



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 05:42 AM UTC

PDB ID : 4OB9 / pdb_00004ob9
Title : Crystal structure of chorismate synthase from *Acinetobacter baumannii* at 2.50Å resolution
Authors : Shukla, P.K.; Chaudhary, A.; Singh, N.; Sinha, M.; Bhushan, A.; Kaur, P.; Sharma, S.; Singh, T.P.
Deposited on : 2014-01-07
Resolution : 2.50 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

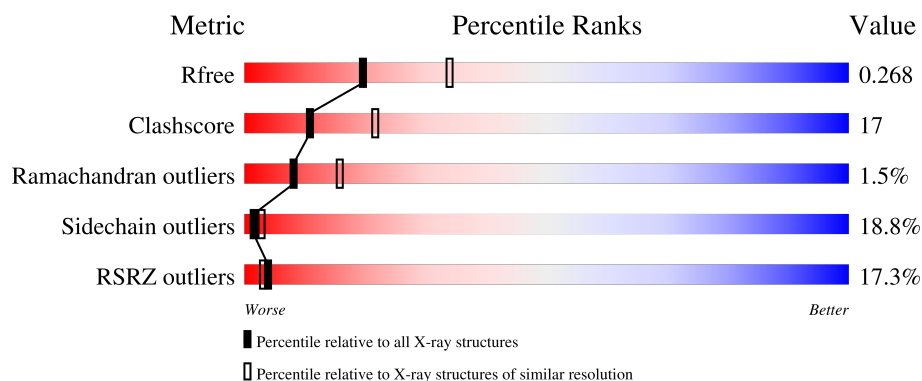
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	363	15% 50% 28% 7% • 14%
1	B	363	15% 53% 25% 8% • 14%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4881 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 Chorismate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	313	Total	C	N	O	S	0	0	0
			2335	1463	421	440	11			
1	B	313	Total	C	N	O	S	0	0	0
			2335	1463	421	440	11			

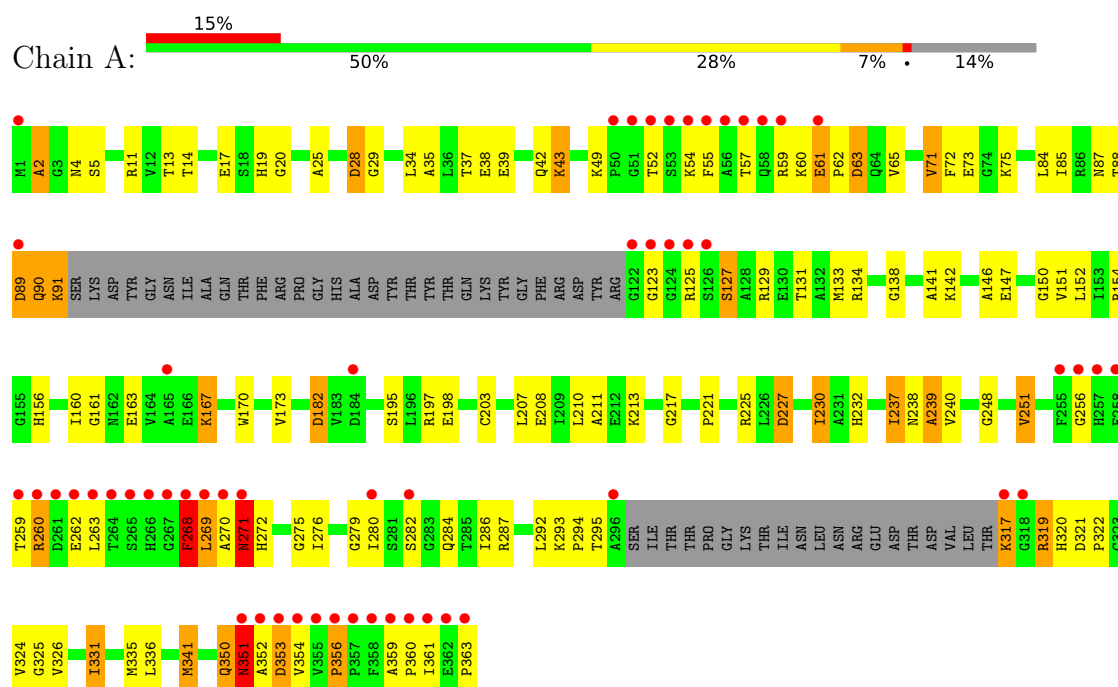
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	107	Total	O	0	0
			107	107		
2	B	104	Total	O	0	0
			104	104		

