



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 20, 2026 – 09:14 AM UTC

PDB ID : 3BN9 / pdb_00003bn9
Title : Crystal Structure of MT-SP1 in complex with Fab Inhibitor E2
Authors : Farady, C.J.; Schneider, E.L.; Egea, P.F.; Goetz, D.H.; Craik, C.S.
Deposited on : 2007-12-13
Resolution : 2.17 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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
Mogul	:	2022.3.0, CSD as543be (2022)
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

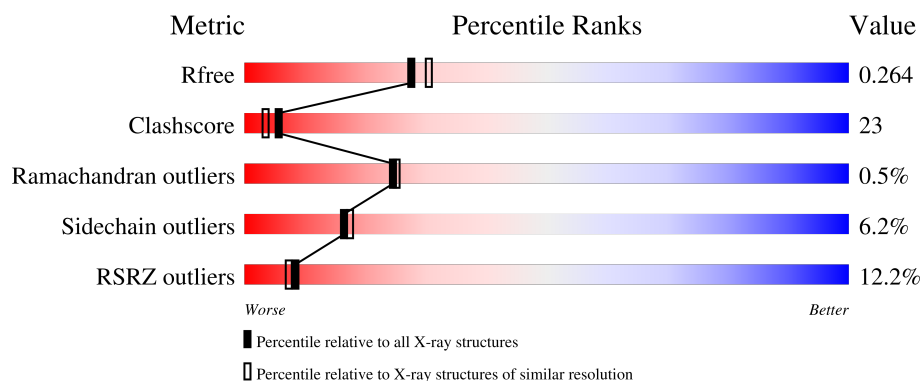
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.17 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	8975 (2.20-2.16)
Clashscore	190562	9786 (2.20-2.16)
Ramachandran outliers	187476	9664 (2.20-2.16)
Sidechain outliers	187428	9664 (2.20-2.16)
RSRZ outliers	180081	8979 (2.20-2.16)

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	241	% 73% 22% .
1	B	241	% 78% 20% .
2	C	214	27% 60% 34% ..
2	E	214	13% 57% 35% 6% ..
3	D	257	16% 51% 27% 18%

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Mol	Chain	Length	Quality of chain
3	F	257	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	EDO	A	2	-	-	X	-
4	EDO	B	6	-	-	X	-
4	EDO	B	7	-	-	X	-
4	EDO	C	216	-	-	X	-

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 11103 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 Membrane-type serine protease 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	241	Total	C	N	O	S	2	3	0
			1882	1188	331	352	11			
1	A	241	Total	C	N	O	S	2	4	0
			1891	1194	334	352	11			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	122	SER	CYS	engineered mutation	UNP Q9Y5Y6
A	122	SER	CYS	engineered mutation	UNP Q9Y5Y6

- Molecule 2 is a protein called E2 Fab Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	210	Total	C	N	O	S	0	0	0
			1593	996	266	326	5			
2	E	211	Total	C	N	O	S	0	1	0
			1609	1007	269	328	5			

- Molecule 3 is a protein called E2 Fab Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	211	Total	C	N	O	S	0	1	0
			1575	998	267	302	8			
3	F	224	Total	C	N	O	S	0	1	0
			1667	1050	285	325	7			

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	C	1	Total	C	O	0	0
			4	2	2		
4	C	1	Total	C	O	0	0
			4	2	2		
4	D	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	E	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	C	1	Total	O	S	0	0
			5	4	1		
5	E	1	Total	O	S	0	0
			5	4	1		

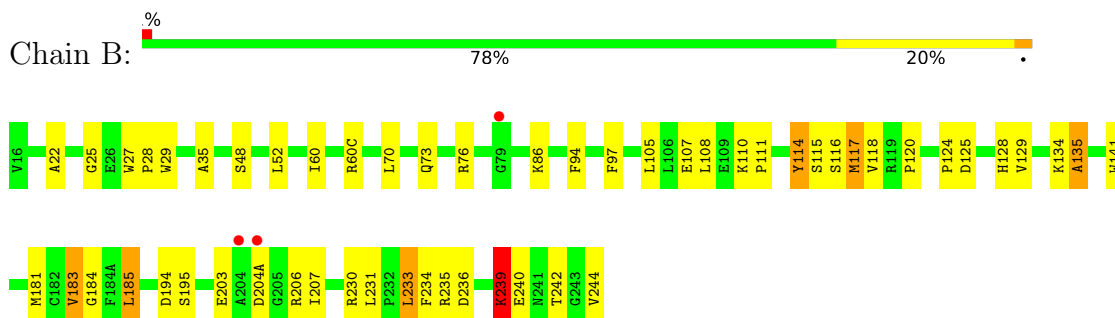
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	199	Total	O	0	0
			199	199		
6	C	118	Total	O	0	0
			118	118		
6	D	105	Total	O	0	0
			105	105		
6	A	175	Total	O	0	0
			175	175		
6	E	124	Total	O	0	0
			124	124		
6	F	103	Total	O	0	0
			103	103		

