



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 09:37 AM EDT

PDB ID : 5D0O / pdb_00005d0o
Title : BamABCDE complex, outer membrane beta barrel assembly machinery entire complex
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Deposited on : 2015-08-03
Resolution : 2.90 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

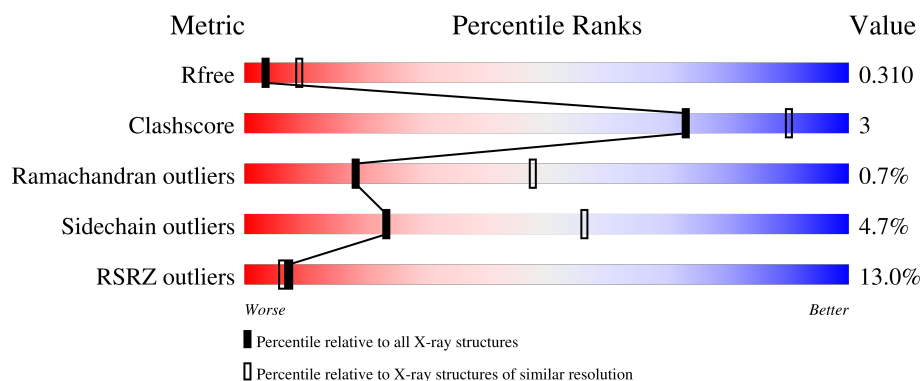
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (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 $\leq 5\%$. 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	810	11% 87% 9% ••
2	B	392	14% 79% 10% • 10%
3	C	344	5% 14% • 84%
4	D	245	9% 76% 9% 15%
5	E	123	11% 45% 20% • 33%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 22815 atoms, of which 11201 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 Outer membrane protein assembly factor BamA.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	786	Total	C	H	N	O	S	0	0	0
			12142	3919	5928	1047	1232	16			

- Molecule 2 is a protein called Outer membrane protein assembly factor BamB.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	354	Total	C	H	N	O	S	0	0	0
			5280	1675	2615	457	527	6			

- Molecule 3 is a protein called Outer membrane protein assembly factor BamC.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	C	56	Total	C	H	N	O	S	0	0	0
			817	258	409	71	78	1			

- Molecule 4 is a protein called Outer membrane protein assembly factor BamD.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
4	D	208	Total	C	H	N	O	S	0	0	0
			3306	1057	1624	296	322	7			

- Molecule 5 is a protein called Outer membrane protein assembly factor BamE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
5	E	83	Total	C	H	N	O	S	0	0	0
			1270	405	625	112	126	2			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	114	GLY	-	expression tag	UNP P0A937
E	115	GLY	-	expression tag	UNP P0A937