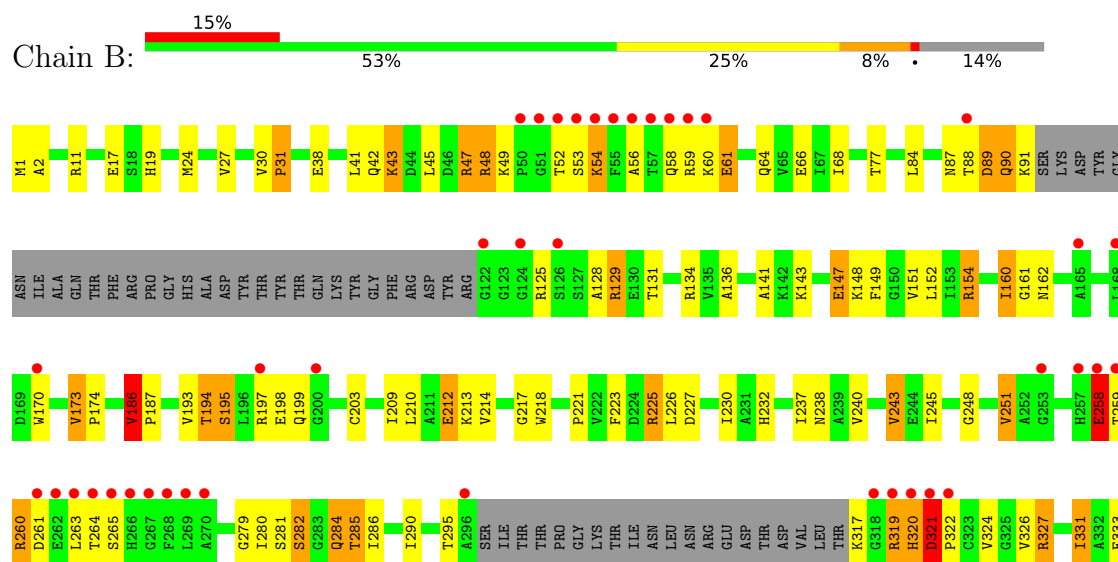
3 Residue-property plots [i](#)

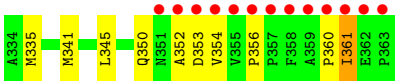
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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



• Molecule 1: Chorismate synthase





4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2 ₁	Depositor
Cell constants a, b, c, α , β , γ	72.98Å 89.79Å 108.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.19 – 2.50 50.19 – 2.50	Depositor EDS
% Data completeness (in resolution range)	91.2 (50.19-2.50) 91.2 (50.19-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.18	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.10 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.218 , 0.264 0.220 , 0.268	Depositor DCC
R_{free} test set	1166 reflections (4.60%)	wwPDB-VP
Wilson B-factor (Å ²)	37.3	Xtriage
Anisotropy	0.589	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 61.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	4881	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.17% 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	1.26	10/2376 (0.4%)	1.35	23/3211 (0.7%)
1	B	1.25	3/2376 (0.1%)	1.44	31/3211 (1.0%)
All	All	1.26	13/4752 (0.3%)	1.39	54/6422 (0.8%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3
1	B	0	3
All	All	0	6

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	240	VAL	C-O	-7.00	1.16	1.24
1	A	28	ASP	C-O	-6.85	1.15	1.23
1	A	272	HIS	CG-ND1	-6.46	1.31	1.38
1	A	271	ASN	CA-C	-6.22	1.45	1.53
1	B	225	ARG	C-O	-6.16	1.16	1.23
1	A	272	HIS	CD2-NE2	-6.06	1.31	1.37
1	A	19	HIS	CG-ND1	-5.89	1.31	1.38
1	A	240	VAL	C-O	-5.46	1.18	1.24
1	B	218	TRP	NE1-CE2	-5.42	1.31	1.37
1	A	182	ASP	C-O	-5.37	1.17	1.24
1	A	237	ILE	C-O	-5.36	1.17	1.24
1	A	71	VAL	C-O	-5.33	1.18	1.24
1	A	19	HIS	CD2-NE2	-5.26	1.32	1.37

