



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 08:14 AM UTC

PDB ID : 7EQI / pdb_00007eqi
Title : ChlB3 [Acetyltransferase]
Authors : Saeed, A.U.; Zheng, J.
Deposited on : 2021-05-02
Resolution : 3.10 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:

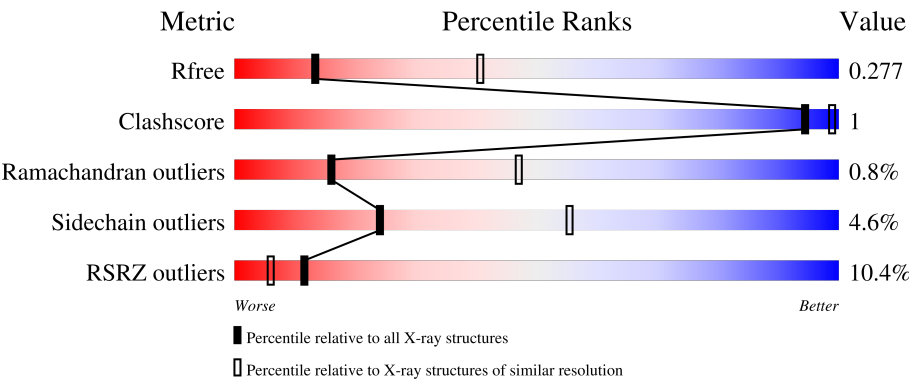
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

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 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	347	10% 92%
1	B	347	9% 90%
1	C	347	7% 91%
1	D	347	8% 88%
1	E	347	13% 87%

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Mol	Chain	Length	Quality of chain
1	F	347	12% 87% 7% 5%
1	G	347	10% 88% 6% 5%
1	H	347	10% 89% 5% 6%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 19137 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 ChlB3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	334	Total	C	N	O	S	0	0	0
			2371	1503	413	443	12			
1	B	335	Total	C	N	O	S	0	0	0
			2450	1550	429	458	13			
1	C	333	Total	C	N	O	S	0	0	0
			2412	1526	427	446	13			
1	D	329	Total	C	N	O	S	0	0	0
			2341	1487	407	434	13			
1	E	332	Total	C	N	O	S	0	0	0
			2324	1478	400	435	11			
1	F	329	Total	C	N	O	S	0	0	0
			2378	1508	415	443	12			
1	G	328	Total	C	N	O	S	0	0	0
			2384	1510	417	445	12			
1	H	327	Total	C	N	O	S	0	0	0
			2392	1515	419	446	12			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	11	Total	O	0	0
			11	11		
2	B	12	Total	O	0	0
			12	12		
2	C	14	Total	O	0	0
			14	14		
2	D	11	Total	O	0	0
			11	11		
2	E	10	Total	O	0	0
			10	10		
2	F	5	Total	O	0	0
			5	5		

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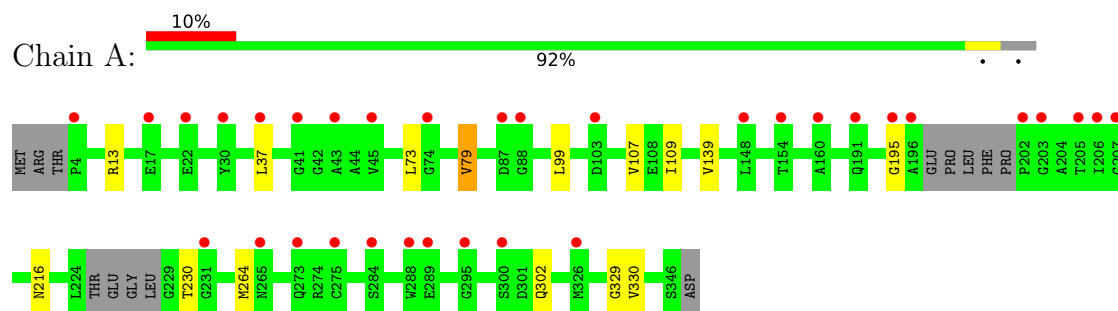
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	G	13	Total	O	0	0
			13	13		
2	H	9	Total	O	0	0
			9	9		

