:HIS:HD2	1.81	0.45
1:A:316:ILE:HG12	1:A:331:ILE:HG12	1.97	0.45
1:B:308:VAL:HG12	1:B:360:ILE:CD1	2.46	0.45
1:A:69:GLN:HB2	1:A:70:PRO:CD	2.46	0.45
1:A:160:LEU:HD23	1:A:160:LEU:N	2.31	0.44
1:A:380:ILE:HD11	1:A:390:VAL:HG11	1.99	0.44
1:B:196:LEU:HD23	1:B:196:LEU:HA	1.80	0.44
1:A:333:HIS:O	1:A:334:ALA:HB3	2.17	0.44
1:A:420:ARG:HB3	1:B:62:TYR:CE1	2.51	0.44
1:B:79:ALA:HA	1:B:88:ILE:HD11	1.99	0.44
1:B:102:ARG:NH1	1:B:128:ASP:O	2.50	0.44
1:B:208:ILE:CD1	1:B:416:LEU:HD13	2.47	0.44
1:B:349:GLN:HE21	1:B:349:GLN:HB3	1.62	0.44
1:B:387:PRO:O	1:B:388:VAL:C	2.61	0.44
1:A:157:LEU:HD11	1:B:157:LEU:HD22	2.00	0.44
1:A:276:ARG:HG2	1:A:276:ARG:NH1	2.31	0.44
1:A:331:ILE:HB	1:A:339:THR:CG2	2.46	0.44
1:B:337:VAL:HG12	1:B:338:GLU:N	2.32	0.44
1:A:380:ILE:C	1:A:382:GLY:N	2.76	0.44
1:B:276:ARG:HG2	1:B:277:ILE:N	2.33	0.44
1:A:133:ARG:HD2	1:A:294:LEU:HD23	1.98	0.43
1:B:105:ARG:O	1:B:108:GLN:HG2	2.18	0.43
1:B:181:GLU:H	1:B:181:GLU:HG3	1.65	0.43
1:B:69:GLN:O	1:B:72:ASP:HB2	2.19	0.43
1:B:316:ILE:HD11	1:B:354:VAL:HG11	2.00	0.43
1:B:308:VAL:CG1	1:B:360:ILE:HD11	2.48	0.43
1:A:67:ALA:HA	1:A:109:SER:CB	2.48	0.43
1:A:279:SER:HB3	1:A:299:ASP:HB2	2.00	0.43
1:B:160:LEU:N	1:B:160:LEU:CD2	2.76	0.43
1:A:66:GLU:HA	1:A:66:GLU:OE1	2.19	0.43
1:A:302:ALA:HB3	1:A:363:VAL:HG21	2.01	0.43
1:B:332:ARG:C	1:B:334:ALA:H	2.27	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:206:ARG:HG2	1:B:419:LEU:HB2	2.01	0.42
1:B:322:LYS:O	1:B:325:TYR:HB2	2.19	0.42
1:B:102:ARG:CB	1:B:102:ARG:NH1	2.82	0.42
1:A:84:ALA:O	1:A:88:ILE:HG13	2.18	0.42
1:B:166:LYS:HD2	1:B:175:ARG:NH1	2.34	0.42
1:A:401:ASP:O	1:A:403:ALA:N	2.51	0.42
1:B:256:GLU:H	1:B:256:GLU:CD	2.27	0.42
1:A:281:PHE:CD2	1:A:281:PHE:C	2.97	0.42
1:B:157:LEU:HA	1:B:158:PRO:HD3	1.92	0.42
1:B:99:ALA:C	1:B:101:LEU:N	2.78	0.42
1:B:252:ASN:HA	1:B:388:VAL:HG11	2.01	0.42
1:A:175:ARG:O	1:A:175:ARG:HG3	2.19	0.42
1:B:186:LEU:HD13	1:B:207:LEU:HD21	2.02	0.42
1:A:391:ALA:O	1:A:392:LEU:HG	2.20	0.41
1:A:399:GLN:C	1:A:401:ASP:N	2.76	0.41
1:A:295:HIS:HE1	1:A:299:ASP:CG	2.28	0.41
1:B:94:LYS:HG3	1:B:95:TYR:CE2	2.55	0.41
1:B:363:VAL:CG1	1:B:364:GLY:N	2.84	0.41
1:A:108:GLN:CG	1:A:109:SER:N	2.82	0.41
1:B:141:LYS:HB2	1:B:146:ARG:HE	1.85	0.41
1:A:70:PRO:O	1:A:71:GLY:C	2.64	0.41
1:B:295:HIS:CE1	1:B:299:ASP:CG	2.99	0.41
1:A:278:SER:HG	1:A:299:ASP:HB3	1.85	0.41
1:A:170:ARG:HE	1:A:170:ARG:HB2	1.78	0.41
1:A:279:SER:HA	1:A:280:PRO:HD3	1.86	0.41
1:A:296:THR:HB	1:A:384:PRO:CB	2.51	0.41
1:A:386:ASN:OD1	1:A:388:VAL:HB	2.21	0.41
1:B:255:ASP:OD1	1:B:255:ASP:C	2.64	0.41
1:B:94:LYS:HE2	1:B:95:TYR:CE2	2.56	0.41
1:A:170:ARG:NH1	1:A:184:GLU:OE2	2.54	0.40
1:A:296:THR:HB	1:A:384:PRO:HB3	2.03	0.40
1:A:115:GLY:HA3	1:A:121:ARG:NH2	2.37	0.40
1:B:267:PHE:CD1	1:B:267:PHE:N	2.89	0.40
1:A:313:ASP:HB3	1:A:314:GLY:H	1.75	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	343/371 (92%)	304 (89%)	29 (8%)	10 (3%)	3	3
1	B	354/371 (95%)	323 (91%)	19 (5%)	12 (3%)	3	2
All	All	697/742 (94%)	627 (90%)	48 (7%)	22 (3%)	3	2