All (54) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	55	PHE	CB-CA-C	-12.65	82.94	109.38
1	B	260	ARG	N-CA-C	11.02	123.29	111.28
1	B	238	ASN	N-CA-C	10.70	122.94	111.28
1	B	264	THR	N-CA-C	10.47	122.45	111.14
1	A	57	THR	CB-CA-C	-10.44	95.70	109.16
1	A	89	ASP	N-CA-C	-9.63	100.62	112.38
1	B	259	THR	N-CA-C	8.88	124.09	112.72
1	B	321	ASP	CA-C-N	8.61	128.60	119.05
1	B	321	ASP	C-N-CA	8.61	128.60	119.05
1	B	31	PRO	CA-C-N	8.56	128.50	119.85
1	B	31	PRO	C-N-CA	8.56	128.50	119.85
1	B	361	ILE	N-CA-C	8.47	119.26	110.62
1	A	29	GLY	N-CA-C	8.31	126.80	115.32
1	A	55	PHE	CA-C-N	8.21	131.49	120.65
1	A	55	PHE	C-N-CA	8.21	131.49	120.65
1	A	61	GLU	N-CA-C	7.78	124.20	113.16
1	B	282	SER	CB-CA-C	-7.72	98.70	110.90
1	B	56	ALA	N-CA-C	-7.70	97.19	109.59
1	B	238	ASN	CA-C-N	-7.65	110.41	122.65
1	B	238	ASN	C-N-CA	-7.65	110.41	122.65
1	A	351	ASN	CA-C-N	7.36	130.00	120.44
1	A	351	ASN	C-N-CA	7.36	130.00	120.44
1	B	319	ARG	N-CA-C	-7.34	97.28	109.46
1	A	55	PHE	N-CA-C	7.26	120.97	109.50
1	B	265	SER	N-CA-C	7.25	118.97	111.14
1	A	295	THR	CB-CA-C	-7.24	97.12	111.60
1	A	270	ALA	N-CA-C	-6.78	97.69	108.73
1	B	53	SER	CA-C-N	6.61	129.14	120.28
1	B	53	SER	C-N-CA	6.61	129.14	120.28
1	B	240	VAL	N-CA-C	6.49	118.13	109.37
1	A	260	ARG	CA-C-N	6.17	130.57	120.63
1	A	260	ARG	C-N-CA	6.17	130.57	120.63
1	B	217	GLY	N-CA-C	6.17	123.97	115.27
1	A	351	ASN	O-C-N	5.95	130.97	123.23
1	B	89	ASP	N-CA-C	-5.91	99.51	108.67
1	B	352	ALA	N-CA-C	-5.80	104.96	111.28
1	B	54	LYS	N-CA-C	5.79	117.59	111.28
1	B	281	SER	CA-C-N	5.79	128.31	120.44
1	B	281	SER	C-N-CA	5.79	128.31	120.44
1	B	320	HIS	CA-C-N	-5.71	113.02	120.44
1	B	320	HIS	C-N-CA	-5.71	113.02	120.44
1	A	341	MET	N-CA-C	-5.63	105.05	111.07
1	B	147	GLU	N-CA-C	5.58	117.04	111.07

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	75	LYS	N-CA-C	5.50	118.42	109.24
1	B	186	VAL	CB-CA-C	-5.49	106.81	114.00
1	A	217	GLY	N-CA-C	5.49	121.28	114.37
1	B	258	GLU	N-CA-C	5.46	122.31	114.39
1	A	268	PHE	CA-C-N	-5.46	113.89	122.08
1	A	268	PHE	C-N-CA	-5.46	113.89	122.08
1	A	35	ALA	N-CA-C	-5.37	101.22	109.76
1	B	354	VAL	N-CA-C	5.37	116.94	109.80
1	A	57	THR	N-CA-C	5.23	121.34	114.75
1	B	261	ASP	N-CA-C	5.17	116.83	108.34
1	A	353	ASP	N-CA-C	5.07	116.66	108.34

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	2	ALA	Peptide
1	A	256	GLY	Peptide
1	A	269	LEU	Peptide
1	B	321	ASP	Peptide,Mainchain
1	B	360	PRO	Peptide

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	2335	0	2342	89	0
1	B	2335	0	2342	78	0
2	A	107	0	0	5	0
2	B	104	0	0	7	0
All	All	4881	0	4684	155	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 17.