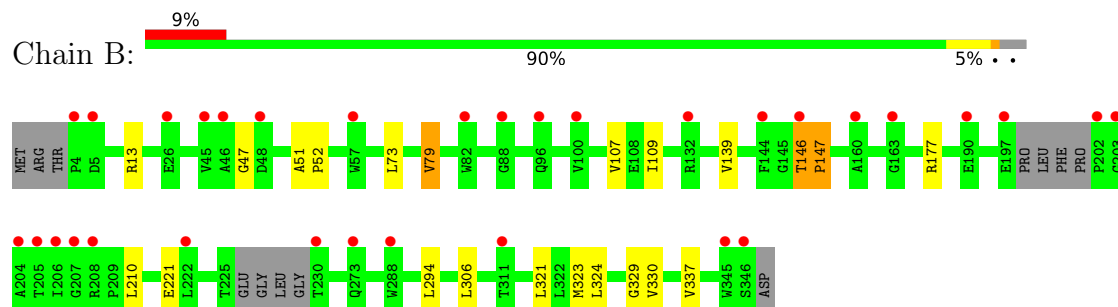
3 Residue-property plots [i](#)

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.

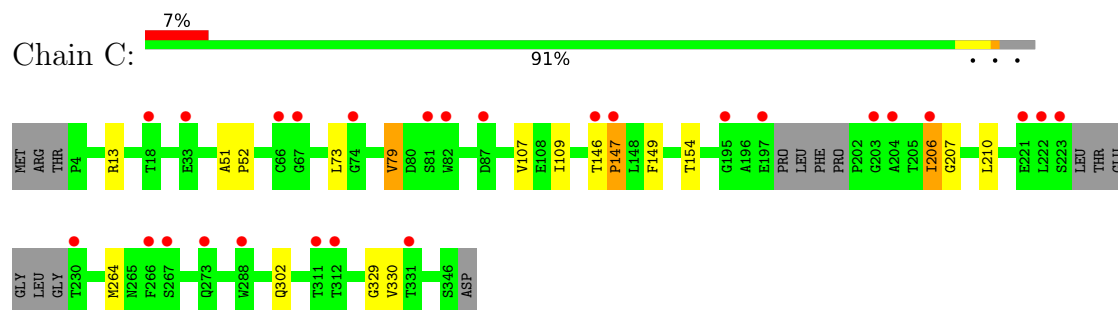
• Molecule 1: ChlB3



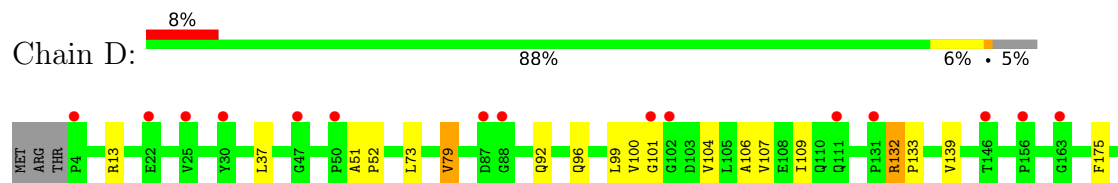
• Molecule 1: ChlB3

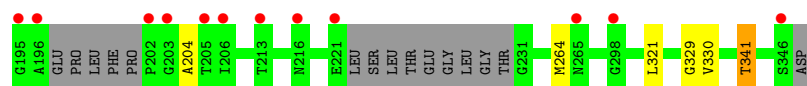


• Molecule 1: ChlB3

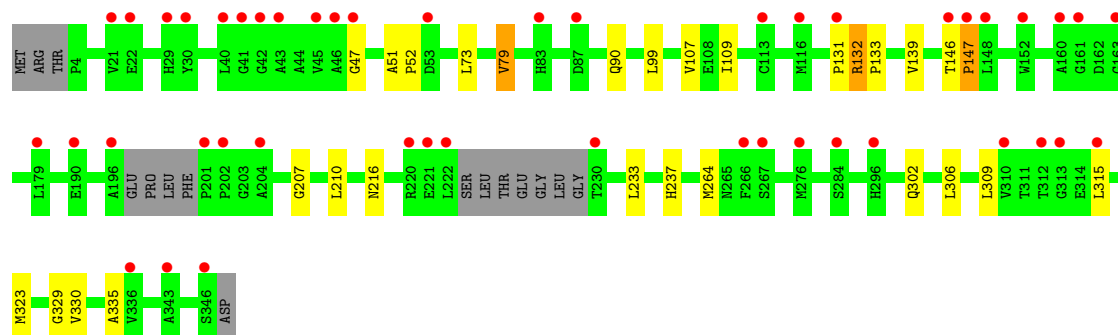
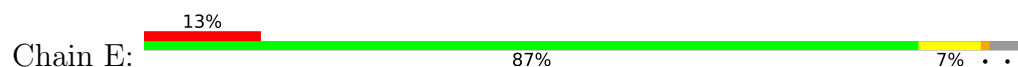