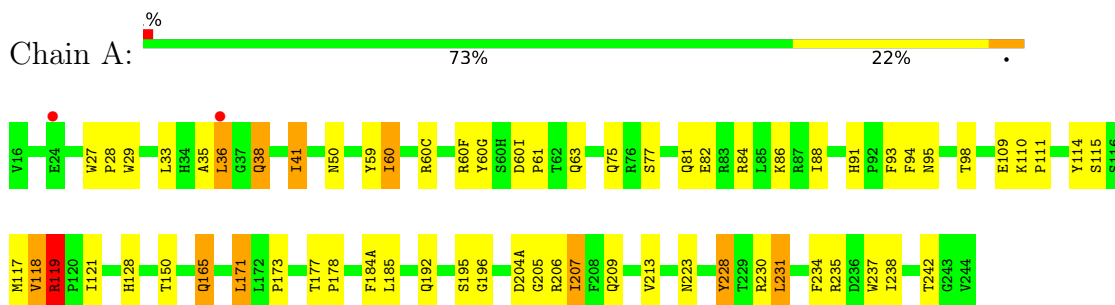
3 Residue-property plots [i](#)

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.

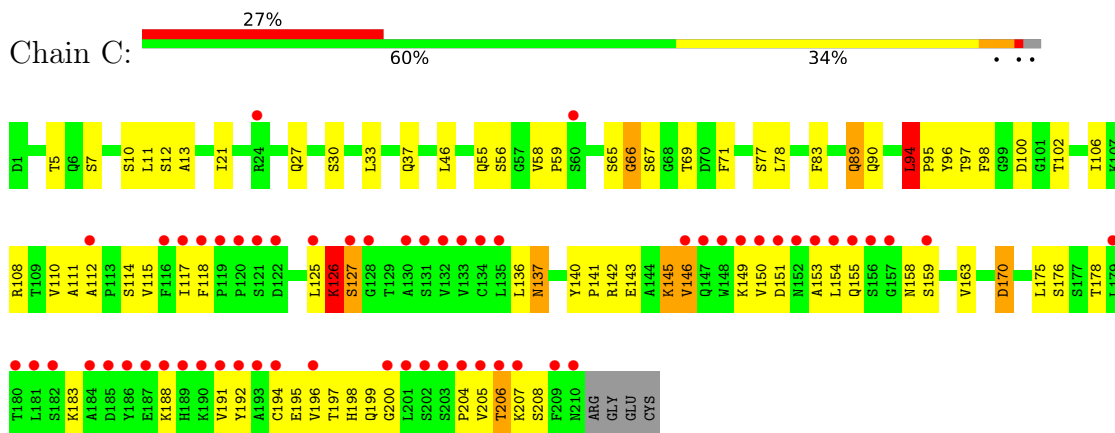
- Molecule 1: Membrane-type serine protease 1



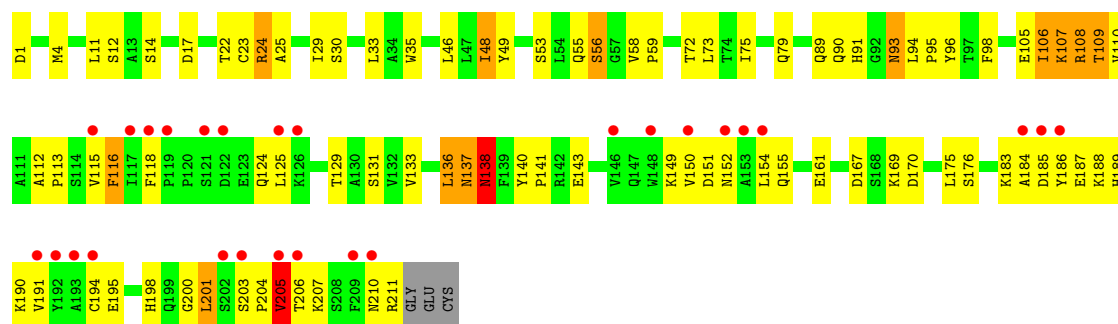
- Molecule 1: Membrane-type serine protease 1