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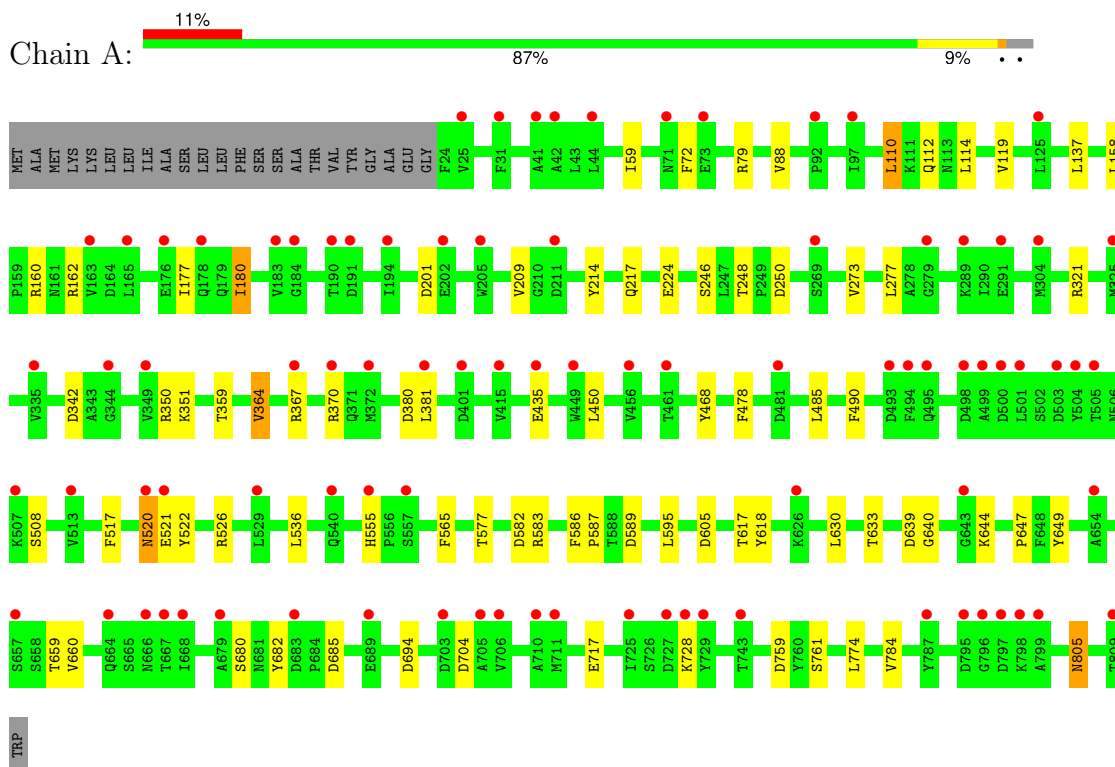
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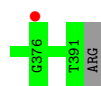
Chain	Residue	Modelled	Actual	Comment	Reference
E	116	HIS	-	expression tag	UNP P0A937
E	117	HIS	-	expression tag	UNP P0A937
E	118	HIS	-	expression tag	UNP P0A937
E	119	HIS	-	expression tag	UNP P0A937
E	120	HIS	-	expression tag	UNP P0A937
E	121	HIS	-	expression tag	UNP P0A937
E	122	HIS	-	expression tag	UNP P0A937
E	123	HIS	-	expression tag	UNP P0A937

3 Residue-property plots [i](#)

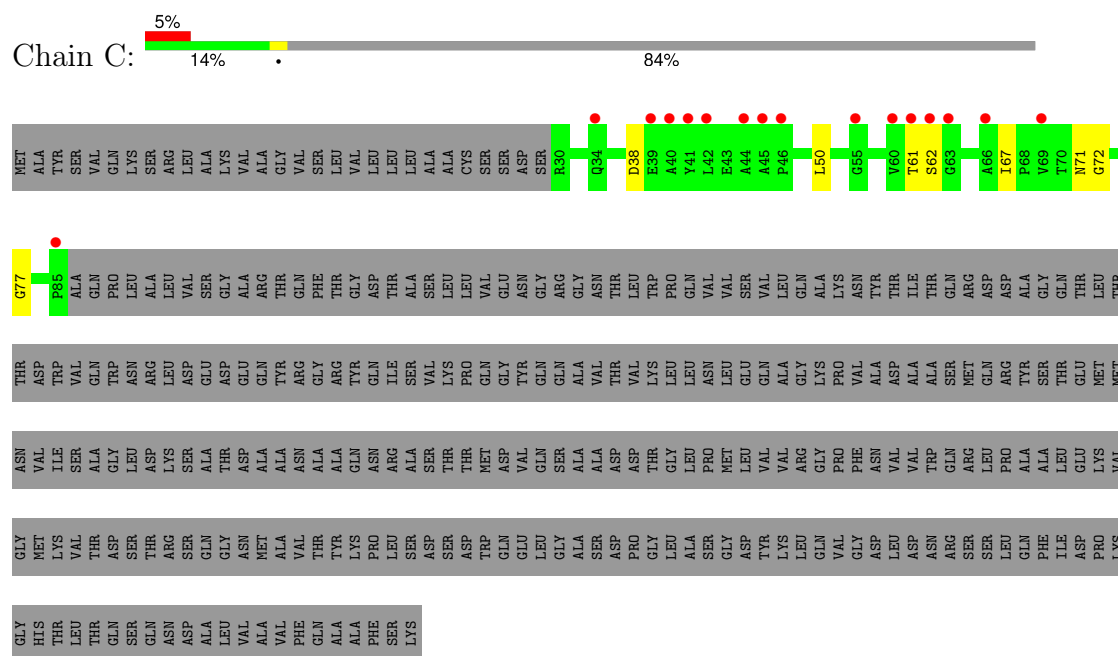
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