• Molecule 1: ChlB3

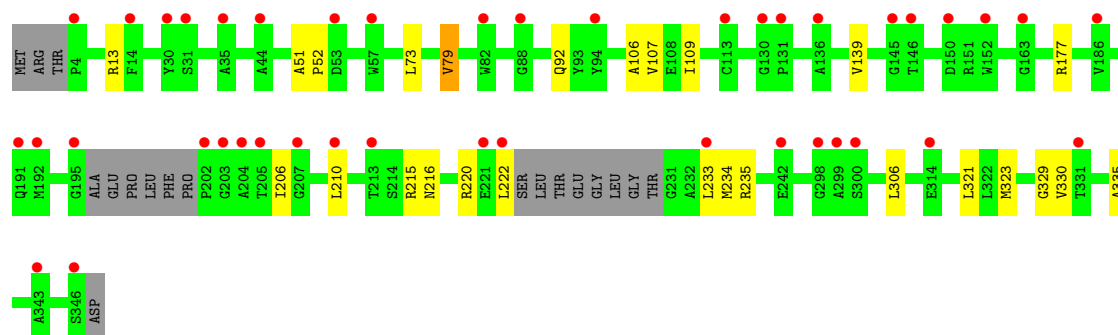
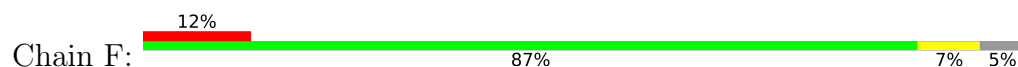




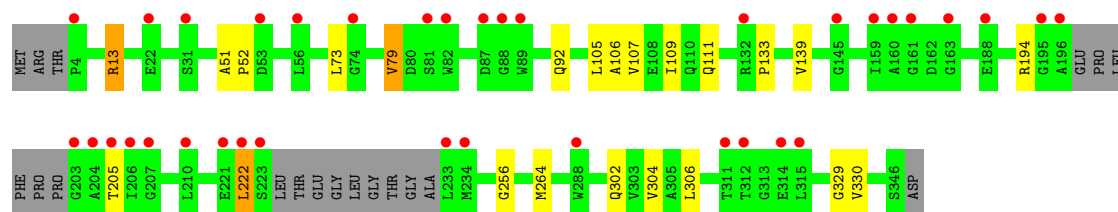
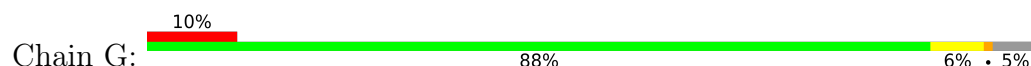
• Molecule 1: ChlB3



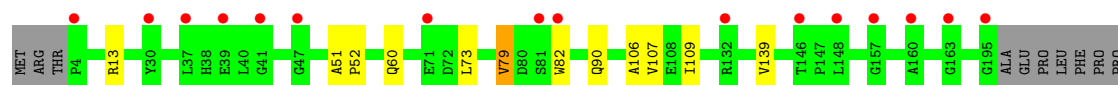
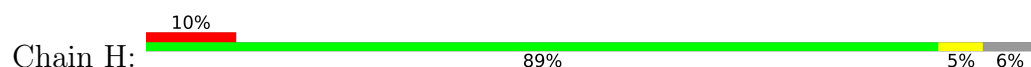
• Molecule 1: ChlB3