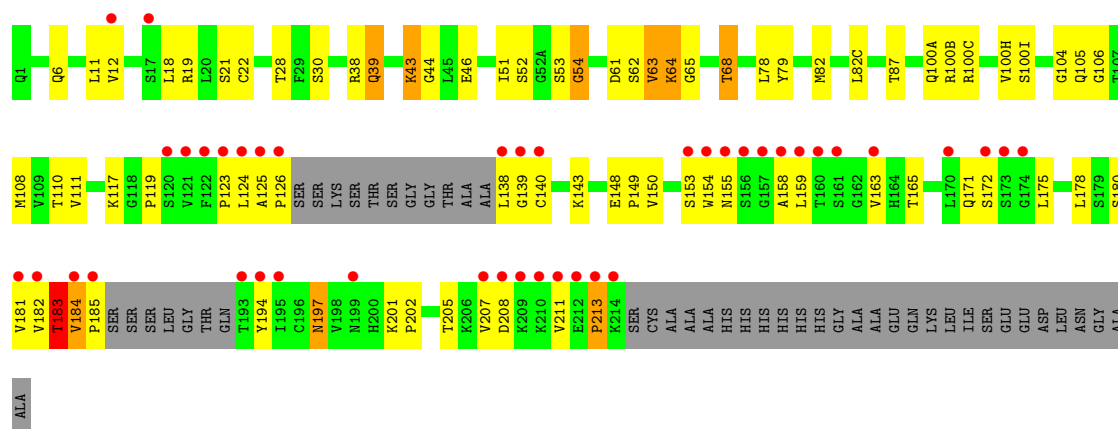
- Molecule 2: E2 Fab Light Chain



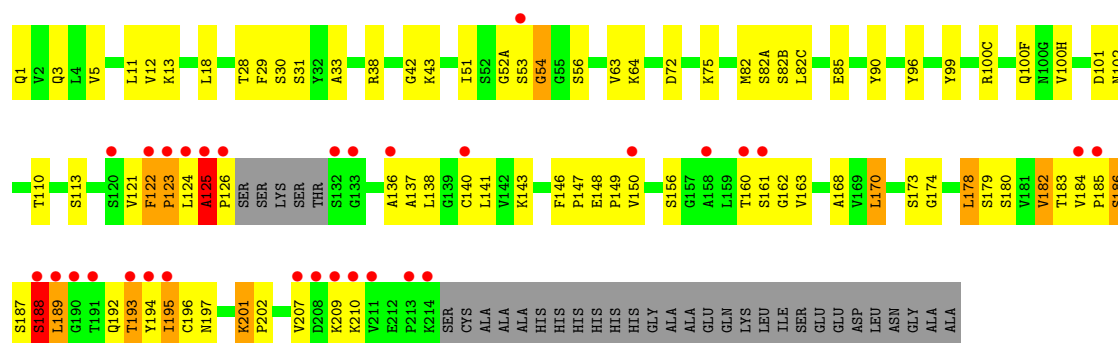
- Molecule 2: E2 Fab Light Chain



• Molecule 3: E2 Fab Heavy Chain



• Molecule 3: E2 Fab Heavy Chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	48.62Å 163.28Å 201.16Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	85.64 – 2.17 85.64 – 2.17	Depositor EDS
% Data completeness (in resolution range)	87.4 (85.64-2.17) 87.4 (85.64-2.17)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.87 (at 2.18Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.223 , 0.267 0.225 , 0.264	Depositor DCC
R_{free} test set	5781 reflections (6.83%)	wwPDB-VP
Wilson B-factor (Å ²)	29.0	Xtriage
Anisotropy	0.731	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 62.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	11103	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 44.76 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.4561e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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, EDO

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	1.32	17/1946 (0.9%)	1.04	11/2647 (0.4%)
1	B	1.25	16/1934 (0.8%)	0.95	0/2630
2	C	1.21	9/1627 (0.6%)	1.03	4/2212 (0.2%)
2	E	1.26	10/1644 (0.6%)	1.09	12/2235 (0.5%)
3	D	0.92	6/1618 (0.4%)	0.96	5/2207 (0.2%)
3	F	1.16	9/1708 (0.5%)	1.11	14/2326 (0.6%)
All	All	1.20	67/10477 (0.6%)	1.03	46/14257 (0.3%)

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
2	C	0	2
3	D	0	4
3	F	0	2
All	All	0	8