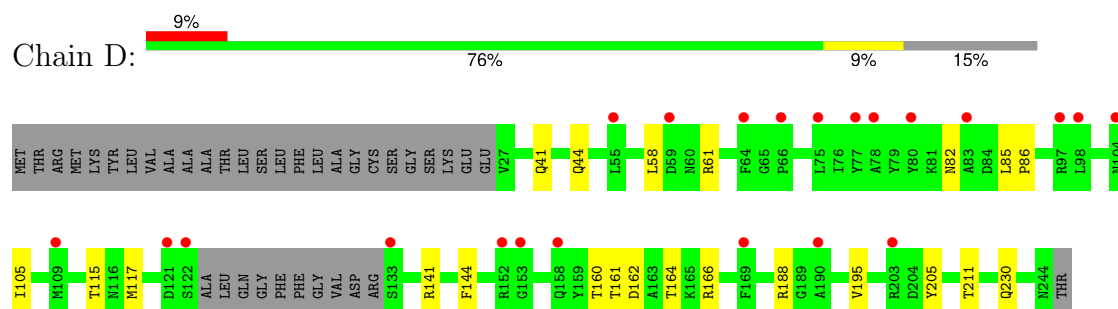




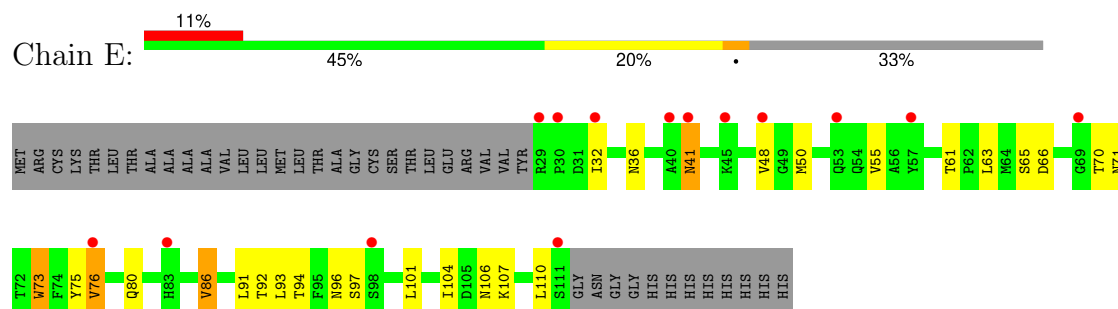
- Molecule 3: Outer membrane protein assembly factor BamC



- Molecule 4: Outer membrane protein assembly factor BamD



- Molecule 5: Outer membrane protein assembly factor BamE



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	116.69Å 116.69Å 435.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.65 – 2.90 49.65 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.5 (49.65-2.90) 100.0 (49.65-2.90)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	0.02	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.16 (at 2.77Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.276 , 0.304 0.281 , 0.310	Depositor DCC
R_{free} test set	3845 reflections (4.84%)	wwPDB-VP
Wilson B-factor (Å ²)	84.2	Xtriage
Anisotropy	0.560	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 58.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	22815	wwPDB-VP
Average B, all atoms (Å ²)	128.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.54% 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 [i](#)

5.1 Standard geometry [i](#)

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	0.30	0/6357	0.66	0/8624
2	B	0.30	0/2714	0.67	0/3700
3	C	0.34	0/417	0.69	0/569
4	D	0.34	0/1719	0.70	0/2336
5	E	0.34	0/659	0.70	0/899
All	All	0.31	0/11866	0.67	0/16128

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 [i](#)

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	6214	5928	5928	36	0
2	B	2665	2615	2615	20	0
3	C	408	409	409	3	0
4	D	1682	1624	1624	11	0
5	E	645	625	625	7	0
All	All	11614	11201	11201	74	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 3.

