Full wwPDB X-ray Structure Validation Report (i)

Aug 6, 2023 – 07:19 AM EDT

PDB ID	:	1JSY
Title	:	Crystal structure of bovine arrestin-2
Authors	:	Milano, S.K.; Pace, H.C.; Kim, Y.M.; Brenner, C.; Benovic, J.L.
Deposited on	:	2001-08-19
Resolution	:	2.90 Å(reported)

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

|		
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.35
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)	:	2.35

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 2.90 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	Percentile Ranks	Value
Rfree		0.236
Clashscore		38
Ramachandran outliers		5.4%
Sidechain outliers		10.2%
RSRZ outliers		3.9%

Worse   *Better*

▮ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution
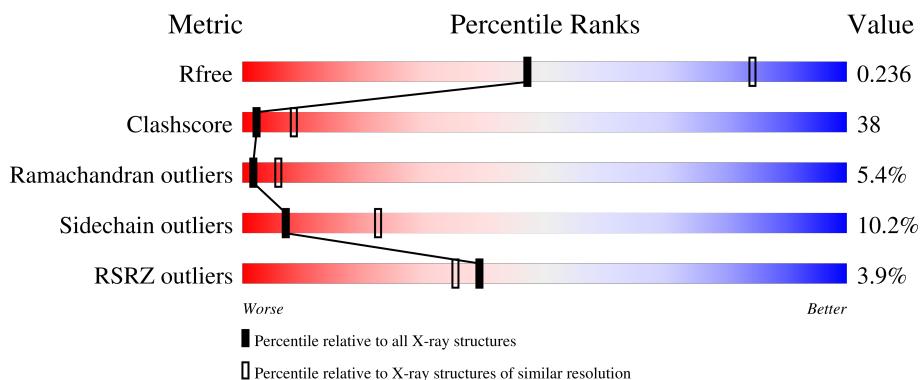
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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 <=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	418	3% — 38% / 40% / 7% · 14%
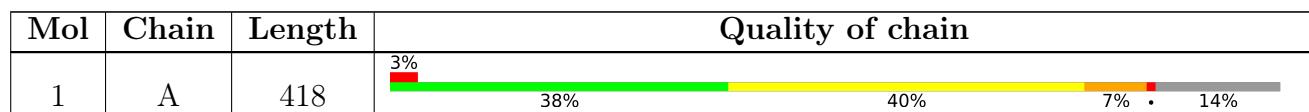
2 Entry composition ⓘ

There are 2 unique types of molecules in this entry. The entry contains 2905 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 Bovine arrestin-2 (full length).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	358	Total 2829	C 1809	N 485	O 524	S 11	0	0	0