The worst 5 of 67 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	43	LYS	C-N	-10.53	1.20	1.33
1	A	60	ILE	C-O	-10.19	1.12	1.24
1	B	184	GLY	C-O	-9.68	1.17	1.23
3	F	42	GLY	C-N	-8.27	1.22	1.33
1	B	115	SER	C-O	-7.50	1.16	1.24

The worst 5 of 46 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	43	LYS	O-C-N	-10.53	108.78	122.78
1	A	119[A]	ARG	CA-C-O	-10.29	110.36	119.72
1	A	119[B]	ARG	CA-C-O	-10.29	110.36	119.72
2	E	137	ASN	N-CA-C	9.11	123.75	108.90
2	E	205	VAL	CB-CA-C	-7.13	101.32	111.31

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	126	LYS	Peptide
2	C	94	LEU	Peptide
3	D	100(A)	GLN	Peptide
3	D	125	ALA	Peptide
3	D	172	SER	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	1891	0	1808	68	0
1	B	1882	0	1793	49	0
2	C	1593	0	1540	85	0
2	E	1609	0	1550	97	0
3	D	1575	0	1527	93	0
3	F	1667	0	1629	96	0
4	A	12	0	18	9	0
4	B	24	0	36	21	0
4	C	8	0	12	8	0
4	D	4	0	6	3	0
4	E	4	0	6	0	0
5	C	5	0	0	0	0
5	E	5	0	0	0	0
6	A	175	0	0	11	0
6	B	199	0	0	9	0
6	C	118	0	0	8	0
6	D	105	0	0	3	0
6	E	124	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	F	103	0	0	7	0
All	All	11103	0	9925	472	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 23.

The worst 5 of 472 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)
3:F:123:PRO:CG	3:F:209:LYS:HE2	1.35	1.54
2:E:187:GLU:C	2:E:211:ARG:NH1	1.74	1.46
3:F:123:PRO:HG3	3:F:209:LYS:CE	1.45	1.44
2:C:151:ASP:HA	2:C:191:VAL:CG2	1.46	1.42
3:F:122:PHE:HA	3:F:209:LYS:NZ	1.27	1.37

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	243/241 (101%)	235 (97%)	8 (3%)	0	100	100
1	B	242/241 (100%)	237 (98%)	5 (2%)	0	100	100
2	C	208/214 (97%)	198 (95%)	9 (4%)	1 (0%)	24	25
2	E	210/214 (98%)	203 (97%)	5 (2%)	2 (1%)	12	10
3	D	206/257 (80%)	190 (92%)	14 (7%)	2 (1%)	12	10
3	F	221/257 (86%)	210 (95%)	10 (4%)	1 (0%)	24	25
All	All	1330/1424 (93%)	1273 (96%)	51 (4%)	6 (0%)	24	25

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	D	184	VAL
3	D	62	SER
2	E	138	ASN
2	C	127	SER
3	F	123	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	201/197 (102%)	193 (96%)	8 (4%)	28	35
1	B	200/197 (102%)	193 (96%)	7 (4%)	32	40
2	C	181/186 (97%)	166 (92%)	15 (8%)	10	10
2	E	182/186 (98%)	164 (90%)	18 (10%)	7	6
3	D	174/210 (83%)	167 (96%)	7 (4%)	28	35
3	F	185/210 (88%)	170 (92%)	15 (8%)	11	11
All	All	1123/1186 (95%)	1053 (94%)	70 (6%)	16	17

5 of 70 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	F	85	GLU
3	F	122	PHE
3	F	187	SER
3	D	64	LYS
3	D	63	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	174	GLN
3	F	197	ASN
2	E	55	GLN
3	F	100(F)	GLN

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Mol	Chain	Res	Type
1	A	223	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](#)