All (155) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:90:GLN:O	1:A:91:LYS:HB2	1.54	1.05
1:A:268:PHE:CD1	1:A:268:PHE:N	2.29	0.98
1:A:293:LYS:HA	1:B:251:VAL:HG13	1.50	0.93
1:A:211:ALA:HB3	1:A:286:ILE:HB	1.54	0.90
1:A:268:PHE:H	1:A:268:PHE:HD1	0.93	0.87
1:A:2:ALA:HB1	2:B:412:HOH:O	1.75	0.85
1:A:268:PHE:N	1:A:268:PHE:HD1	1.69	0.85
1:B:90:GLN:H	1:B:90:GLN:HE21	1.29	0.81
1:A:269:LEU:HG	1:A:284:GLN:HE21	1.46	0.79
1:A:90:GLN:O	1:A:91:LYS:CB	2.30	0.79
1:A:269:LEU:HG	1:A:284:GLN:NE2	1.97	0.79
1:A:351:ASN:ND2	1:A:351:ASN:N	2.31	0.79
1:A:20:GLY:HA3	2:A:417:HOH:O	1.82	0.78
1:A:319:ARG:HG3	1:A:319:ARG:HH11	1.48	0.78
1:A:238:ASN:O	1:A:239:ALA:HB3	1.83	0.78
1:B:186:VAL:HB	1:B:187:PRO:HD2	1.66	0.77
1:A:350:GLN:HB3	1:A:351:ASN:ND2	2.00	0.76
1:B:42:GLN:OE1	1:B:64:GLN:HA	1.86	0.75
1:A:60:LYS:HG3	1:A:61:GLU:H	1.52	0.75
1:A:293:LYS:HA	1:B:251:VAL:CG1	2.19	0.73
1:A:351:ASN:N	1:A:351:ASN:HD22	1.86	0.72
1:A:182:ASP:OD1	1:A:182:ASP:C	2.30	0.71
1:B:285:THR:HG21	2:B:421:HOH:O	1.92	0.69
1:A:89:ASP:O	1:A:90:GLN:HB2	1.93	0.69
1:A:238:ASN:O	1:A:239:ALA:CB	2.38	0.69
1:A:208:GLU:OE1	1:A:287:ARG:HD3	1.93	0.68
1:B:89:ASP:O	1:B:90:GLN:C	2.37	0.68
1:B:160:ILE:HG22	1:B:203:CYS:SG	2.35	0.67
1:A:350:GLN:C	1:A:351:ASN:HD22	2.02	0.66
1:B:90:GLN:H	1:B:90:GLN:NE2	1.94	0.65
1:B:90:GLN:HE21	1:B:90:GLN:N	1.94	0.65
1:B:237:ILE:HG12	1:B:331:ILE:HD11	1.79	0.65
1:B:61:GLU:HA	1:B:61:GLU:OE1	1.96	0.64
1:A:319:ARG:HG3	1:A:319:ARG:NH1	2.10	0.64
1:A:42:GLN:OE1	1:A:65:VAL:HG12	1.98	0.63
1:A:269:LEU:CG	1:A:284:GLN:HE21	2.12	0.63
1:B:17:GLU:HG3	2:B:467:HOH:O	1.98	0.63
1:A:127:SER:C	1:A:129:ARG:H	2.05	0.63
1:B:160:ILE:CG2	1:B:203:CYS:SG	2.87	0.63
1:B:186:VAL:HB	1:B:187:PRO:CD	2.28	0.62
1:A:221:PRO:O	1:B:2:ALA:HA	1.99	0.62
1:B:321:ASP:HB3	2:B:496:HOH:O	2.00	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:225:ARG:HB3	1:B:227:ASP:OD1	2.00	0.61
1:A:87:ASN:HB3	1:A:89:ASP:OD1	2.02	0.60
1:B:186:VAL:CB	1:B:187:PRO:CD	2.80	0.59
1:B:282:SER:HB3	1:B:284:GLN:HG2	1.84	0.59
1:A:350:GLN:HG3	1:B:1:MET:SD	2.42	0.59
1:A:293:LYS:CA	1:B:251:VAL:HG13	2.29	0.58
1:A:225:ARG:HG2	1:A:279:GLY:HA3	1.85	0.58
1:B:68:ILE:HD11	1:B:84:LEU:HB3	1.84	0.58
1:B:143:LYS:O	1:B:147:GLU:HG3	2.04	0.57
1:A:150:GLY:O	1:A:213:LYS:HD3	2.04	0.57