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	76	Total 76	O 76	0	0

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: Bovine arrestin-2 (full length)
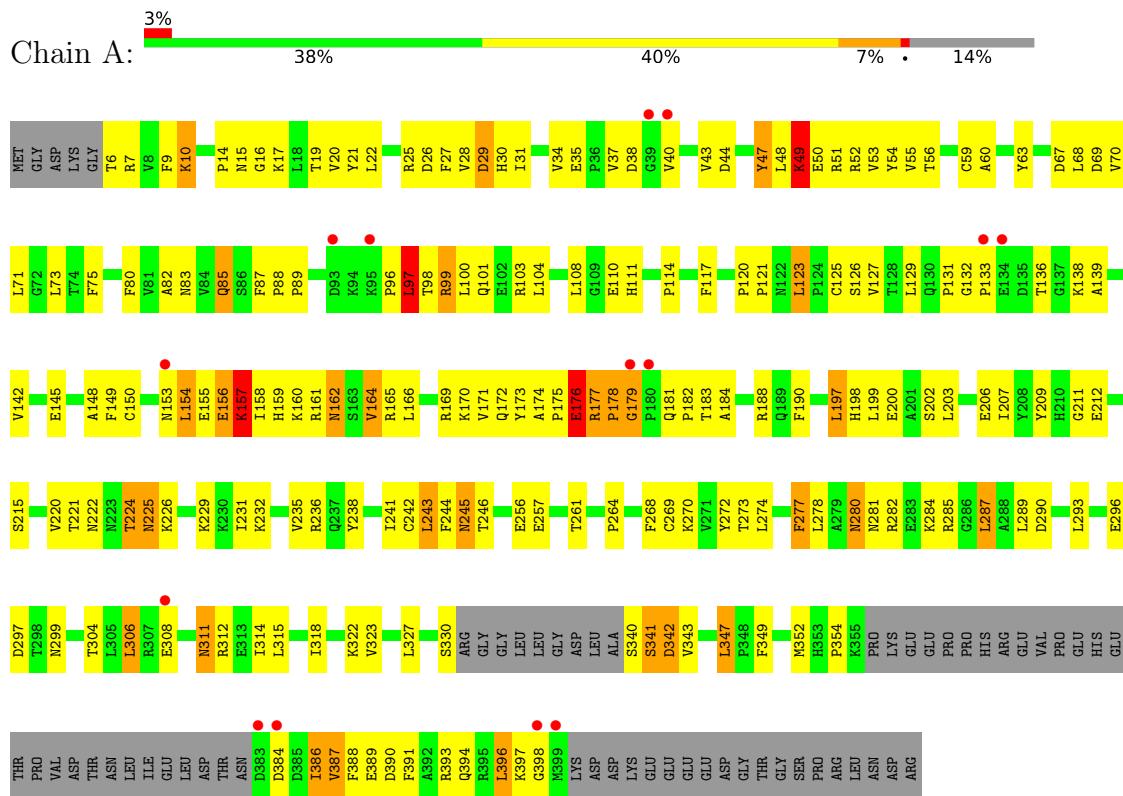
4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α, β, γ	78.95Å 78.95Å 158.92Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.00 – 2.90 19.77 – 2.78	Depositor EDS
% Data completeness (in resolution range)	97.4 (19.00-2.90) 97.9 (19.77-2.78)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	7.40	Depositor
$< I/\sigma(I) >$ [1]	2.97 (at 2.79Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.230 , 0.238 0.230 , 0.236	Depositor DCC
R_{free} test set	1347 reflections (9.11%)	wwPDB-VP
Wilson B-factor (Å^2)	58.6	Xtriage
Anisotropy	0.091	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 41.9	EDS
L-test for twinning [2]	$< |L| > = 0.49, < L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.032 for -h,-k,l	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	2905	wwPDB-VP
Average B, all atoms (Å^2)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.15% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $< |L| >$, $< L^2 >$ 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	0.54	1/2887 (0.0%)	0.73	1/3912 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	269	CYS	CB-SG	-6.79	1.70	1.82

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	157	LYS	CB-CG-CD	-5.23	98.00	111.60

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	2829	0	2866	219	0
2	A	76	0	0	8	0
All	All	2905	0	2866	219	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 38.