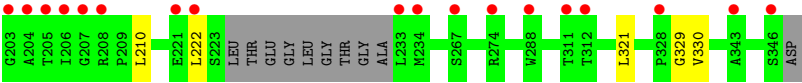


• Molecule 1: ChlB3



• Molecule 1: ChlB3





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	99.47Å 186.58Å 189.75Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 3.10 50.00 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.4 (50.00-3.10) 99.9 (50.00-3.10)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.94 (at 2.91Å)	Xtriage
Refinement program	REFMAC 5	Depositor
R, R_{free}	0.226 , 0.256 0.264 , 0.277	Depositor DCC
R_{free} test set	3931 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	70.4	Xtriage
Anisotropy	0.086	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 37.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.007 for -h,l,k	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	19137	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.92% 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	0.39	0/2428	0.65	0/3324
1	B	0.40	0/2507	0.67	0/3420
1	C	0.40	0/2469	0.66	0/3371
1	D	0.40	0/2398	0.66	0/3282
1	E	0.39	0/2381	0.67	0/3267
1	F	0.40	0/2435	0.69	0/3328
1	G	0.39	0/2440	0.65	0/3332
1	H	0.40	0/2448	0.66	0/3341
All	All	0.40	0/19506	0.66	0/26665

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	2371	0	2215	3	0
1	B	2450	0	2361	6	0
1	C	2412	0	2299	6	0
1	D	2341	0	2201	10	0
1	E	2324	0	2157	9	0
1	F	2378	0	2257	5	0
1	G	2384	0	2274	8	0
1	H	2392	0	2293	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	11	0	0	0	0
2	B	12	0	0	0	0
2	C	14	0	0	0	0
2	D	11	0	0	0	0
2	E	10	0	0	0	0
2	F	5	0	0	0	0
2	G	13	0	0	0	0
2	H	9	0	0	0	0
All	All	19137	0	18057	49	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 1.

All (49) 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:D:132:ARG:CB	1:D:133:PRO:CD	2.66	0.74
1:D:132:ARG:CB	1:D:133:PRO:HD2	2.26	0.66
1:B:146:THR:HB	1:B:147:PRO:HA	1.80	0.64
1:A:329:GLY:N	1:A:330:VAL:HA	2.22	0.55
1:E:132:ARG:CB	1:E:133:PRO:CD	2.86	0.53
1:C:329:GLY:N	1:C:330:VAL:HA	2.25	0.51
1:E:329:GLY:N	1:E:330:VAL:HA	2.25	0.51
1:B:329:GLY:N	1:B:330:VAL:HA	2.26	0.50
1:D:100:VAL:HG12	1:D:104:VAL:HG11	1.94	0.50
1:F:329:GLY:N	1:F:330:VAL:HA	2.26	0.50
1:D:79:VAL:HG12	1:D:109:ILE:HB	1.94	0.49
1:G:329:GLY:N	1:G:330:VAL:HA	2.27	0.49
1:D:329:GLY:N	1:D:330:VAL:HA	2.28	0.49
1:H:329:GLY:N	1:H:330:VAL:HA	2.26	0.49
1:F:79:VAL:HG12	1:F:109:ILE:HB	1.95	0.48
1:A:79:VAL:HG12	1:A:109:ILE:HB	1.94	0.48
1:G:13:ARG:HG3	1:G:304:VAL:HG23	1.96	0.48
1:C:79:VAL:HG12	1:C:109:ILE:HB	1.96	0.48
1:B:79:VAL:HG12	1:B:109:ILE:HB	1.95	0.47
1:E:233:LEU:O	1:E:237:HIS:ND1	2.46	0.47
1:H:79:VAL:HG12	1:H:109:ILE:HB	1.95	0.47
1:E:79:VAL:HG12	1:E:109:ILE:HB	1.96	0.47
1:G:79:VAL:HG12	1:G:109:ILE:HB	1.96	0.46
1:C:146:THR:N	1:C:147:PRO:HD3	2.31	0.46
1:D:96:GLN:HG2	1:D:101:GLY:HA2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:100:VAL:HG12	1:D:100:VAL:O	2.17	0.45
1:E:132:ARG:CB	1:E:133:PRO:HD2	2.48	0.44
1:G:222:LEU:C	1:G:222:LEU:HD22	2.43	0.44
1:A:230:THR:HG22	1:G:256:GLY:HA2	2.00	0.44
1:E:146:THR:N	1:E:147:PRO:HD3	2.32	0.44
1:F:323:MET:HE3	1:F:335:ALA:HB3	2.01	0.43
1:B:146:THR:HB	1:B:147:PRO:CA	2.48	0.43
1:E:309:LEU:HB3	1:E:315:LEU:HD23	2.00	0.43
1:C:206:ILE:HA	1:C:207:GLY:HA2	1.76	0.42
1:F:92:GLN:HG3	1:F:106:ALA:HB1	2.02	0.42
1:E:51:ALA:N	1:E:52:PRO:CD	2.83	0.41
1:D:51:ALA:N	1:D:52:PRO:CD	2.84	0.41
1:C:149:PHE:CE2	1:C:154:THR:HG21	2.56	0.41
1:G:111:GLN:NE2	1:H:106:ALA:O	2.52	0.41
1:C:51:ALA:N	1:C:52:PRO:CD	2.84	0.41
1:E:323:MET:HE3	1:E:335:ALA:HB3	2.03	0.41
1:G:51:ALA:N	1:G:52:PRO:CD	2.84	0.41
1:B:51:ALA:N	1:B:52:PRO:CD	2.84	0.41
1:D:92:GLN:HG3	1:D:106:ALA:HB1	2.03	0.41
1:B:323:MET:HE2	1:B:337:VAL:HG23	2.03	0.40
1:F:51:ALA:N	1:F:52:PRO:CD	2.84	0.40
1:G:92:GLN:HG3	1:G:106:ALA:HB1	2.03	0.40
1:D:175:PHE:HA	1:D:341:THR:HG22	2.03	0.40
1:H:51:ALA:N	1:H:52:PRO:CD	2.84	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	328/347 (94%)	303 (92%)	23 (7%)	2 (1%)	21 52

