



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 22, 2024 – 11:19 PM EDT

PDB ID : 6RFY
Title : Crystal structure of Eis2 form Mycobacterium abscessus
Authors : Blaise, M.; Kremer, L.; Olieric, V.; Alsarraf, H.; Ung, K.L.
Deposited on : 2019-04-16
Resolution : 2.20 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 : 4.02b-467
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 1.20.1
EDS : 2.37.1
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) : 2.37.1

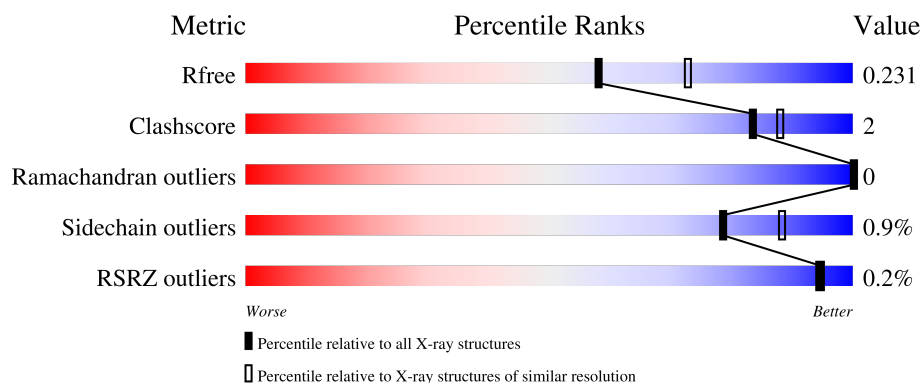
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


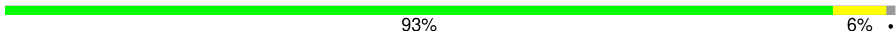
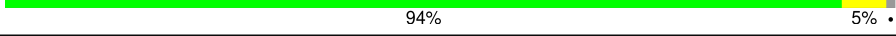
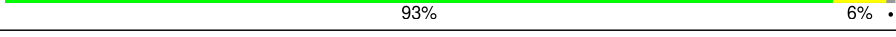

The reported resolution of this entry is 2.20 Å.

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}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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	411	 91% 8% .
1	B	411	 93% 6% .
1	C	411	 94% 5% .
1	D	411	 93% 6% .
1	E	411	 91% 8% .

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	411	 A horizontal bar chart showing the quality of the chain. The bar is divided into three segments: a long green segment representing 90%, a short yellow segment representing 8%, and a very short grey segment representing the remaining 2%. The percentages '90%' and '8%' are printed below the green and yellow segments respectively. A small black dot is visible at the end of the grey segment.

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 19964 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 Eis2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	405	Total	C	N	O	S	0	0	0
			3146	1982	551	603	10			
1	B	405	Total	C	N	O	S	0	0	0
			3147	1984	551	602	10			
1	C	406	Total	C	N	O	S	0	0	0
			3151	1986	552	603	10			
1	D	407	Total	C	N	O	S	0	0	0
			3156	1989	553	604	10			
1	E	404	Total	C	N	O	S	0	0	0
			3140	1979	550	601	10			
1	F	404	Total	C	N	O	S	0	0	0
			3138	1979	550	599	10			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	expression tag	UNP A0A3A1BNP8
B	1	GLY	-	expression tag	UNP A0A3A1BNP8
C	1	GLY	-	expression tag	UNP A0A3A1BNP8
D	1	GLY	-	expression tag	UNP A0A3A1BNP8
E	1	GLY	-	expression tag	UNP A0A3A1BNP8
F	1	GLY	-	expression tag	UNP A0A3A1BNP8

- Molecule 2 is 2-[BIS-(2-HYDROXY-ETHYL)-AMINO]-2-HYDROXYMETHYL-PROPAN E-1,3-DIOL (three-letter code: BTB) (formula: C₈H₁₉NO₅).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	D	1	Total	C	N	O	0	0
			14	8	1	5		
2	E	1	Total	C	N	O	0	0
			14	8	1	5		
2	F	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0
3	C	1	Total O S 5 4 1	0	0
3	D	1	Total O S 5 4 1	0	0
3	E	1	Total O S 5 4 1	0	0
3	F	1	Total O S 5 4 1	0	0