All (74) 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:160:ARG:NH1	4:D:61:ARG:O	2.11	0.83
1:A:364:VAL:O	1:A:367:ARG:NH1	2.15	0.79
1:A:217:GLN:N	1:A:217:GLN:OE1	2.25	0.69
1:A:582:ASP:OD2	1:A:589:ASP:N	2.30	0.65
1:A:605:ASP:O	1:A:644:LYS:NZ	2.32	0.62
2:B:281:ARG:NH1	2:B:315:THR:OG1	2.33	0.62
2:B:138:ASP:N	2:B:138:ASP:OD1	2.35	0.60
1:A:201:ASP:N	1:A:201:ASP:OD1	2.36	0.59
1:A:435:GLU:OE1	1:A:805:ASN:ND2	2.36	0.57
2:B:166:THR:HG22	2:B:168:ASN:H	1.69	0.57
4:D:161:THR:O	4:D:164:THR:OG1	2.21	0.57
1:A:526:ARG:NH2	1:A:577:THR:OG1	2.38	0.57
1:A:248:THR:OG1	1:A:250:ASP:OD1	2.22	0.56
2:B:337:LEU:HB2	2:B:349:ILE:HG23	1.89	0.54
4:D:205:TYR:O	4:D:211:THR:OG1	2.16	0.53
1:A:321:ARG:NH1	1:A:342:ASP:OD2	2.41	0.53
2:B:109:ALA:O	2:B:126:SER:OG	2.28	0.51
1:A:380:ASP:OD1	1:A:381:LEU:N	2.43	0.51
2:B:341:ASP:OD1	2:B:345:TYR:N	2.38	0.50
1:A:364:VAL:HG13	1:A:367:ARG:HH12	1.77	0.50
1:A:639:ASP:OD1	1:A:640:GLY:N	2.45	0.50
1:A:110:LEU:HD21	1:A:137:LEU:HD22	1.95	0.49
2:B:245:SER:OG	2:B:246:ASP:N	2.45	0.48
1:A:759:ASP:OD1	1:A:761:SER:OG	2.32	0.48
1:A:630:LEU:HB3	1:A:717:GLU:HB2	1.95	0.48
3:C:67:ILE:HD11	4:D:144:PHE:CZ	2.49	0.47
1:A:370:ARG:O	1:A:370:ARG:NH1	2.48	0.47
4:D:41:GLN:NE2	4:D:44:GLN:OE1	2.47	0.47
4:D:162:ASP:OD1	4:D:166:ARG:NE	2.48	0.47
1:A:520:ASN:C	1:A:522:TYR:H	2.23	0.47
2:B:223:GLN:OE1	2:B:225:GLN:N	2.48	0.46
2:B:246:ASP:HA	2:B:263:TYR:HB3	1.98	0.46
2:B:110:LEU:HD13	2:B:128:LYS:HG2	1.97	0.46
4:D:85:LEU:HB2	4:D:86:PRO:HD3	1.98	0.46
4:D:230:GLN:NE2	5:E:66:ASP:OD2	2.47	0.45
1:A:177:ILE:HD12	1:A:177:ILE:N	2.32	0.45
1:A:468:TYR:HE1	1:A:490:PHE:HB2	1.80	0.45
1:A:618:TYR:CE1	1:A:630:LEU:HD13	2.51	0.45
2:B:248:ASP:O	2:B:249:THR:CB	2.64	0.45
1:A:582:ASP:OD1	1:A:583:ARG:N	2.50	0.45
2:B:200:PRO:HB3	2:B:209:VAL:HB	1.99	0.45
2:B:281:ARG:NH2	2:B:313:GLY:O	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:319:GLN:NE2	2:B:354:GLY:O	2.51	0.44
5:E:70:THR:OG1	5:E:71:ASN:N	2.50	0.44
2:B:226:MET:HE2	2:B:229:GLN:HB2	2.00	0.43
5:E:73:TRP:HB2	5:E:93:LEU:HB2	1.99	0.43
2:B:148:ALA:N	2:B:172:GLN:OE1	2.47	0.43
5:E:36:ASN:N	5:E:76:VAL:O	2.51	0.43
1:A:536:LEU:N	1:A:565:PHE:O	2.51	0.43
1:A:647:PRO:HB3	1:A:649:TYR:CE2	2.53	0.43
1:A:478:PHE:HB2	1:A:485:LEU:HB2	2.00	0.42
5:E:80:GLN:HB2	5:E:86:VAL:HG12	2.01	0.42
2:B:300:ASP:HB3	2:B:304:ARG:H	1.85	0.42
5:E:93:LEU:HB3	5:E:101:LEU:HD11	2.00	0.42
1:A:72:PHE:CD1	1:A:88:VAL:HG21	2.55	0.42
1:A:704:ASP:OD1	1:A:704:ASP:N	2.53	0.42
2:B:248:ASP:HB3	2:B:249:THR:H	1.74	0.41
3:C:71:ASN:OD1	3:C:72:GLY:N	2.53	0.41
2:B:363:ASP:OD1	2:B:365:SER:N	2.49	0.41
4:D:160:THR:HG23	4:D:161:THR:N	2.35	0.41
4:D:188:ARG:HE	4:D:188:ARG:C	2.27	0.41
1:A:177:ILE:HD11	1:A:214:TYR:HB2	2.03	0.41
2:B:150:GLU:OE2	2:B:195:ARG:NH2	2.46	0.41
1:A:177:ILE:HG21	1:A:180:ILE:HD12	2.02	0.41
1:A:586:PHE:N	1:A:587:PRO:CD	2.83	0.41
1:A:659:THR:OG1	1:A:660:VAL:N	2.52	0.41
1:A:784:VAL:HG13	1:A:805:ASN:HB2	2.03	0.41
1:A:682:TYR:OH	1:A:694:ASP:OD1	2.26	0.41
3:C:61:THR:O	3:C:62:SER:OG	2.30	0.40
1:A:158:LEU:HB2	1:A:162:ARG:HB2	2.02	0.40
1:A:350:ARG:HG2	1:A:351:LYS:HG2	2.02	0.40
1:A:114:LEU:HB3	1:A:119:VAL:HG13	2.03	0.40
5:E:75:TYR:HB2	5:E:91:LEU:HB3	2.03	0.40
4:D:82:ASN:ND2	4:D:82:ASN:O	2.55	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	784/810 (97%)	736 (94%)	45 (6%)	3 (0%)	30 59
2	B	350/392 (89%)	318 (91%)	28 (8%)	4 (1%)	11 36
3	C	54/344 (16%)	46 (85%)	6 (11%)	2 (4%)	2 11
4	D	204/245 (83%)	196 (96%)	8 (4%)	0	100 100
5	E	81/123 (66%)	74 (91%)	6 (7%)	1 (1%)	10 34
All	All	1473/1914 (77%)	1370 (93%)	93 (6%)	10 (1%)	18 48

