Full wwPDB X-ray Structure Validation Report

May 13, 2020 – 01:48 pm BST

PDB ID	:	4KD5
Title	:	substrate binding domain of putative molybdenum ABC transporter from Clostridium difficile
Authors	:	Maltseva, N.; Kim, Y.; Grimshaw, S.; Anderson, W.F.; Joachimiak, A.; Center for Structural Genomics of Infectious Diseases (CSGID)
Deposited on	:	2013-04-24
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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

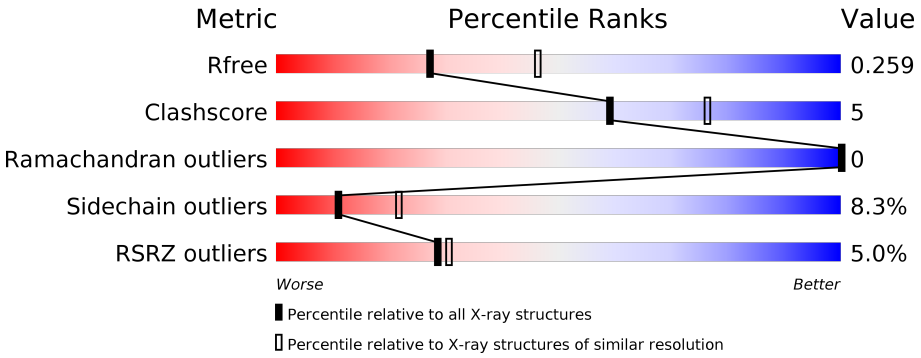
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 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}	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (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 on 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 <=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	233	2% 80% 16%
1	B	233	6% 76% 20%
1	C	233	2% 83% 14%
1	D	233	9% 82% 14%

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	FMT	C	303	-	-	-	X

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 7210 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.

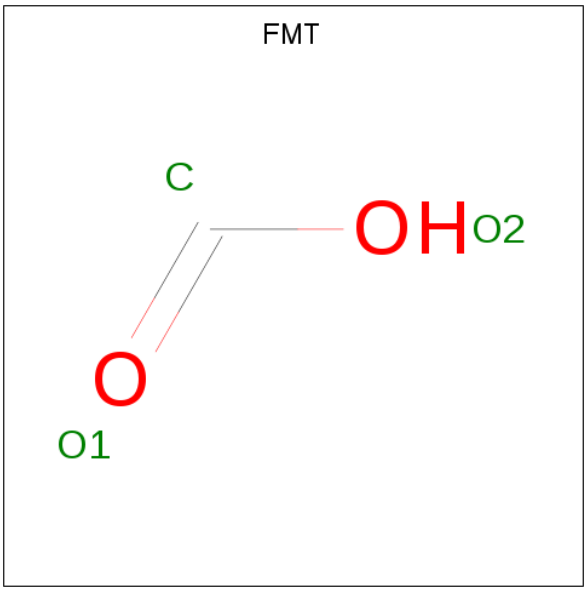
- Molecule 1 is a protein called ABC-type transport system, molybdenum-specific extracellular solute-binding protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	C	229	Total	C	N	O	S	Se	0	5	0
			1802	1140	287	369	2	4			
1	A	229	Total	C	N	O	S	Se	0	1	0
			1770	1121	283	361	1	4			
1	B	228	Total	C	N	O	S	Se	0	1	0
			1761	1116	282	357	2	4			
1	D	227	Total	C	N	O	S	Se	0	2	0
			1761	1116	282	357	2	4			

There are 16 discrepancies between the modelled and reference sequences:

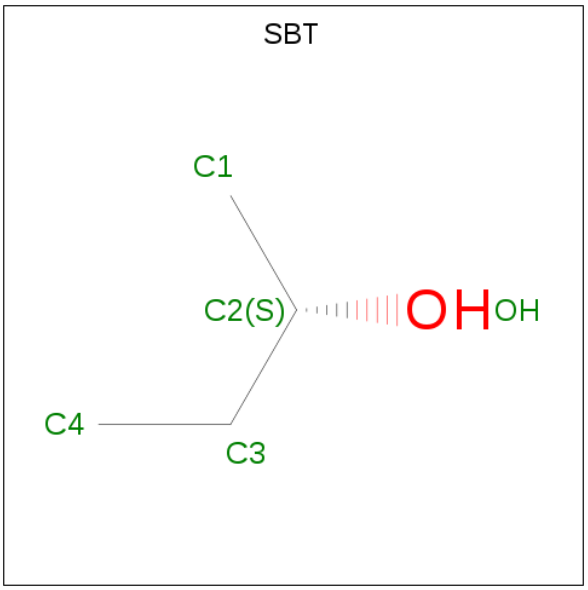
Chain	Residue	Modelled	Actual	Comment	Reference
C	38	SER	-	EXPRESSION TAG	UNP Q18A64
C	39	ASN	-	EXPRESSION TAG	UNP Q18A64
C	40	ALA	-	EXPRESSION TAG	UNP Q18A64
C	41	ASP	-	EXPRESSION TAG	UNP Q18A64
A	38	SER	-	EXPRESSION TAG	UNP Q18A64
A	39	ASN	-	EXPRESSION TAG	UNP Q18A64
A	40	ALA	-	EXPRESSION TAG	UNP Q18A64
A	41	ASP	-	EXPRESSION TAG	UNP Q18A64
B	38	SER	-	EXPRESSION TAG	UNP Q18A64
B	39	ASN	-	EXPRESSION TAG	UNP Q18A64
B	40	ALA	-	EXPRESSION TAG	UNP Q18A64
B	41	ASP	-	EXPRESSION TAG	UNP Q18A64
D	38	SER	-	EXPRESSION TAG	UNP Q18A64
D	39	ASN	-	EXPRESSION TAG	UNP Q18A64
D	40	ALA	-	EXPRESSION TAG	UNP Q18A64
D	41	ASP	-	EXPRESSION TAG	UNP Q18A64

- Molecule 2 is FORMIC ACID (three-letter code: FMT) (formula: CH_2O_2).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	C	1	Total C O 3 1 2	0	0
2	C	1	Total C O 3 1 2	0	0
2	C	1	Total C O 3 1 2	0	0

- Molecule 3 is 2-BUTANOL (three-letter code: SBT) (formula: $C_4H_{10}O$).



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

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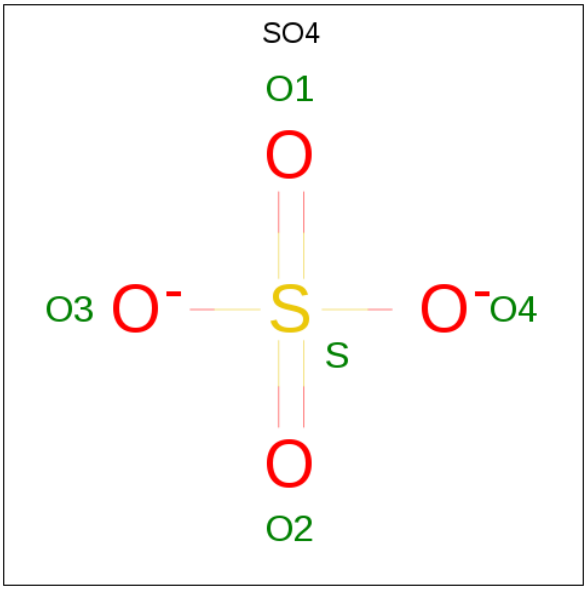
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	C	1	Total C O 5 4 1	0	0
3	B	1	Total C O 5 4 1	0	0

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total O S 5 4 1	0	0
4	D	1	Total O S 5 4 1	0	0