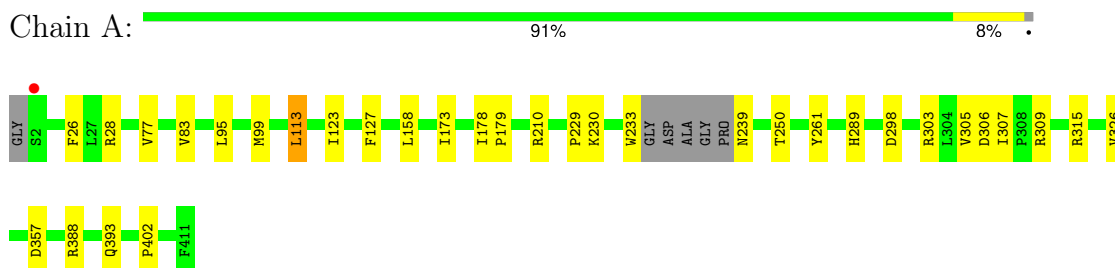
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	193	Total O 193 193	0	0
4	B	194	Total O 194 194	0	0
4	C	174	Total O 174 174	0	0
4	D	167	Total O 167 167	0	0
4	E	157	Total O 157 157	0	0
4	F	101	Total O 101 101	0	0

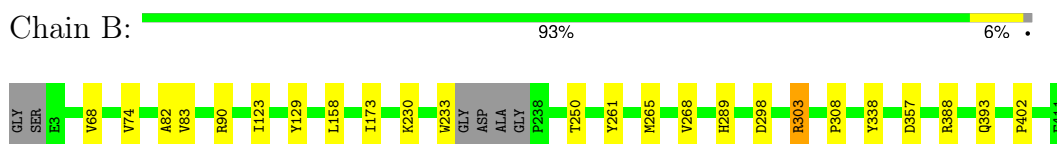
3 Residue-property plots [i](#)

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.