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	249	THR
3	C	38	ASP
5	E	41	ASN
3	C	77	GLY
1	A	277	LEU
1	A	520	ASN
1	A	680	SER
2	B	250	THR
2	B	227	ILE
2	B	34	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	670/688 (97%)	647 (97%)	23 (3%)	32 66
2	B	287/321 (89%)	277 (96%)	10 (4%)	32 66
3	C	41/276 (15%)	40 (98%)	1 (2%)	43 75
4	D	176/204 (86%)	170 (97%)	6 (3%)	32 66

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	E	72/103 (70%)	53 (74%)	19 (26%)	0	2
All	All	1246/1592 (78%)	1187 (95%)	59 (5%)	23	56

All (59) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	59	ILE
1	A	79	ARG
1	A	110	LEU
1	A	112	GLN
1	A	180	ILE
1	A	209	VAL
1	A	224	GLU
1	A	246	SER
1	A	273	VAL
1	A	359	THR
1	A	364	VAL
1	A	450	LEU
1	A	508	SER
1	A	517	PHE
1	A	521	GLU
1	A	555	HIS
1	A	595	LEU
1	A	617	THR
1	A	633	THR
1	A	685	ASP
1	A	728	LYS
1	A	774	LEU
1	A	805	ASN
2	B	38	VAL
2	B	104	PHE
2	B	163	LEU
2	B	166	THR
2	B	223	GLN
2	B	248	ASP
2	B	283	LEU
2	B	286	VAL
2	B	306	MET
2	B	368	GLN
3	C	50	LEU
4	D	58	LEU
4	D	105	ILE