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	329/347 (95%)	306 (93%)	20 (6%)	3 (1%)	14	44
1	C	327/347 (94%)	302 (92%)	24 (7%)	1 (0%)	36	67
1	D	323/347 (93%)	300 (93%)	20 (6%)	3 (1%)	14	44
1	E	326/347 (94%)	303 (93%)	17 (5%)	6 (2%)	6	28
1	F	323/347 (93%)	301 (93%)	20 (6%)	2 (1%)	21	52
1	G	322/347 (93%)	298 (92%)	21 (6%)	3 (1%)	14	44
1	H	321/347 (92%)	308 (96%)	13 (4%)	0	100	100
All	All	2599/2776 (94%)	2421 (93%)	158 (6%)	20 (1%)	16	47

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	132	ARG
1	E	132	ARG
1	E	147	PRO
1	E	207	GLY
1	F	206	ILE
1	D	204	ALA
1	F	220	ARG
1	G	133	PRO
1	B	146	THR
1	G	205	THR
1	C	147	PRO
1	D	99	LEU
1	E	99	LEU
1	G	194	ARG
1	A	99	LEU
1	E	131	PRO
1	A	195	GLY
1	B	47	GLY
1	E	47	GLY
1	B	147	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	221/265 (83%)	212 (96%)	9 (4%)	27	59
1	B	241/265 (91%)	229 (95%)	12 (5%)	22	53
1	C	231/265 (87%)	223 (96%)	8 (4%)	32	62
1	D	220/265 (83%)	211 (96%)	9 (4%)	27	59
1	E	214/265 (81%)	204 (95%)	10 (5%)	23	55
1	F	228/265 (86%)	213 (93%)	15 (7%)	15	43
1	G	231/265 (87%)	221 (96%)	10 (4%)	26	57
1	H	234/265 (88%)	223 (95%)	11 (5%)	23	55
All	All	1820/2120 (86%)	1736 (95%)	84 (5%)	24	55

All (84) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	ARG
1	A	37	LEU
1	A	73	LEU
1	A	79	VAL
1	A	107	VAL
1	A	139	VAL
1	A	216	ASN
1	A	264	MET
1	A	302	GLN
1	B	13	ARG
1	B	73	LEU
1	B	79	VAL
1	B	107	VAL
1	B	139	VAL
1	B	177	ARG
1	B	210	LEU
1	B	221	GLU
1	B	294	LEU
1	B	306	LEU
1	B	321	LEU
1	B	324	LEU
1	C	13	ARG
1	C	73	LEU
1	C	79	VAL
1	C	107	VAL