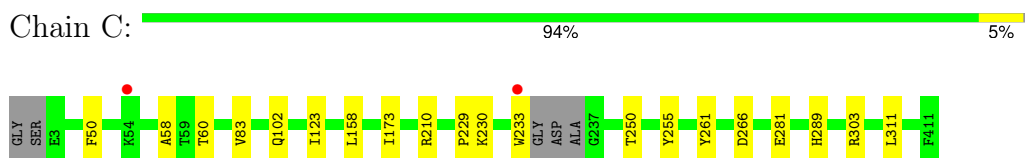
- Molecule 1: Eis2



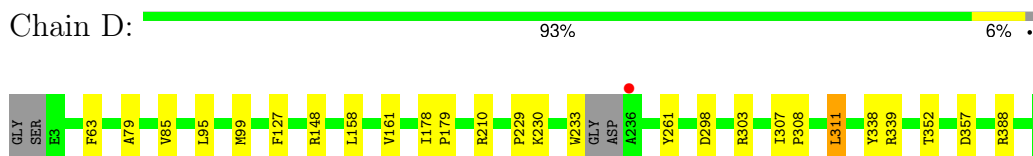
- Molecule 1: Eis2



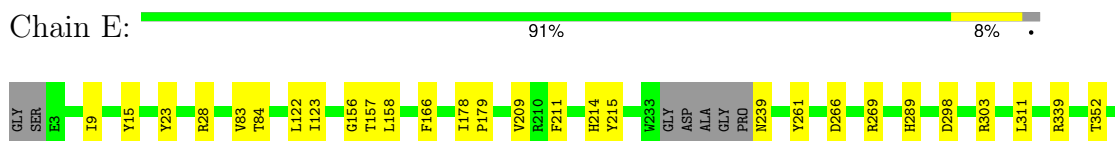
- Molecule 1: Eis2



- Molecule 1: Eis2

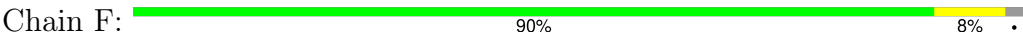


- Molecule 1: Eis2





● Molecule 1: Eis2



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	112.69Å 79.86Å 152.83Å 90.00° 90.24° 90.00°	Depositor
Resolution (Å)	49.52 – 2.20 49.52 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.9 (49.52-2.20) 99.9 (49.52-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.33 (at 2.20Å)	Xtriage
Refinement program	PHENIX (1.15rc3_3435: ???)	Depositor
R, R_{free}	0.199 , 0.230 0.202 , 0.231	Depositor DCC
R_{free} test set	2006 reflections (1.45%)	wwPDB-VP
Wilson B-factor (Å ²)	42.3	Xtriage
Anisotropy	0.312	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 29.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.025 for h,-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	19964	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 4.33% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, BTB

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	0.25	0/3213	0.45	0/4368
1	B	0.25	0/3215	0.45	0/4371
1	C	0.25	0/3219	0.45	0/4377
1	D	0.25	0/3224	0.45	0/4384
1	E	0.25	0/3207	0.45	0/4360
1	F	0.25	0/3206	0.45	0/4359
All	All	0.25	0/19284	0.45	0/26219

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	3146	0	3082	19	0
1	B	3147	0	3085	15	0
1	C	3151	0	3087	9	0
1	D	3156	0	3092	13	0
1	E	3140	0	3077	16	0
1	F	3138	0	3079	18	0
2	A	14	0	19	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	14	0	19	2	0
2	D	14	0	19	3	0
2	E	14	0	19	3	0
2	F	14	0	19	2	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
3	C	5	0	0	0	0
3	D	5	0	0	0	0
3	E	5	0	0	0	0
3	F	5	0	0	0	0
4	A	193	0	0	2	0
4	B	194	0	0	0	0
4	C	174	0	0	0	0
4	D	167	0	0	1	0
4	E	157	0	0	0	0
4	F	101	0	0	0	0
All	All	19964	0	18597	91	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 2.