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Mol	Chain	Res	Type
4	D	115	THR
4	D	117	MET
4	D	141	ARG
4	D	195	VAL
5	E	32	ILE
5	E	41	ASN
5	E	48	VAL
5	E	50	MET
5	E	55	VAL
5	E	61	THR
5	E	63	LEU
5	E	65	SER
5	E	73	TRP
5	E	76	VAL
5	E	86	VAL
5	E	92	THR
5	E	94	THR
5	E	96	ASN
5	E	97	SER
5	E	104	ILE
5	E	106	ASN
5	E	107	LYS
5	E	110	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	523	ASN
1	A	666	ASN
2	B	170	GLN
2	B	266	ASN
2	B	319	GLN
4	D	41	GLN
4	D	224	GLN
5	E	88	GLN

5.3.3 RNA ⓘ

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 [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	786/810 (97%)	0.71	88 (11%) 10 9	100, 122, 164, 204	0
2	B	354/392 (90%)	0.91	54 (15%) 5 4	102, 124, 166, 233	0
3	C	56/344 (16%)	1.51	16 (28%) 1 1	101, 131, 199, 209	0
4	D	208/245 (84%)	0.70	22 (10%) 11 9	104, 124, 176, 234	0
5	E	83/123 (67%)	1.13	14 (16%) 4 3	109, 135, 171, 204	0
All	All	1487/1914 (77%)	0.81	194 (13%) 7 6	100, 124, 170, 234	0

All (194) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	196	GLY	9.4
2	B	247	VAL	7.5
5	E	45	LYS	6.7
4	D	66	PRO	6.0
1	A	415	VAL	5.7
3	C	41	TYR	5.4
1	A	499	ALA	5.2
2	B	248	ASP	5.1
3	C	55	GLY	4.9
2	B	264	ASN	4.8
1	A	799	ALA	4.7
2	B	234	GLN	4.6
4	D	80	TYR	4.5
2	B	201	THR	4.5
2	B	250	THR	4.5
1	A	798	LYS	4.4
1	A	729	TYR	4.4
3	C	42	LEU	4.4
2	B	263	TYR	4.3
1	A	728	LYS	4.3

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Mol	Chain	Res	Type	RSRZ
2	B	56	ILE	4.2
3	C	63	GLY	4.1
1	A	795	ASP	4.1
5	E	83	HIS	4.1
1	A	125	LEU	4.0
1	A	42	ALA	4.0
2	B	265	GLY	4.0
1	A	501	LEU	4.0
2	B	242	ASP	3.9
2	B	283	LEU	3.8
3	C	45	ALA	3.7
4	D	77	TYR	3.7
4	D	152	ARG	3.7
5	E	111	SER	3.7
1	A	481	ASP	3.6
4	D	64	PHE	3.6
1	A	667	THR	3.6
5	E	69	GLY	3.6
5	E	41	ASN	3.6
1	A	507	LYS	3.6
4	D	203	ARG	3.5
1	A	725	ILE	3.5
2	B	284	GLY	3.5
4	D	97	ARG	3.5
1	A	787	TYR	3.5
2	B	37	THR	3.5
1	A	495	GLN	3.5
2	B	134	LEU	3.5
2	B	246	ASP	3.5
1	A	706	VAL	3.5
2	B	249	THR	3.4
1	A	279	GLY	3.4
1	A	513	VAL	3.4
4	D	78	ALA	3.3
1	A	664	GLN	3.3
4	D	190	ALA	3.3
4	D	75	LEU	3.3
5	E	76	VAL	3.3
2	B	141	VAL	3.3
1	A	557	SER	3.3
1	A	191	ASP	3.2
2	B	76	ASP	3.2