All (219) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

W O R L D W I D E
wwPDB
PROTEIN DATA BANK

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:285:ARG:HH22	1:A:293:LEU:HD12	1.16	1.10
1:A:285:ARG:NH2	1:A:293:LEU:HD12	1.66	1.09
1:A:29:ASP:HB2	1:A:34:VAL:HG13	1.42	1.00
1:A:129:LEU:HD13	1:A:241:ILE:HD11	1.45	0.98
1:A:154:LEU:HD22	1:A:154:LEU:H	1.27	0.98
1:A:98:THR:HG22	1:A:101:GLN:HG3	1.44	0.97
1:A:155:GLU:O	1:A:156:GLU:O	1.82	0.96
1:A:177:ARG:HB3	1:A:178:PRO:HD2	1.47	0.96
1:A:280:ASN:H	1:A:280:ASN:HD22	1.15	0.94
1:A:224:THR:CG2	1:A:226:LYS:H	1.80	0.94
1:A:224:THR:HG23	1:A:226:LYS:H	1.35	0.91
1:A:153:ASN:HD22	1:A:155:GLU:HG2	1.39	0.88
1:A:177:ARG:HB3	1:A:178:PRO:CD	2.04	0.87
1:A:285:ARG:NH2	1:A:293:LEU:CD1	2.38	0.86
1:A:153:ASN:ND2	1:A:155:GLU:HG2	1.91	0.85
1:A:87:PHE:HB3	1:A:88:PRO:HD3	1.59	0.83
1:A:96:PRO:O	1:A:97:LEU:HB2	1.82	0.79
1:A:222:ASN:HD21	1:A:224:THR:HB	1.47	0.79
1:A:63:TYR:HE1	1:A:138:LYS:HG2	1.49	0.78
1:A:340:SER:O	1:A:341:SER:O	2.03	0.77
1:A:120:PRO:HG2	1:A:123:LEU:HD22	1.66	0.76
1:A:222:ASN:ND2	1:A:224:THR:HB	2.00	0.76
1:A:63:TYR:CE1	1:A:138:LYS:HG2	2.22	0.75
1:A:176:GLU:HA	1:A:207:ILE:HD12	1.68	0.75
1:A:280:ASN:H	1:A:280:ASN:ND2	1.85	0.74
1:A:104:LEU:O	1:A:108:LEU:HD23	1.87	0.74
1:A:162:ASN:C	1:A:162:ASN:HD22	1.92	0.73
1:A:98:THR:HG22	1:A:101:GLN:CG	2.16	0.73
1:A:178:PRO:HG2	1:A:179:GLY:H	1.54	0.72
1:A:314:ILE:HG23	2:A:445:HOH:O	1.90	0.71
1:A:285:ARG:CZ	1:A:293:LEU:HD12	2.20	0.70
1:A:48:LEU:HB2	1:A:51:ARG:HB3	1.75	0.68
1:A:30:HIS:C	1:A:31:ILE:HD12	2.13	0.68
1:A:59:CYS:HB3	1:A:80:PHE:HB3	1.74	0.68
1:A:27:PHE:CE2	1:A:37:VAL:HA	2.29	0.67
1:A:38:ASP:OD2	1:A:98:THR:HG21	1.95	0.67
1:A:17:LYS:NZ	1:A:47:TYR:HB2	2.11	0.66
1:A:98:THR:CG2	1:A:101:GLN:HG3	2.22	0.66
1:A:197:LEU:HD13	1:A:343:VAL:HG21	1.77	0.66
1:A:182:PRO:HA	2:A:444:HOH:O	1.96	0.65
1:A:285:ARG:CZ	1:A:293:LEU:CD1	2.74	0.65
1:A:280:ASN:ND2	1:A:280:ASN:N	2.43	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:229:LYS:CD	1:A:330:SER:HB2	2.28	0.64
1:A:87:PHE:O	1:A:89:PRO:HD3	1.98	0.64
1:A:44:ASP:O	1:A:48:LEU:HD23	1.98	0.64
1:A:235:VAL:HG23	1:A:274:LEU:HD12	1.81	0.62
1:A:245:ASN:C	1:A:245:ASN:HD22	2.03	0.62
1:A:226:LYS:O	1:A:264:PRO:HG3	2.01	0.61
1:A:220:VAL:HB	1:A:268:PHE:HB3	1.82	0.61
1:A:40:VAL:HG12	1:A:114:PRO:HA	1.83	0.61
1:A:17:LYS:HE3	1:A:47:TYR:CD1	2.36	0.60
1:A:178:PRO:O	1:A:179:GLY:O	2.20	0.60