All (91) 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:F:112:SER:HB3	1:F:309:ARG:HH11	1.54	0.73
1:B:90:ARG:NH2	1:E:266:ASP:OD1	2.26	0.64
1:A:239:ASN:N	4:A:602:HOH:O	2.33	0.61
1:A:402:PRO:HG2	1:B:393:GLN:HG2	1.82	0.60
1:A:393:GLN:HG2	1:B:402:PRO:HG2	1.86	0.58
1:A:158:LEU:HD13	1:A:261:TYR:HB2	1.88	0.56
1:C:158:LEU:HD13	1:C:261:TYR:HB2	1.88	0.55
1:B:173:ILE:HG23	1:B:250:THR:HG23	1.88	0.54
1:C:83:VAL:HG11	1:C:123:ILE:HD13	1.89	0.54
1:D:63:PHE:HB2	1:D:79:ALA:HB3	1.90	0.54
1:F:282:LEU:HA	1:F:285:LEU:HD22	1.90	0.53
1:E:158:LEU:HD13	1:E:261:TYR:HB2	1.90	0.53
1:D:148:ARG:NH2	4:D:607:HOH:O	2.43	0.52
1:E:84:THR:HA	1:E:122:LEU:HD12	1.92	0.52
1:F:307:ILE:HD13	1:F:326:VAL:HG11	1.91	0.51
1:A:357:ASP:OD1	1:A:388:ARG:HD3	2.11	0.50
1:B:308:PRO:HG3	1:B:338:TYR:CE1	2.47	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:357:ASP:OD1	1:D:388:ARG:HD3	2.12	0.49
1:E:83:VAL:HG11	1:E:123:ILE:HD13	1.94	0.49
1:A:306:ASP:OD2	1:A:309:ARG:HD3	2.12	0.49
1:A:77:VAL:HG23	1:A:113:LEU:HD13	1.94	0.49
1:C:210:ARG:HD3	1:C:229:PRO:HD3	1.95	0.48
1:E:339:ARG:HB2	1:E:352:THR:HG21	1.96	0.48
1:B:158:LEU:HD13	1:B:261:TYR:HB2	1.95	0.48
1:F:198:ASP:OD1	1:F:209:VAL:HG23	2.13	0.48
1:A:230:LYS:HE3	1:A:233:TRP:CZ3	2.49	0.47
1:D:339:ARG:HB2	1:D:352:THR:HG21	1.94	0.47
1:F:357:ASP:OD1	1:F:388:ARG:HD3	2.15	0.47
1:F:83:VAL:HG11	1:F:123:ILE:HD13	1.97	0.47
1:A:173:ILE:HG23	1:A:250:THR:HG23	1.97	0.47
1:F:158:LEU:HD13	1:F:261:TYR:HB2	1.96	0.47
1:B:357:ASP:OD1	1:B:388:ARG:HD3	2.15	0.46
1:F:230:LYS:HE3	1:F:233:TRP:CH2	2.51	0.46
1:F:161:VAL:HG21	1:F:165:THR:HG21	1.97	0.46
2:B:501:BTB:H12	2:B:501:BTB:H72	1.55	0.46
2:E:501:BTB:H52	2:E:501:BTB:H31	1.77	0.46
1:D:99:MET:HG2	1:D:127:PHE:CD2	2.51	0.46
2:D:501:BTB:H52	2:D:501:BTB:H31	1.74	0.46
1:A:309:ARG:NH2	4:A:613:HOH:O	2.49	0.45
1:B:129:TYR:CE2	1:B:303:ARG:HB2	2.52	0.45
2:A:501:BTB:H51	2:A:501:BTB:H32	1.68	0.45
1:D:158:LEU:HD13	1:D:261:TYR:HB2	1.97	0.45
1:F:210:ARG:HD3	1:F:229:PRO:HD3	1.97	0.45
1:E:166:PHE:CD1	1:E:211:PHE:HB3	2.51	0.45
1:A:99:MET:HG2	1:A:127:PHE:CD2	2.52	0.45
2:D:501:BTB:H12	2:D:501:BTB:H72	1.57	0.45
1:E:23:TYR:HE1	1:E:28:ARG:NH2	2.15	0.45
1:E:9:ILE:HD13	1:E:15:TYR:HA	1.99	0.44
2:F:501:BTB:H72	2:F:501:BTB:H11	1.53	0.44
1:B:83:VAL:HG11	1:B:123:ILE:HD13	1.99	0.44
2:E:501:BTB:H12	2:E:501:BTB:H72	1.61	0.44
1:C:60:THR:HG22	1:C:102:GLN:HE21	1.81	0.44
1:C:289:HIS:HB2	1:D:298:ASP:OD2	2.17	0.44