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Mol	Chain	Res	Type
1	C	206	ILE
1	C	210	LEU
1	C	264	MET
1	C	302	GLN
1	D	13	ARG
1	D	37	LEU
1	D	73	LEU
1	D	79	VAL
1	D	107	VAL
1	D	139	VAL
1	D	264	MET
1	D	321	LEU
1	D	341	THR
1	E	73	LEU
1	E	79	VAL
1	E	90	GLN
1	E	107	VAL
1	E	139	VAL
1	E	210	LEU
1	E	216	ASN
1	E	264	MET
1	E	302	GLN
1	E	306	LEU
1	F	13	ARG
1	F	73	LEU
1	F	79	VAL
1	F	107	VAL
1	F	139	VAL
1	F	177	ARG
1	F	210	LEU
1	F	215	ARG
1	F	216	ASN
1	F	222	LEU
1	F	233	LEU
1	F	234	MET
1	F	235	ARG
1	F	306	LEU
1	F	321	LEU
1	G	13	ARG
1	G	73	LEU
1	G	79	VAL
1	G	105	LEU

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Mol	Chain	Res	Type
1	G	107	VAL
1	G	139	VAL
1	G	222	LEU
1	G	264	MET
1	G	302	GLN
1	G	306	LEU
1	H	13	ARG
1	H	60	GLN
1	H	73	LEU
1	H	79	VAL
1	H	82	TRP
1	H	90	GLN
1	H	107	VAL
1	H	139	VAL
1	H	210	LEU
1	H	222	LEU
1	H	321	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (35) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	83	HIS
1	A	90	GLN
1	A	110	GLN
1	A	216	ASN
1	A	273	GLN
1	B	83	HIS
1	B	216	ASN
1	B	238	GLN
1	C	83	HIS
1	C	90	GLN
1	C	110	GLN
1	C	211	ASN
1	D	83	HIS
1	D	110	GLN
1	D	211	ASN
1	D	216	ASN
1	D	238	GLN
1	E	83	HIS
1	E	90	GLN
1	E	191	GLN
1	E	216	ASN

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Mol	Chain	Res	Type
1	F	83	HIS
1	F	110	GLN
1	F	211	ASN
1	F	216	ASN
1	G	83	HIS
1	G	98	HIS
1	G	110	GLN
1	G	191	GLN
1	H	60	GLN
1	H	83	HIS
1	H	90	GLN
1	H	110	GLN
1	H	211	ASN
1	H	238	GLN

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 [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	334/347 (96%)	0.88	33 (9%) 13 7	44, 63, 94, 129	0
1	B	335/347 (96%)	0.83	32 (9%) 13 7	40, 55, 83, 106	0
1	C	333/347 (95%)	0.72	26 (7%) 19 10	40, 56, 84, 109	0
1	D	329/347 (94%)	0.75	27 (8%) 17 10	40, 54, 82, 102	0
1	E	332/347 (95%)	1.15	46 (13%) 6 4	50, 76, 100, 138	0
1	F	329/347 (94%)	1.00	42 (12%) 7 4	49, 72, 100, 129	0
1	G	328/347 (94%)	0.95	36 (10%) 10 5	45, 69, 103, 133	0
1	H	327/347 (94%)	0.93	34 (10%) 11 6	42, 65, 92, 136	0
All	All	2647/2776 (95%)	0.90	276 (10%) 11 6	40, 64, 95, 138	0

All (276) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	201	PRO	6.2
1	A	206	ILE	5.8
1	E	41	GLY	5.8
1	B	206	ILE	5.6
1	A	202	PRO	5.4
1	B	202	PRO	5.3
1	H	206	ILE	5.2
1	C	206	ILE	5.1
1	G	233	LEU	5.1
1	E	146	THR	5.1
1	F	202	PRO	5.1
1	G	206	ILE	5.0
1	H	195	GLY	4.9
1	G	196	ALA	4.9
1	G	163	GLY	4.8
1	H	207	GLY	4.7