1:A:242:CYS:HA	1:A:246:THR:HG22	1.84	0.60
1:A:224:THR:HG22	1:A:226:LYS:H	1.65	0.60
1:A:15:ASN:O	1:A:17:LYS:N	2.35	0.59
1:A:43:VAL:HG12	1:A:44:ASP:N	2.17	0.59
1:A:56:THR:HA	1:A:82:ALA:O	2.02	0.59
1:A:154:LEU:HD22	1:A:154:LEU:N	2.08	0.59
1:A:53:VAL:HB	1:A:87:PHE:HB2	1.84	0.58
1:A:131:PRO:HG2	1:A:138:LYS:C	2.22	0.58
1:A:25:ARG:HB3	1:A:391:PHE:CE1	2.38	0.58
1:A:188:ARG:HH22	1:A:341:SER:CB	2.16	0.58
1:A:222:ASN:HD21	1:A:224:THR:CB	2.17	0.58
1:A:25:ARG:NH1	1:A:391:PHE:O	2.37	0.57
1:A:177:ARG:HB2	2:A:434:HOH:O	2.03	0.57
1:A:87:PHE:O	1:A:89:PRO:CD	2.53	0.57
1:A:188:ARG:HH22	1:A:341:SER:HB2	1.70	0.56
1:A:280:ASN:HD22	1:A:280:ASN:N	1.91	0.56
1:A:6:THR:O	1:A:386:ILE:O	2.24	0.56
1:A:224:THR:HG23	1:A:225:ASN:N	2.21	0.56
1:A:393:ARG:HG2	1:A:393:ARG:HH11	1.70	0.56
1:A:155:GLU:O	1:A:156:GLU:C	2.42	0.55
1:A:53:VAL:HB	1:A:87:PHE:CB	2.37	0.55
1:A:28:VAL:O	1:A:35:GLU:HG3	2.06	0.55
1:A:49:LYS:NZ	1:A:49:LYS:HA	2.21	0.55
1:A:85:GLN:OE1	1:A:88:PRO:HB2	2.07	0.55
1:A:15:ASN:ND2	1:A:17:LYS:HB2	2.21	0.55
1:A:125:CYS:HB3	1:A:170:LYS:O	2.06	0.55
1:A:306:LEU:HD23	1:A:306:LEU:N	2.22	0.55
1:A:149:PHE:CD2	1:A:158:ILE:HG12	2.42	0.54
1:A:277:PHE:HB3	1:A:280:ASN:ND2	2.22	0.54
1:A:56:THR:HG22	1:A:83:ASN:HA	1.90	0.54
1:A:211:GLY:HA2	1:A:277:PHE:CE2	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:60:ALA:HB3	1:A:68:LEU:HD21	1.90	0.53
1:A:132:GLY:HA2	1:A:285:ARG:CB	2.38	0.53
1:A:171:VAL:HA	2:A:449:HOH:O	2.09	0.53
1:A:98:THR:HG23	1:A:100:LEU:N	2.24	0.53
1:A:131:PRO:HD3	1:A:139:ALA:HA	1.91	0.52
1:A:211:GLY:HA2	1:A:277:PHE:CZ	2.43	0.52
1:A:231:ILE:HG12	1:A:327:LEU:HD23	1.91	0.52
1:A:178:PRO:HG2	1:A:179:GLY:N	2.24	0.52
1:A:281:ASN:ND2	1:A:284:LYS:NZ	2.57	0.52
1:A:145:GLU:HG3	1:A:165:ARG:HE	1.74	0.52
1:A:224:THR:CG2	1:A:225:ASN:N	2.73	0.52
1:A:245:ASN:C	1:A:245:ASN:ND2	2.60	0.52
1:A:154:LEU:H	1:A:154:LEU:CD2	2.06	0.51
1:A:225:ASN:HD22	1:A:225:ASN:H	1.58	0.51
1:A:20:VAL:HG23	1:A:164:VAL:HG21	1.91	0.51
1:A:162:ASN:C	1:A:162:ASN:ND2	2.63	0.51
1:A:229:LYS:HD2	1:A:330:SER:HB2	1.91	0.51
1:A:14:PRO:HG2	1:A:160:LYS:O	2.11	0.51
1:A:224:THR:CG2	1:A:226:LYS:N	2.63	0.51
1:A:273:THR:C	1:A:274:LEU:HD23	2.32	0.50
1:A:136:THR:HG22	2:A:466:HOH:O	2.12	0.50
1:A:343:VAL:HG13	2:A:437:HOH:O	2.10	0.50
1:A:235:VAL:HG22	1:A:323:VAL:HG22	1.94	0.50
1:A:174:ALA:HB2	1:A:352:MET:SD	2.51	0.50
1:A:287:LEU:HD12	1:A:287:LEU:O	2.11	0.50
1:A:297:ASP:OD2	1:A:393:ARG:NH1	2.45	0.50