1:D:210:ARG:HD3	1:D:229:PRO:HD3	2.00	0.44
1:F:308:PRO:HG3	1:F:338:TYR:CE1	2.53	0.44
1:C:50:PHE:HB2	1:C:58:ALA:HB3	2.00	0.44
1:F:281:GLU:O	1:F:285:LEU:HD13	2.18	0.44
1:B:230:LYS:HE3	1:B:233:TRP:CH2	2.53	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:308:PRO:HG3	1:D:338:TYR:CE1	2.53	0.44
1:E:156:GLY:HA3	1:E:214:HIS:NE2	2.33	0.43
1:C:255:TYR:CE2	1:C:281:GLU:HB2	2.53	0.43
1:A:289:HIS:HB2	1:B:298:ASP:OD2	2.19	0.43
1:A:315:ARG:HA	1:A:315:ARG:HD3	1.80	0.43
1:D:307:ILE:O	1:D:311:LEU:HD22	2.19	0.42
1:B:265:MET:HB3	1:B:268:VAL:HG21	2.00	0.42
1:A:307:ILE:HD13	1:A:326:VAL:HG11	2.02	0.42
1:C:230:LYS:HE3	1:C:233:TRP:CH2	2.54	0.42
1:D:178:ILE:HG13	1:D:179:PRO:HD3	2.01	0.42
2:E:501:BTB:H71	2:E:501:BTB:H61	1.54	0.42
2:D:501:BTB:H71	2:D:501:BTB:H61	1.52	0.42
1:E:157:THR:HG23	1:E:215:TYR:HB2	2.02	0.42
1:E:239:ASN:HA	1:E:269:ARG:HG3	2.02	0.42
1:F:173:ILE:HG23	1:F:250:THR:HG23	2.01	0.42
1:B:68:VAL:HG22	1:B:74:VAL:HG22	2.00	0.42
1:E:402:PRO:HG2	1:F:393:GLN:HG2	2.01	0.42
1:A:298:ASP:OD2	1:B:289:HIS:HB2	2.19	0.42
1:B:82:ALA:HA	2:B:501:BTB:H81	2.02	0.42
1:D:85:VAL:CG2	1:D:95:LEU:HG	2.50	0.41
1:D:230:LYS:HE3	1:D:233:TRP:CZ3	2.54	0.41
1:A:83:VAL:HG11	1:A:123:ILE:HD13	2.01	0.41
1:A:210:ARG:HD3	1:A:229:PRO:HD3	2.02	0.41
1:E:298:ASP:OD2	1:F:289:HIS:HB2	2.21	0.41
1:C:173:ILE:HG23	1:C:250:THR:HG23	2.03	0.41
1:A:26:PHE:O	1:A:28:ARG:HG3	2.21	0.41
1:F:178:ILE:HG13	1:F:179:PRO:HD3	2.02	0.41
1:E:178:ILE:HG13	1:E:179:PRO:HD3	2.02	0.41
1:E:289:HIS:HB2	1:F:298:ASP:OD2	2.21	0.41
1:E:357:ASP:OD1	1:E:388:ARG:HD3	2.21	0.41
1:A:178:ILE:HG13	1:A:179:PRO:HD3	2.02	0.41
1:F:106:ILE:HG23	1:F:111:GLU:HB2	2.02	0.41
2:F:501:BTB:H32	2:F:501:BTB:H51	1.82	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	401/411 (98%)	396 (99%)	5 (1%)	0	100	100
1	B	401/411 (98%)	395 (98%)	6 (2%)	0	100	100
1	C	402/411 (98%)	396 (98%)	6 (2%)	0	100	100
1	D	403/411 (98%)	398 (99%)	5 (1%)	0	100	100
1	E	400/411 (97%)	395 (99%)	5 (1%)	0	100	100
1	F	400/411 (97%)	393 (98%)	7 (2%)	0	100	100
All	All	2407/2466 (98%)	2373 (99%)	34 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	330/332 (99%)	326 (99%)	4 (1%)	71	83
1	B	330/332 (99%)	329 (100%)	1 (0%)	92	97
1	C	330/332 (99%)	327 (99%)	3 (1%)	78	88
1	D	330/332 (99%)	327 (99%)	3 (1%)	78	88
1	E	329/332 (99%)	326 (99%)	3 (1%)	78	88
1	F	329/332 (99%)	325 (99%)	4 (1%)	71	83
All	All	1978/1992 (99%)	1960 (99%)	18 (1%)	78	88