15 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	$\# Z > 2$
4	EDO	A	13	-	3,3,3	0.41	0	2,2,2	0.38	0
4	EDO	A	2	-	3,3,3	0.39	0	2,2,2	0.97	0
4	EDO	B	8	-	3,3,3	0.31	0	2,2,2	0.18	0
5	SO4	E	215	-	4,4,4	0.24	0	6,6,6	0.15	0
4	EDO	B	7	-	3,3,3	0.26	0	2,2,2	0.32	0
4	EDO	E	216	-	3,3,3	0.20	0	2,2,2	1.13	0
4	EDO	C	217	-	3,3,3	0.40	0	2,2,2	0.45	0
4	EDO	B	4	-	3,3,3	0.30	0	2,2,2	0.45	0
4	EDO	B	1	-	3,3,3	0.45	0	2,2,2	0.14	0
4	EDO	D	243	-	3,3,3	0.19	0	2,2,2	1.02	0
4	EDO	B	6	-	3,3,3	0.41	0	2,2,2	0.56	0
5	SO4	C	215	-	4,4,4	0.24	0	6,6,6	0.11	0
4	EDO	A	12	-	3,3,3	0.28	0	2,2,2	0.54	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	EDO	B	3	-	3,3,3	0.55	0	2,2,2	0.52	0
4	EDO	C	216	-	3,3,3	0.45	0	2,2,2	0.24	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
4	EDO	A	13	-	-	1/1/1/1	-
4	EDO	A	2	-	-	1/1/1/1	-
4	EDO	B	8	-	-	1/1/1/1	-
4	EDO	B	7	-	-	0/1/1/1	-
4	EDO	E	216	-	-	0/1/1/1	-
4	EDO	C	217	-	-	1/1/1/1	-
4	EDO	B	4	-	-	1/1/1/1	-
4	EDO	B	1	-	-	0/1/1/1	-
4	EDO	D	243	-	-	1/1/1/1	-
4	EDO	B	6	-	-	0/1/1/1	-
4	EDO	A	12	-	-	1/1/1/1	-
4	EDO	B	3	-	-	0/1/1/1	-
4	EDO	C	216	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	217	EDO	O1-C1-C2-O2
4	A	2	EDO	O1-C1-C2-O2
4	B	4	EDO	O1-C1-C2-O2
4	B	8	EDO	O1-C1-C2-O2
4	A	12	EDO	O1-C1-C2-O2

There are no ring outliers.

12 monomers are involved in 41 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	13	EDO	3	0
4	A	2	EDO	5	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	8	EDO	1	0
4	B	7	EDO	5	0
4	C	217	EDO	2	0
4	B	4	EDO	3	0
4	B	1	EDO	3	0
4	D	243	EDO	3	0
4	B	6	EDO	6	0
4	A	12	EDO	1	0
4	B	3	EDO	3	0
4	C	216	EDO	6	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
3	D	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D	43:LYS	C	44:GLY	N	1.20

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	241/241 (100%)	-0.16	2 (0%) 82 82	11, 30, 47, 74	5 (2%)
1	B	241/241 (100%)	-0.34	3 (1%) 76 76	11, 26, 44, 63	4 (1%)
2	C	210/214 (98%)	0.88	58 (27%) 1 1	16, 37, 122, 138	0
2	E	211/214 (98%)	0.49	27 (12%) 7 6	15, 37, 90, 110	1 (0%)
3	D	211/257 (82%)	0.83	42 (19%) 3 2	17, 42, 95, 111	1 (0%)
3	F	224/257 (87%)	0.65	31 (13%) 6 6	19, 44, 83, 108	1 (0%)
All	All	1338/1424 (93%)	0.37	163 (12%) 8 7	11, 33, 95, 138	12 (0%)

The worst 5 of 163 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	F	189	LEU	7.5
3	D	138	LEU	6.3
3	D	185	PRO	5.9
3	D	126	PRO	5.8
3	D	125	ALA	5.7

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

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
4	EDO	A	12	4/4	0.76	0.17	59,60,61,65	0
4	EDO	A	13	4/4	0.83	0.17	33,39,45,54	0
4	EDO	C	216	4/4	0.88	0.21	44,46,53,53	0
4	EDO	A	2	4/4	0.89	0.12	40,42,42,54	0
4	EDO	B	7	4/4	0.89	0.19	47,53,61,63	0
4	EDO	B	4	4/4	0.89	0.13	40,45,48,52	0
4	EDO	B	8	4/4	0.90	0.10	42,42,53,61	0
4	EDO	B	3	4/4	0.92	0.13	21,38,41,47	0
4	EDO	B	1	4/4	0.92	0.14	55,60,61,63	0
4	EDO	D	243	4/4	0.93	0.23	58,61,64,64	0
4	EDO	B	6	4/4	0.93	0.12	23,27,31,32	0
5	SO4	C	215	5/5	0.93	0.10	60,64,70,77	0
4	EDO	C	217	4/4	0.94	0.10	42,43,44,48	0
4	EDO	E	216	4/4	0.95	0.10	48,51,51,55	0
5	SO4	E	215	5/5	0.95	0.12	51,57,63,65	0

6.5 Other polymers

There are no such residues in this entry.