1:A:293:LYS:CA	1:B:251:VAL:CG1	2.83	0.57
1:B:87:ASN:HB3	1:B:129:ARG:NH2	2.19	0.57
1:B:258:GLU:HG2	2:B:478:HOH:O	2.03	0.56
1:B:38:GLU:HB2	2:B:418:HOH:O	2.05	0.56
1:A:232:HIS:HB2	1:B:232:HIS:HB2	1.87	0.56
1:B:210:LEU:HA	1:B:286:ILE:O	2.05	0.56
1:B:186:VAL:HG12	1:B:187:PRO:HD3	1.87	0.56
1:A:156:HIS:NE2	1:A:208:GLU:OE2	2.37	0.56
1:B:66:GLU:O	1:B:68:ILE:HD12	2.05	0.56
1:B:320:HIS:O	1:B:321:ASP:C	2.48	0.56
1:A:320:HIS:CE1	2:A:414:HOH:O	2.58	0.55
1:A:317:LYS:HA	1:A:317:LYS:HE2	1.88	0.55
1:B:243:VAL:HG13	1:B:290:ILE:HG22	1.88	0.55
1:B:160:ILE:O	1:B:161:GLY:C	2.48	0.55
1:A:269:LEU:CD2	1:A:284:GLN:HE21	2.20	0.55
1:A:170:TRP:O	1:A:173:VAL:HG22	2.06	0.55
1:B:227:ASP:OD1	1:B:227:ASP:N	2.40	0.54
1:A:11:ARG:HB3	1:A:28:ASP:HB2	1.90	0.54
1:A:293:LYS:HB3	1:B:251:VAL:HG11	1.89	0.54
1:A:350:GLN:HB3	1:A:351:ASN:HD21	1.72	0.53
1:A:13:THR:O	1:A:25:ALA:HA	2.09	0.52
1:A:88:THR:C	1:A:90:GLN:N	2.63	0.52
1:A:195:SER:O	1:A:198:GLU:HG3	2.09	0.52
1:A:248:GLY:O	1:A:251:VAL:HB	2.10	0.52
1:B:148:LYS:HG2	1:B:149:PHE:CE2	2.45	0.51
1:A:230:ILE:HD13	1:A:336:LEU:CD1	2.40	0.51
1:A:2:ALA:HA	1:B:221:PRO:O	2.10	0.51
1:A:227:ASP:OD1	1:A:227:ASP:N	2.33	0.51
1:A:127:SER:C	1:A:129:ARG:N	2.63	0.51
1:B:68:ILE:CD1	1:B:84:LEU:HB3	2.41	0.51
1:B:186:VAL:HG12	1:B:187:PRO:CD	2.41	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:275:GLY:C	1:A:276:ILE:HG13	2.36	0.50
1:B:248:GLY:O	1:B:251:VAL:HB	2.12	0.50
1:A:63:ASP:HB2	2:A:476:HOH:O	2.12	0.49
1:A:134:ARG:HG2	1:A:335:MET:HE1	1.93	0.49
1:B:335:MET:N	1:B:335:MET:HE2	2.27	0.49
1:A:138:GLY:O	1:A:142:LYS:HB2	2.12	0.49
1:A:60:LYS:HG3	1:A:61:GLU:N	2.26	0.49
1:A:352:ALA:O	1:A:353:ASP:OD1	2.30	0.49
1:A:17:GLU:HA	2:A:428:HOH:O	2.13	0.48
1:A:356:PRO:HB3	2:A:420:HOH:O	2.14	0.48
1:A:146:ALA:O	1:A:150:GLY:HA2	2.14	0.48
1:B:41:LEU:HD22	1:B:136:ALA:O	2.14	0.47
1:A:271:ASN:ND2	1:A:275:GLY:H	2.13	0.47
1:B:321:ASP:HB2	1:B:322:PRO:HA	1.95	0.47
1:B:282:SER:CB	1:B:284:GLN:HG2	2.44	0.47
1:A:134:ARG:CG	1:A:335:MET:HE1	2.45	0.47
1:B:134:ARG:HG2	1:B:335:MET:HE1	1.95	0.47
1:A:320:HIS:O	1:A:322:PRO:CD	2.63	0.47
1:A:134:ARG:HD3	1:B:223:PHE:HE1	1.80	0.47
1:B:173:VAL:HG22	1:B:174:PRO:HD3	1.97	0.46
1:B:195:SER:O	1:B:199:GLN:HG2	2.16	0.46
1:A:225:ARG:HB3	1:A:227:ASP:OD1	2.16	0.46
1:B:48:ARG:NH1	1:B:128:ALA:O	2.40	0.46