1:A:278:LEU:HD22	1:A:289:LEU:HD22	1.93	0.50
1:A:98:THR:HG23	1:A:99:ARG:N	2.26	0.49
1:A:311:ASN:C	1:A:311:ASN:HD22	2.15	0.49
1:A:232:LYS:NZ	1:A:232:LYS:HB3	2.26	0.49
1:A:129:LEU:O	1:A:131:PRO:HD3	2.12	0.49
1:A:311:ASN:HD22	1:A:312:ARG:N	2.10	0.49
1:A:284:LYS:O	1:A:285:ARG:HD3	2.13	0.49
1:A:15:ASN:HD22	1:A:17:LYS:CG	2.26	0.49
1:A:236:ARG:HG3	1:A:236:ARG:NH1	2.26	0.49
1:A:103:ARG:NH2	1:A:384:ASP:CB	2.76	0.49
1:A:327:LEU:O	1:A:342:ASP:HB3	2.13	0.49
1:A:323:VAL:HG23	1:A:349:PHE:CE1	2.49	0.48
1:A:236:ARG:HG3	1:A:236:ARG:HH11	1.79	0.48
1:A:282:ARG:NH1	1:A:396:LEU:HD11	2.28	0.48
1:A:157:LYS:O	1:A:159:HIS:CD2	2.67	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:48:LEU:HG	1:A:48:LEU:O	2.13	0.48
1:A:17:LYS:HZ2	1:A:47:TYR:HB2	1.76	0.48
1:A:34:VAL:O	1:A:35:GLU:C	2.52	0.48
1:A:54:TYR:O	1:A:148:ALA:HA	2.14	0.47
1:A:225:ASN:N	1:A:225:ASN:HD22	2.10	0.47
1:A:396:LEU:HB3	1:A:397:LYS:H	1.50	0.47
1:A:285:ARG:CZ	1:A:293:LEU:HD11	2.45	0.47
1:A:293:LEU:HD23	1:A:293:LEU:HA	1.77	0.47
1:A:98:THR:HG23	1:A:101:GLN:H	1.80	0.47
1:A:131:PRO:CD	1:A:139:ALA:HA	2.45	0.47
1:A:296:GLU:OE1	1:A:394:GLN:CD	2.53	0.46
1:A:290:ASP:OD1	1:A:299:ASN:N	2.39	0.46
1:A:9:PHE:HA	1:A:389:GLU:O	2.15	0.46
1:A:49:LYS:HA	1:A:49:LYS:HZ3	1.79	0.46
1:A:278:LEU:CD2	1:A:289:LEU:HD22	2.46	0.46
1:A:87:PHE:O	1:A:89:PRO:N	2.49	0.46
1:A:190:PHE:CG	1:A:226:LYS:HE3	2.51	0.46
1:A:198:HIS:HB3	1:A:221:THR:HB	1.97	0.46
1:A:48:LEU:HD23	1:A:48:LEU:H	1.81	0.46
1:A:87:PHE:HB3	1:A:88:PRO:CD	2.39	0.45
1:A:178:PRO:CG	1:A:179:GLY:H	2.24	0.45
1:A:49:LYS:HB3	1:A:50:GLU:H	1.54	0.45
1:A:241:ILE:N	1:A:241:ILE:HD12	2.32	0.45
1:A:285:ARG:NH1	1:A:293:LEU:CD1	2.79	0.45
1:A:386:ILE:O	1:A:387:VAL:HB	2.16	0.45
1:A:52:ARG:O	1:A:150:CYS:HA	2.17	0.45
1:A:393:ARG:HG2	1:A:393:ARG:NH1	2.31	0.45
1:A:14:PRO:HD2	1:A:161:ARG:O	2.16	0.44
1:A:142:VAL:HG23	1:A:142:VAL:O	2.17	0.44
1:A:340:SER:O	1:A:341:SER:C	2.55	0.44
1:A:34:VAL:CG2	1:A:121:PRO:HA	2.47	0.44
1:A:70:VAL:CG1	2:A:486:HOH:O	2.65	0.44
1:A:98:THR:CG2	1:A:101:GLN:H	2.31	0.44
1:A:243:LEU:HD12	1:A:243:LEU:HA	1.84	0.44
1:A:175:PRO:O	1:A:176:GLU:CD	2.56	0.44
1:A:287:LEU:HD12	1:A:287:LEU:C	2.38	0.44
1:A:43:VAL:HG12	1:A:44:ASP:H	1.82	0.44
1:A:199:LEU:HD13	1:A:327:LEU:HD11	2.00	0.44
1:A:304:THR:HG21	1:A:318:ILE:HG13	1.99	0.44
1:A:342:ASP:OD1	1:A:342:ASP:N	2.41	0.44
1:A:56:THR:HG22	1:A:83:ASN:CG	2.39	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:154:LEU:N	1:A:154:LEU:HD13	2.33	0.43