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Mol	Chain	Res	Type	RSRZ
1	G	288	TRP	4.7
1	B	146	THR	4.7
1	E	42	GLY	4.7
1	E	222	LEU	4.6
1	F	222	LEU	4.5
1	F	207	GLY	4.5
1	F	195	GLY	4.5
1	D	206	ILE	4.5
1	C	197	GLU	4.4
1	C	146	THR	4.4
1	A	196	ALA	4.2
1	H	146	THR	4.2
1	A	207	GLY	4.1
1	D	101	GLY	4.1
1	E	131	PRO	3.9
1	B	207	GLY	3.9
1	E	346	SER	3.9
1	F	31	SER	3.9
1	E	29	HIS	3.8
1	B	163	GLY	3.8
1	H	160	ALA	3.7
1	G	207	GLY	3.7
1	E	160	ALA	3.7
1	A	103	ASP	3.6
1	D	22	GLU	3.6
1	A	43	ALA	3.6
1	D	102	GLY	3.6
1	A	74	GLY	3.5
1	B	197	GLU	3.5
1	H	205	THR	3.5
1	G	204	ALA	3.5
1	E	147	PRO	3.5
1	F	163	GLY	3.4
1	F	146	THR	3.4
1	D	25	VAL	3.4
1	H	157	GLY	3.4
1	F	186	VAL	3.3
1	D	4	PRO	3.3
1	D	221	GLU	3.3
1	A	87	ASP	3.3
1	E	30	TYR	3.3
1	H	204	ALA	3.3

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Mol	Chain	Res	Type	RSRZ
1	F	343	ALA	3.3
1	C	147	PRO	3.3
1	B	311	THR	3.3
1	A	41	GLY	3.3
1	F	30	TYR	3.3
1	C	288	TRP	3.2
1	H	203	GLY	3.2
1	G	222	LEU	3.2
1	E	87	ASP	3.2
1	E	230	THR	3.2
1	G	223	SER	3.2
1	C	203	GLY	3.2
1	H	4	PRO	3.1
1	D	196	ALA	3.1
1	H	233	LEU	3.1
1	C	195	GLY	3.1
1	E	161	GLY	3.1
1	H	163	GLY	3.1
1	F	88	GLY	3.1
1	E	47	GLY	3.0
1	G	145	GLY	3.0
1	D	156	PRO	3.0
1	C	221	GLU	3.0
1	F	298	GLY	3.0
1	A	22	GLU	3.0
1	A	195	GLY	3.0
1	F	145	GLY	3.0
1	C	204	ALA	2.9
1	E	43	ALA	2.9
1	B	45	VAL	2.9
1	D	203	GLY	2.9
1	H	47	GLY	2.9
1	C	311	THR	2.9
1	H	132	ARG	2.9
1	C	87	ASP	2.9
1	H	312	THR	2.9
1	H	30	TYR	2.9
1	F	14	PHE	2.9
1	D	47	GLY	2.9
1	H	81	SER	2.9
1	E	113	CYS	2.9
1	B	144	PHE	2.8

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Mol	Chain	Res	Type	RSRZ
1	E	83	HIS	2.8
1	H	267	SER	2.8
1	B	5	ASP	2.8
1	D	205	THR	2.8
1	H	82	TRP	2.8
1	H	288	TRP	2.8
1	H	41	GLY	2.8
1	G	88	GLY	2.8
1	H	39	GLU	2.8
1	G	89	TRP	2.7
1	B	160	ALA	2.7
1	H	343	ALA	2.7
1	A	148	LEU	2.7
1	C	312	THR	2.7
1	F	221	GLU	2.7
1	B	4	PRO	2.7
1	A	191	GLN	2.7
1	F	4	PRO	2.7
1	G	132	ARG	2.7
1	E	21	VAL	2.7
1	E	313	GLY	2.7
1	B	57	TRP	2.7
1	G	160	ALA	2.7
1	C	82	TRP	2.6
1	F	150	ASP	2.6
1	G	56	LEU	2.6
1	F	205	THR	2.6
1	F	94	TYR	2.6
1	A	37	LEU	2.6
1	E	152	TRP	2.6
1	D	131	PRO	2.6
1	B	46	ALA	2.6
1	F	213	THR	2.6
1	C	223	SER	2.5
1	A	88	GLY	2.5
1	B	88	GLY	2.5
1	D	87	ASP	2.5
1	E	312	THR	2.5
1	A	284	SER	2.5
1	B	26	GLU	2.5
1	E	196	ALA	2.5
1	G	87	ASP	2.5