1:B:43:LYS:HE3	1:B:43:LYS:HB2	1.45	0.46
1:A:88:THR:C	1:A:90:GLN:H	2.22	0.46
1:A:207:LEU:HD13	1:A:292:LEU:HD13	1.98	0.45
1:A:293:LYS:HB3	1:B:251:VAL:CG1	2.47	0.45
1:A:197:ARG:NH1	1:A:320:HIS:O	2.49	0.45
1:B:320:HIS:O	1:B:321:ASP:O	2.34	0.45
1:B:11:ARG:O	1:B:27:VAL:HA	2.15	0.45
1:A:65:VAL:HA	1:A:85:ILE:HG12	1.99	0.45
1:B:30:VAL:HA	1:B:31:PRO:HD3	1.80	0.45
1:B:42:GLN:OE1	1:B:64:GLN:CA	2.59	0.44
1:B:151:VAL:HA	1:B:212:GLU:O	2.17	0.44
1:B:214:VAL:HG21	1:B:286:ILE:HD12	1.98	0.44
1:A:42:GLN:O	1:A:43:LYS:C	2.61	0.44
1:A:141:ALA:HB1	1:A:341:MET:HB2	1.99	0.44
1:B:61:GLU:OE1	1:B:61:GLU:CA	2.63	0.44
1:A:167:LYS:HE2	1:A:167:LYS:HB2	1.57	0.43
1:B:19:HIS:CD2	1:B:19:HIS:H	2.36	0.43
1:B:141:ALA:HB1	1:B:341:MET:HB2	2.01	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:47:ARG:NH1	1:B:333:GLU:OE1	2.43	0.43
1:B:327:ARG:NH1	2:B:462:HOH:O	2.52	0.43
1:B:154:ARG:HA	1:B:333:GLU:OE2	2.20	0.42
1:B:225:ARG:HG2	1:B:279:GLY:HA3	2.02	0.42
1:B:237:ILE:HG12	1:B:331:ILE:CD1	2.48	0.42
1:A:72:PHE:O	1:A:73:GLU:C	2.63	0.42
1:B:88:THR:O	1:B:88:THR:HG22	2.18	0.42
1:A:4:ASN:HB2	1:A:14:THR:O	2.19	0.42
1:B:197:ARG:HD2	1:B:320:HIS:ND1	2.34	0.42
1:A:230:ILE:HD13	1:A:336:LEU:HD13	2.00	0.42
1:A:230:ILE:CD1	1:A:336:LEU:CD1	2.97	0.42
1:B:1:MET:O	1:B:2:ALA:HB2	2.20	0.42
1:B:45:LEU:O	1:B:48:ARG:HB2	2.19	0.42
1:B:170:TRP:HZ2	1:B:210:LEU:HD12	1.83	0.42
1:A:71:VAL:O	1:A:71:VAL:HG23	2.18	0.42
1:B:226:LEU:O	1:B:230:ILE:HG13	2.20	0.42
1:A:293:LYS:HB2	1:A:294:PRO:CD	2.50	0.42
1:A:167:LYS:O	1:A:182:ASP:HB2	2.20	0.42
1:A:237:ILE:HG12	1:A:331:ILE:HG12	2.02	0.41
1:A:160:ILE:HG22	1:A:203:CYS:SG	2.61	0.41
1:B:194:THR:O	1:B:198:GLU:HG3	2.21	0.41
1:A:85:ILE:HG13	1:A:133:MET:HE1	2.02	0.41
1:A:170:TRP:HZ2	1:A:210:LEU:HD12	1.86	0.41
1:A:352:ALA:C	1:A:353:ASP:OD1	2.64	0.41
1:A:320:HIS:O	1:A:322:PRO:HD2	2.20	0.41
1:A:134:ARG:HD3	1:B:223:PHE:CE1	2.55	0.41
1:B:335:MET:HE2	1:B:335:MET:CA	2.51	0.41
1:A:147:GLU:O	1:A:363:PRO:HA	2.20	0.41
1:B:284:GLN:HG2	1:B:284:GLN:H	1.49	0.40
1:B:345:LEU:HD23	1:B:345:LEU:HA	1.87	0.40
1:A:282:SER:HB3	1:A:284:GLN:HG3	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	307/363 (85%)	285 (93%)	14 (5%)	8 (3%)	4	7
1	B	307/363 (85%)	287 (94%)	19 (6%)	1 (0%)	36	55
All	All	614/726 (85%)	572 (93%)	33 (5%)	9 (2%)	8	16