1:A:87:PHE:CB	1:A:88:PRO:HD3	2.38	0.43
1:A:166:LEU:O	1:A:166:LEU:HD12	2.18	0.43
1:A:174:ALA:CB	1:A:352:MET:SD	3.07	0.43
1:A:224:THR:HG22	1:A:226:LYS:N	2.32	0.43
1:A:132:GLY:HA2	1:A:285:ARG:HB3	2.00	0.43
1:A:224:THR:HG21	1:A:226:LYS:HB2	2.01	0.43
1:A:44:ASP:O	1:A:48:LEU:CD2	2.67	0.43
1:A:69:ASP:OD1	1:A:69:ASP:O	2.37	0.43
1:A:120:PRO:HA	1:A:121:PRO:HD3	1.66	0.43
1:A:87:PHE:HD1	1:A:88:PRO:HG3	1.84	0.43
1:A:173:TYR:CD2	1:A:173:TYR:C	2.92	0.43
1:A:181:GLN:HB3	1:A:203:LEU:O	2.18	0.43
1:A:80:PHE:HB2	1:A:123:LEU:HD21	2.01	0.42
1:A:238:TYR:CE1	1:A:322:LYS:HE3	2.54	0.42
1:A:30:HIS:O	1:A:172:GLN:NE2	2.51	0.42
1:A:182:PRO:O	1:A:202:SER:HA	2.19	0.42
1:A:202:SER:HA	1:A:347:LEU:CD2	2.50	0.42
1:A:55:VAL:HG22	1:A:148:ALA:CB	2.49	0.42
1:A:75:PHE:CD2	1:A:244:PHE:HB2	2.54	0.42
1:A:17:LYS:HG3	1:A:47:TYR:CE1	2.54	0.42
1:A:285:ARG:NH1	1:A:293:LEU:HD12	2.33	0.42
1:A:108:LEU:N	1:A:108:LEU:HD22	2.35	0.42
1:A:52:ARG:HD2	1:A:54:TYR:OH	2.20	0.42
1:A:127:VAL:HG12	1:A:142:VAL:HG22	2.01	0.42
1:A:270:LYS:HD3	1:A:272:TYR:CZ	2.55	0.42
1:A:278:LEU:O	1:A:282:ARG:N	2.53	0.42
1:A:6:THR:HG22	1:A:7:ARG:H	1.84	0.42
1:A:241:ILE:O	1:A:246:THR:HA	2.20	0.42
1:A:129:LEU:C	1:A:129:LEU:HD23	2.40	0.41
1:A:19:THR:HG22	1:A:21:TYR:CE1	2.55	0.41
1:A:232:LYS:HE2	1:A:257:GLU:HB3	2.02	0.41
1:A:284:LYS:HE3	1:A:284:LYS:HB2	1.66	0.41
1:A:9:PHE:N	1:A:22:LEU:O	2.47	0.41
1:A:15:ASN:HD21	1:A:17:LYS:HB2	1.85	0.41
1:A:26:ASP:OD1	1:A:169:ARG:NH2	2.47	0.41
1:A:184:ALA:O	1:A:200:GLU:HA	2.20	0.41
1:A:10:LYS:HG2	1:A:388:PHE:HB3	2.02	0.41
1:A:37:VAL:HB	1:A:117:PHE:HB2	2.02	0.41
1:A:225:ASN:C	1:A:225:ASN:ND2	2.74	0.41
1:A:99:ARG:C	1:A:101:GLN:N	2.73	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:315:LEU:HB2	1:A:318:ILE:HD11	2.02	0.41
1:A:55:VAL:HA	1:A:148:ALA:HA	2.03	0.41
1:A:68:LEU:HD12	1:A:68:LEU:HA	1.71	0.41
1:A:98:THR:HG22	1:A:101:GLN:CB	2.50	0.41
1:A:178:PRO:CG	1:A:179:GLY:N	2.83	0.41
1:A:153:ASN:ND2	1:A:155:GLU:H	2.19	0.41
1:A:70:VAL:HG11	2:A:486:HOH:O	2.21	0.40
1:A:176:GLU:HG3	1:A:209:TYR:OH	2.22	0.40
1:A:274:LEU:HD23	1:A:274:LEU:N	2.35	0.40
1:A:110:GLU:HG3	1:A:111:HIS:ND1	2.37	0.40
1:A:166:LEU:HB2	1:A:391:PHE:CE2	2.56	0.40
1:A:209:TYR:O	1:A:212:GLU:HB3	2.22	0.40
1:A:229:LYS:HD3	1:A:330:SER:HB2	2.01	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	352/418 (84%)	285 (81%)	48 (14%)	19 (5%)	2	6