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Mol	Chain	Res	Type	RSRZ
2	B	273	ARG	3.2
3	C	60	VAL	3.2
2	B	376	GLY	3.2
2	B	103	TRP	3.2
4	D	59	ASP	3.2
1	A	165	LEU	3.2
4	D	169	PHE	3.2
1	A	176	GLU	3.2
1	A	529	LEU	3.2
1	A	796	GLY	3.2
1	A	73	GLU	3.2
1	A	710	ALA	3.1
2	B	111	LEU	3.1
1	A	666	ASN	3.1
1	A	500	ASP	3.1
1	A	520	ASN	3.0
5	E	98	SER	3.0
2	B	253	VAL	3.0
2	B	176	GLU	3.0
3	C	61	THR	3.0
5	E	40	ALA	3.0
1	A	370	ARG	3.0
1	A	41	ALA	3.0
1	A	679	ALA	3.0
2	B	245	SER	3.0
2	B	142	ALA	2.9
3	C	39	GLU	2.9
4	D	121	ASP	2.9
1	A	31	PHE	2.9
1	A	705	ALA	2.9
2	B	117	VAL	2.9
1	A	194	ILE	2.9
1	A	163	VAL	2.8
2	B	97	LEU	2.8
1	A	683	ASP	2.8
1	A	504	TYR	2.8
4	D	122	SER	2.8
4	D	133	SER	2.8
1	A	494	PHE	2.8
2	B	194	LEU	2.8
2	B	58	ASN	2.8
2	B	359	GLN	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	183	VAL	2.7
1	A	668	ILE	2.7
1	A	498	ASP	2.7
1	A	797	ASP	2.7
1	A	44	LEU	2.7
1	A	202	GLU	2.6
4	D	98	LEU	2.6
3	C	69	VAL	2.6
1	A	727	ASP	2.6
1	A	657	SER	2.6
2	B	54	SER	2.6
1	A	456	VAL	2.6
2	B	213	ASN	2.6
2	B	298	LEU	2.5
1	A	493	ASP	2.5
5	E	32	ILE	2.5
1	A	809	THR	2.5
2	B	290	ILE	2.5
1	A	190	THR	2.5
2	B	68	ALA	2.5
3	C	85	PRO	2.5
5	E	57	TYR	2.5
1	A	205	TRP	2.4
1	A	689	GLU	2.4
1	A	71	ASN	2.4
1	A	325	MET	2.4
1	A	711	MET	2.4
2	B	109	ALA	2.4
1	A	703	ASP	2.4
1	A	626	LYS	2.4
1	A	291	GLU	2.4
2	B	226	MET	2.4
3	C	46	PRO	2.4
1	A	449	TRP	2.4
2	B	146	LYS	2.3
5	E	29	ARG	2.3
1	A	211	ASP	2.3
2	B	320	SER	2.3
4	D	55	LEU	2.3
5	E	30	PRO	2.3
1	A	344	GLY	2.3
1	A	503	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
4	D	158	GLN	2.3
1	A	269	SER	2.3
1	A	381	LEU	2.3
1	A	743	THR	2.3
5	E	48	VAL	2.3
2	B	79	GLY	2.3
1	A	435	GLU	2.2
4	D	104	ASN	2.2
1	A	540	GLN	2.2
1	A	505	THR	2.2
1	A	654	ALA	2.2
3	C	66	ALA	2.2
2	B	163	LEU	2.2
4	D	109	MET	2.2
4	D	83	ALA	2.2
1	A	97	ILE	2.2
1	A	367	ARG	2.2
3	C	34	GLN	2.2
3	C	62	SER	2.2
2	B	244	LEU	2.2
1	A	461	THR	2.2
1	A	184	GLY	2.2
2	B	179	GLY	2.2
2	B	132	TYR	2.2
2	B	164	ILE	2.1
2	B	243	ARG	2.1
1	A	92	PRO	2.1
2	B	34	PRO	2.1
2	B	251	PRO	2.1
4	D	153	GLY	2.1
2	B	167	SER	2.1
3	C	40	ALA	2.1
1	A	335	VAL	2.1
2	B	177	ALA	2.1
5	E	53	GLN	2.1
1	A	555	HIS	2.1
3	C	44	ALA	2.1
1	A	372	MET	2.1
1	A	401	ASP	2.1
1	A	521	GLU	2.1
1	A	349	VAL	2.0
1	A	178	GLN	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	643	GLY	2.0
2	B	300	ASP	2.0
1	A	289	LYS	2.0
1	A	304	MET	2.0
1	A	25	VAL	2.0
2	B	286	VAL	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.