All (22) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	313	ASP
1	A	351	GLN
1	A	381	ASN
1	A	402	LYS
1	B	94	LYS
1	B	98	GLU
1	B	130	ASP
1	B	335	ASN
1	B	402	LYS
1	A	348	SER
1	A	349	GLN
1	B	142	GLY
1	B	388	VAL
1	A	333	HIS
1	B	333	HIS
1	B	334	ALA
1	A	167	THR
1	A	389	SER
1	B	100	ASP
1	A	384	PRO
1	B	99	ALA
1	B	143	GLY

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	260/280 (93%)	239 (92%)	21 (8%)	11	17
1	B	269/280 (96%)	254 (94%)	15 (6%)	19	31
All	All	529/560 (94%)	493 (93%)	36 (7%)	14	24

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	94	LYS
1	A	104	LEU
1	A	108	GLN
1	A	110	VAL
1	A	123	VAL
1	A	124	GLN
1	A	132	GLU
1	A	151	GLU
1	A	160	LEU
1	A	163	VAL
1	A	181	GLU
1	A	211	SER
1	A	272	LEU
1	A	288	ILE
1	A	304	GLN
1	A	341	TYR
1	A	351	GLN
1	A	384	PRO
1	A	388	VAL
1	A	416	LEU
1	A	418	ARG
1	B	60	THR
1	B	160	LEU
1	B	163	VAL
1	B	223	ASP
1	B	229	VAL
1	B	242	ARG

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Mol	Chain	Res	Type
1	B	262	GLN
1	B	268	ASN
1	B	276	ARG
1	B	304	GLN
1	B	315	VAL
1	B	388	VAL
1	B	411	LYS
1	B	416	LEU
1	B	418	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	65	GLN
1	A	108	GLN
1	A	217	GLN
1	A	327	ASN
1	A	349	GLN
1	B	69	GLN
1	B	218	GLN
1	B	252	ASN
1	B	262	GLN
1	B	290	HIS
1	B	304	GLN
1	B	327	ASN
1	B	349	GLN
1	B	353	ASN
1	B	381	ASN
1	B	399	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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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

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	351/371 (94%)	1.03	52 (14%) 5 4	39, 88, 122, 135	0
1	B	358/371 (96%)	0.71	19 (5%) 32 28	54, 80, 105, 112	0
All	All	709/742 (95%)	0.87	71 (10%) 12 9	39, 83, 114, 135	0

All (71) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	334	ALA	5.0
1	B	58	VAL	4.9
1	A	102	ARG	4.8
1	A	350	ALA	4.1
1	A	244	ASP	4.0
1	A	245	LYS	4.0
1	A	334	ALA	3.6
1	B	388	VAL	3.5
1	B	251	GLY	3.5
1	B	244	ASP	3.4
1	A	95	TYR	3.2
1	B	62	TYR	3.2
1	A	107	ASP	3.1
1	A	302	ALA	3.1
1	A	106	ALA	3.0
1	B	98	GLU	2.9
1	B	144	ILE	2.9
1	B	245	LYS	2.9
1	A	293	ARG	2.9
1	A	196	LEU	2.9
1	B	106	ALA	2.7
1	A	277	ILE	2.7
1	B	105	ARG	2.7
1	A	132	GLU	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	105	ARG	2.6
1	A	103	HIS	2.6
1	A	384	PRO	2.6
1	A	330	MET	2.6
1	A	389	SER	2.6
1	A	368	ARG	2.5
1	A	380	ILE	2.5
1	A	383	GLN	2.5
1	A	311	SER	2.5
1	A	274	TYR	2.5
1	A	167	THR	2.5
1	A	382	GLY	2.4
1	A	252	ASN	2.4
1	A	378	ALA	2.4
1	A	266	GLY	2.4
1	B	376	TYR	2.4
1	A	312	ALA	2.4
1	B	77	VAL	2.4
1	A	268	ASN	2.4
1	A	170	ARG	2.3
1	A	104	LEU	2.3
1	A	165	VAL	2.3
1	A	303	PRO	2.3
1	A	337	VAL	2.3
1	B	263	GLU	2.3
1	B	262	GLN	2.3
1	A	321	ARG	2.3
1	A	372	PRO	2.3
1	A	400	ALA	2.2
1	A	271	PRO	2.2
1	B	85	ARG	2.2
1	A	288	ILE	2.2
1	B	88	ILE	2.2
1	B	333	HIS	2.2
1	A	318	PHE	2.2
1	A	342	ALA	2.2
1	A	250	GLY	2.2
1	A	57	GLY	2.1
1	A	324	GLY	2.1
1	A	344	LEU	2.1
1	A	360	ILE	2.1
1	A	297	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	325	TYR	2.1
1	A	335	ASN	2.1
1	A	363	VAL	2.0
1	A	357	GLY	2.0
1	B	181	GLU	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](#)

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($\text{\AA}^2$)	Q<0.9
2	NI	A	1	1/1	0.98	0.09	78,78,78,78	0
2	NI	B	2	1/1	0.99	0.11	67,67,67,67	0

6.5 Other polymers [i](#)

There are no such residues in this entry.