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Mol	Chain	Res	Type	RSRZ
1	G	159	ILE	2.5
1	A	30	TYR	2.5
1	A	295	GLY	2.5
1	C	74	GLY	2.5
1	E	45	VAL	2.5
1	E	46	ALA	2.5
1	G	188	GLU	2.5
1	D	146	THR	2.5
1	G	205	THR	2.5
1	H	222	LEU	2.5
1	D	195	GLY	2.5
1	G	195	GLY	2.5
1	D	202	PRO	2.4
1	C	81	SER	2.4
1	E	221	GLU	2.4
1	G	22	GLU	2.4
1	G	210	LEU	2.4
1	B	345	TRP	2.4
1	C	230	THR	2.4
1	B	205	THR	2.4
1	F	82	TRP	2.4
1	G	312	THR	2.4
1	E	310	VAL	2.4
1	E	163	GLY	2.4
1	C	66	CYS	2.4
1	A	288	TRP	2.4
1	G	82	TRP	2.4
1	F	331	THR	2.4
1	B	48	ASP	2.4
1	G	203	GLY	2.4
1	A	275	CYS	2.4
1	F	152	TRP	2.4
1	D	213	THR	2.3
1	F	130	GLY	2.3
1	E	179	LEU	2.3
1	E	266	PHE	2.3
1	F	242	GLU	2.3
1	B	288	TRP	2.3
1	A	205	THR	2.3
1	E	276	MET	2.3
1	G	234	MET	2.3
1	E	315	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	F	210	LEU	2.3
1	G	315	LEU	2.3
1	C	33	GLU	2.3
1	E	202	PRO	2.3
1	A	160	ALA	2.3
1	A	326	MET	2.3
1	D	30	TYR	2.3
1	G	314	GLU	2.3
1	F	204	ALA	2.3
1	D	216	ASN	2.3
1	A	289	GLU	2.3
1	H	221	GLU	2.3
1	D	298	GLY	2.3
1	G	161	GLY	2.3
1	E	148	LEU	2.3
1	C	267	SER	2.3
1	D	88	GLY	2.2
1	F	299	ALA	2.2
1	G	74	GLY	2.2
1	H	311	THR	2.2
1	B	190	GLU	2.2
1	H	71	GLU	2.2
1	E	40	LEU	2.2
1	F	44	ALA	2.2
1	A	300	SER	2.2
1	B	346	SER	2.2
1	A	4	PRO	2.2
1	B	222	LEU	2.2
1	F	131	PRO	2.2
1	F	300	SER	2.2
1	A	17	GLU	2.2
1	D	265	ASN	2.2
1	H	148	LEU	2.2
1	E	343	ALA	2.2
1	H	328	PRO	2.2
1	A	154	THR	2.2
1	B	230	THR	2.2
1	B	273	GLN	2.2
1	H	346	SER	2.2
1	A	265	ASN	2.2
1	G	4	PRO	2.2
1	B	208	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	F	113	CYS	2.2
1	E	296	HIS	2.2
1	A	273	GLN	2.1
1	G	31	SER	2.1
1	G	221	GLU	2.1
1	E	336	VAL	2.1
1	H	234	MET	2.1
1	B	203	GLY	2.1
1	E	267	SER	2.1
1	C	18	THR	2.1
1	B	132	ARG	2.1
1	F	192	MET	2.1
1	B	204	ALA	2.1
1	E	204	ALA	2.1
1	D	163	GLY	2.1
1	B	82	TRP	2.1
1	H	208	ARG	2.1
1	F	35	ALA	2.1
1	B	96	GLN	2.1
1	D	111	GLN	2.1
1	F	191	GLN	2.1
1	C	266	PHE	2.1
1	E	22	GLU	2.1
1	F	346	SER	2.1
1	G	81	SER	2.1
1	F	57	TRP	2.1
1	C	331	THR	2.1
1	G	311	THR	2.1
1	A	203	GLY	2.1
1	C	273	GLN	2.1
1	E	190	GLU	2.1
1	D	346	SER	2.0
1	B	100	VAL	2.0
1	E	220	ARG	2.0
1	F	233	LEU	2.0
1	E	284	SER	2.0
1	E	116	MET	2.0
1	F	136	ALA	2.0
1	E	53	ASP	2.0
1	F	53	ASP	2.0
1	G	53	ASP	2.0
1	A	231	GLY	2.0

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Mol	Chain	Res	Type	RSRZ
1	C	67	GLY	2.0
1	F	203	GLY	2.0
1	D	50	PRO	2.0
1	A	45	VAL	2.0
1	F	314	GLU	2.0
1	H	274	ARG	2.0
1	C	222	LEU	2.0
1	H	37	LEU	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.