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	95	LEU
1	A	113	LEU
1	A	303	ARG
1	A	305	VAL
1	B	303	ARG
1	C	266	ASP
1	C	303	ARG
1	C	311	LEU
1	D	161	VAL
1	D	303	ARG
1	D	311	LEU
1	E	209	VAL
1	E	303	ARG
1	E	311	LEU
1	F	161	VAL
1	F	285	LEU
1	F	303	ARG
1	F	311	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

11 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and

the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	SO4	E	502	-	4,4,4	0.24	0	6,6,6	0.13	0
2	BTB	B	501	-	13,13,13	0.54	0	7,16,16	0.75	0
3	SO4	B	502	-	4,4,4	0.24	0	6,6,6	0.08	0
3	SO4	D	502	-	4,4,4	0.23	0	6,6,6	0.11	0
3	SO4	A	502	-	4,4,4	0.23	0	6,6,6	0.05	0
3	SO4	F	502	-	4,4,4	0.23	0	6,6,6	0.12	0
2	BTB	E	501	-	13,13,13	0.47	0	7,16,16	0.46	0
2	BTB	D	501	-	13,13,13	0.49	0	7,16,16	0.47	0
3	SO4	C	501	-	4,4,4	0.24	0	6,6,6	0.13	0
2	BTB	F	501	-	13,13,13	0.52	0	7,16,16	0.55	0
2	BTB	A	501	-	13,13,13	0.54	0	7,16,16	0.49	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	BTB	B	501	-	-	12/21/21/21	-
2	BTB	E	501	-	-	7/21/21/21	-
2	BTB	D	501	-	-	7/21/21/21	-
2	BTB	F	501	-	-	4/21/21/21	-
2	BTB	A	501	-	-	1/21/21/21	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (31) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	501	BTB	O1-C1-C2-C3
2	B	501	BTB	O1-C1-C2-C4
2	B	501	BTB	O1-C1-C2-N
2	B	501	BTB	C3-C2-C4-O4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
2	B	501	BTB	C1-C2-N-C5
2	B	501	BTB	C1-C2-N-C7
2	B	501	BTB	C3-C2-N-C5
2	B	501	BTB	C3-C2-N-C7
2	B	501	BTB	C4-C2-N-C5
2	B	501	BTB	C4-C2-N-C7
2	D	501	BTB	C1-C2-C4-O4
2	D	501	BTB	C3-C2-C4-O4
2	D	501	BTB	N-C2-C4-O4
2	D	501	BTB	C6-C5-N-C7
2	E	501	BTB	C1-C2-C4-O4
2	E	501	BTB	C3-C2-C4-O4
2	E	501	BTB	N-C2-C4-O4
2	E	501	BTB	C6-C5-N-C7
2	F	501	BTB	C1-C2-C3-O3
2	F	501	BTB	C4-C2-C3-O3
2	F	501	BTB	N-C2-C3-O3
2	F	501	BTB	N-C5-C6-O6
2	E	501	BTB	N-C7-C8-O8
2	A	501	BTB	N-C5-C6-O6
2	B	501	BTB	N-C7-C8-O8
2	B	501	BTB	N-C2-C4-O4
2	D	501	BTB	C3-C2-N-C7
2	D	501	BTB	N-C7-C8-O8
2	D	501	BTB	C1-C2-N-C7
2	E	501	BTB	C1-C2-N-C7
2	E	501	BTB	C3-C2-N-C7

There are no ring outliers.

5 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	501	BTB	2	0
2	E	501	BTB	3	0
2	D	501	BTB	3	0
2	F	501	BTB	2	0
2	A	501	BTB	1	0

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 [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	405/411 (98%)	-0.50	1 (0%) 95 94	31, 46, 70, 119	0
1	B	405/411 (98%)	-0.44	0 100 100	31, 47, 71, 99	0
1	C	406/411 (98%)	-0.46	2 (0%) 91 90	34, 49, 68, 100	0
1	D	407/411 (99%)	-0.30	1 (0%) 95 94	34, 53, 78, 106	0
1	E	404/411 (98%)	-0.45	0 100 100	36, 52, 73, 106	0
1	F	404/411 (98%)	-0.08	1 (0%) 95 94	39, 69, 93, 106	0
All	All	2431/2466 (98%)	-0.37	5 (0%) 95 94	31, 51, 82, 119	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	2	SER	3.5
1	D	236	ALA	2.9
1	C	54	LYS	2.6
1	F	54	LYS	2.4
1	C	233	TRP	2.3

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 monosaccharides 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(Å ²)	Q<0.9
2	BTB	E	501	14/14	0.81	0.22	81,88,95,95	0
2	BTB	D	501	14/14	0.83	0.20	82,87,88,90	0
2	BTB	B	501	14/14	0.84	0.21	75,81,84,85	0
2	BTB	F	501	14/14	0.87	0.17	81,86,88,89	0
2	BTB	A	501	14/14	0.89	0.18	79,88,91,94	0
3	SO4	D	502	5/5	0.95	0.14	59,63,69,70	0
3	SO4	C	501	5/5	0.96	0.13	52,57,61,68	0
3	SO4	F	502	5/5	0.97	0.09	72,72,75,75	0
3	SO4	A	502	5/5	0.98	0.10	58,61,62,62	0
3	SO4	E	502	5/5	0.99	0.07	60,61,64,66	0
3	SO4	B	502	5/5	0.99	0.08	55,56,58,59	0

6.5 Other polymers [i](#)

There are no such residues in this entry.