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	16	GLY
1	A	49	LYS
1	A	156	GLU
1	A	179	GLY
1	A	341	SER
1	A	354	PRO
1	A	308	GLU
1	A	398	GLY

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Mol	Chain	Res	Type
1	A	177	ARG
1	A	178	PRO
1	A	386	ILE
1	A	97	LEU
1	A	126	SER
1	A	133	PRO
1	A	176	GLU
1	A	390	ASP
1	A	396	LEU
1	A	47	TYR
1	A	387	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	314/372 (84%)	282 (90%)	32 (10%)	7	22

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	LYS
1	A	29	ASP
1	A	49	LYS
1	A	67	ASP
1	A	71	LEU
1	A	73	LEU
1	A	85	GLN
1	A	97	LEU
1	A	99	ARG
1	A	123	LEU
1	A	154	LEU
1	A	157	LYS
1	A	162	ASN
1	A	164	VAL
1	A	176	GLU

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Mol	Chain	Res	Type
1	A	183	THR
1	A	197	LEU
1	A	206	GLU
1	A	215	SER
1	A	224	THR
1	A	225	ASN
1	A	243	LEU
1	A	245	ASN
1	A	256	GLU
1	A	261	THR
1	A	277	PHE
1	A	280	ASN
1	A	287	LEU
1	A	306	LEU
1	A	311	ASN
1	A	342	ASP
1	A	347	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	130	GLN
1	A	153	ASN
1	A	159	HIS
1	A	162	ASN
1	A	172	GLN
1	A	189	GLN
1	A	222	ASN
1	A	225	ASN
1	A	245	ASN
1	A	280	ASN
1	A	281	ASN
1	A	311	ASN
1	A	394	GLN

5.3.3 RNA (i)

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 monosaccharides 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	358/418 (85%)	-0.08	14 (3%)	39	35	21, 50, 99, 141	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	399	MET	7.0
1	A	133	PRO	3.7
1	A	93	ASP	3.7
1	A	383	ASP	3.3
1	A	384	ASP	2.8
1	A	95	LYS	2.6
1	A	179	GLY	2.6
1	A	398	GLY	2.6
1	A	40	VAL	2.3
1	A	39	GLY	2.2
1	A	180	PRO	2.2
1	A	153	ASN	2.1
1	A	308	GLU	2.0
1	A	134	GLU	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 monosaccharides 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.