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	62	PRO
1	B	356	PRO
1	A	325	GLY
1	A	356	PRO
1	A	360	PRO
1	A	123	GLY
1	A	239	ALA
1	A	359	ALA
1	A	161	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	242/286 (85%)	200 (83%)	42 (17%)	2	3
1	B	242/286 (85%)	193 (80%)	49 (20%)	1	2
All	All	484/572 (85%)	393 (81%)	91 (19%)	1	3

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

Mol	Chain	Res	Type
1	A	5	SER
1	A	34	LEU
1	A	37	THR
1	A	38	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	39	GLU
1	A	43	LYS
1	A	49	LYS
1	A	52	THR
1	A	54	LYS
1	A	59	ARG
1	A	63	ASP
1	A	84	LEU
1	A	90	GLN
1	A	91	LYS
1	A	125	ARG
1	A	127	SER
1	A	131	THR
1	A	151	VAL
1	A	152	LEU
1	A	154	ARG
1	A	163	GLU
1	A	167	LYS
1	A	227	ASP
1	A	230	ILE
1	A	251	VAL
1	A	259	THR
1	A	260	ARG
1	A	262	GLU
1	A	263	LEU
1	A	268	PHE
1	A	271	ASN
1	A	280	ILE
1	A	317	LYS
1	A	319	ARG
1	A	321	ASP
1	A	324	VAL
1	A	326	VAL
1	A	331	ILE
1	A	350	GLN
1	A	351	ASN
1	A	354	VAL
1	A	361	ILE
1	B	24	MET
1	B	43	LYS
1	B	47	ARG
1	B	48	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	49	LYS
1	B	52	THR
1	B	54	LYS
1	B	58	GLN
1	B	59	ARG
1	B	60	LYS
1	B	61	GLU
1	B	77	THR
1	B	90	GLN
1	B	91	LYS
1	B	125	ARG
1	B	129	ARG
1	B	131	THR
1	B	152	LEU
1	B	154	ARG
1	B	160	ILE
1	B	162	ASN
1	B	173	VAL
1	B	186	VAL
1	B	193	VAL
1	B	194	THR
1	B	195	SER
1	B	209	ILE
1	B	212	GLU
1	B	213	LYS
1	B	243	VAL
1	B	245	ILE
1	B	251	VAL
1	B	258	GLU
1	B	260	ARG
1	B	263	LEU
1	B	280	ILE
1	B	284	GLN
1	B	285	THR
1	B	295	THR
1	B	317	LYS
1	B	319	ARG
1	B	321	ASP
1	B	324	VAL
1	B	326	VAL
1	B	327	ARG
1	B	331	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	350	GLN
1	B	353	ASP
1	B	361	ILE

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

Mol	Chain	Res	Type
1	A	175	ASN
1	A	199	GLN
1	A	284	GLN
1	A	351	ASN
1	B	8	GLN
1	B	19	HIS
1	B	64	GLN
1	B	90	GLN
1	B	175	ASN
1	B	238	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

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	313/363 (86%)	0.94	55 (17%) 4 3	17, 31, 99, 150	30 (9%)
1	B	313/363 (86%)	1.04	53 (16%) 4 3	18, 35, 114, 158	24 (7%)
All	All	626/726 (86%)	0.99	108 (17%) 4 3	17, 33, 108, 158	54 (8%)

All (108) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	356	PRO	14.0
1	B	361	ILE	12.3
1	B	357	PRO	11.8
1	B	358	PHE	11.7
1	B	355	VAL	11.6
1	A	354	VAL	11.4
1	A	357	PRO	10.1
1	A	359	ALA	9.8
1	B	359	ALA	9.8
1	B	354	VAL	9.6
1	B	363	PRO	9.3
1	B	56	ALA	9.1
1	A	263	LEU	8.8
1	B	360	PRO	8.5
1	B	57	THR	8.3
1	A	363	PRO	8.2
1	A	355	VAL	8.2
1	A	55	PHE	7.6
1	A	57	THR	7.4
1	A	259	THR	7.4
1	A	361	ILE	7.3
1	B	55	PHE	7.2
1	A	358	PHE	7.1
1	A	54	LYS	7.0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	362	GLU	6.9
1	A	264	THR	6.7
1	B	52	THR	6.6
1	A	356	PRO	6.4
1	A	56	ALA	6.3
1	B	59	ARG	6.2
1	A	257	HIS	6.1
1	B	318	GLY	6.1
1	A	51	GLY	5.9
1	A	266	HIS	5.8
1	B	320	HIS	5.7
1	B	353	ASP	5.7
1	A	360	PRO	5.7
1	B	261	ASP	5.5
1	B	53	SER	5.5
1	A	58	GLN	5.5
1	B	319	ARG	5.2
1	A	52	THR	5.1
1	B	58	GLN	5.0
1	A	260	ARG	4.9
1	A	352	ALA	4.8
1	A	258	GLU	4.8
1	A	362	GLU	4.7
1	B	263	LEU	4.6
1	B	257	HIS	4.5
1	A	265	SER	4.5
1	B	54	LYS	4.4
1	A	59	ARG	4.3
1	B	268	PHE	4.1
1	B	60	LYS	4.0
1	A	262	GLU	3.9
1	A	261	ASP	3.9
1	A	53	SER	3.9
1	B	126	SER	3.9
1	A	353	ASP	3.7
1	A	165	ALA	3.6
1	A	124	GLY	3.5
1	A	126	SER	3.5
1	A	351	ASN	3.4
1	B	267	GLY	3.4
1	B	265	SER	3.2
1	A	122	GLY	3.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	50	PRO	3.1
1	A	123	GLY	3.1
1	B	262	GLU	3.0
1	B	50	PRO	3.0
1	B	266	HIS	2.9
1	A	184	ASP	2.9
1	B	124	GLY	2.9
1	B	321	ASP	2.8
1	A	282	SER	2.8
1	B	264	THR	2.8
1	A	268	PHE	2.8
1	A	296	ALA	2.7
1	A	267	GLY	2.7
1	A	318	GLY	2.7
1	B	253	GLY	2.7
1	A	256	GLY	2.6
1	A	89	ASP	2.5
1	B	270	ALA	2.5
1	B	122	GLY	2.4
1	B	200	GLY	2.4
1	B	351	ASN	2.4
1	B	296	ALA	2.4
1	A	270	ALA	2.4
1	A	317	LYS	2.4
1	B	88	THR	2.4
1	A	269	LEU	2.4
1	B	197	ARG	2.3
1	A	280	ILE	2.3
1	B	352	ALA	2.3
1	B	258	GLU	2.2
1	A	255	PHE	2.2
1	B	51	GLY	2.2
1	B	269	LEU	2.2
1	B	170	TRP	2.2
1	A	271	ASN	2.2
1	A	125	ARG	2.2
1	A	61	GLU	2.1
1	B	165	ALA	2.1
1	B	168	LEU	2.1
1	A	1	MET	2.1
1	B	259	THR	2.1
1	B	322	PRO	2.1

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

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

6.3 Carbohydrates [i](#)

There are no 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.