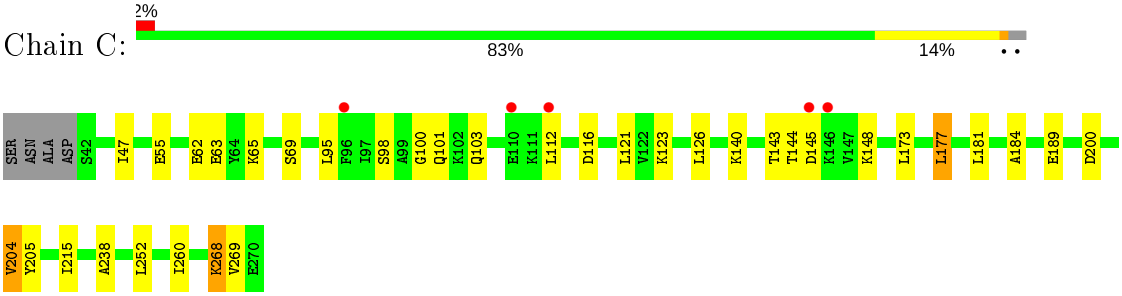
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	C	27	Total O 27 27	0	0
5	A	26	Total O 26 26	0	0
5	B	18	Total O 18 18	0	0
5	D	11	Total O 11 11	0	0

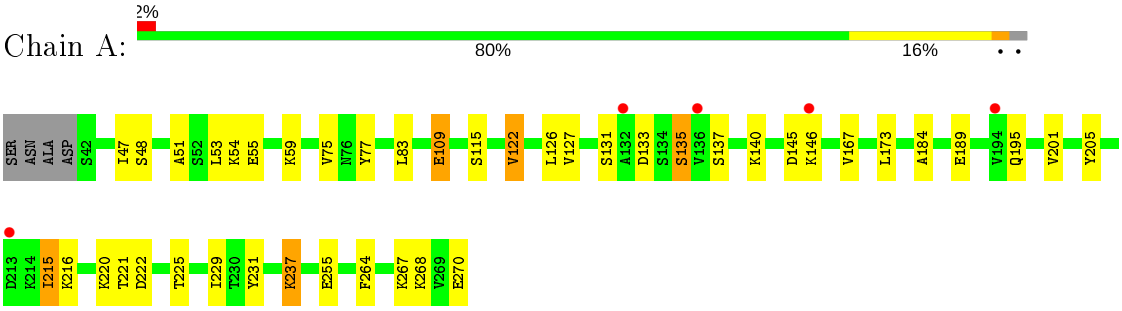
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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.

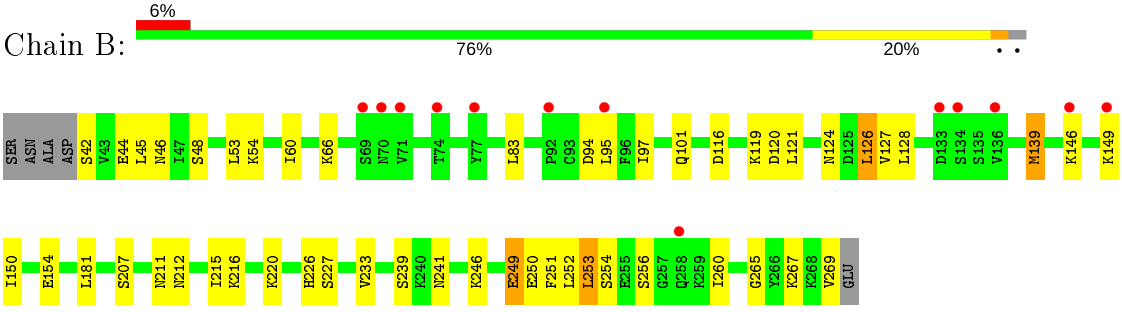
• Molecule 1: ABC-type transport system, molybdenum-specific extracellular solute-binding protein



• Molecule 1: ABC-type transport system, molybdenum-specific extracellular solute-binding protein

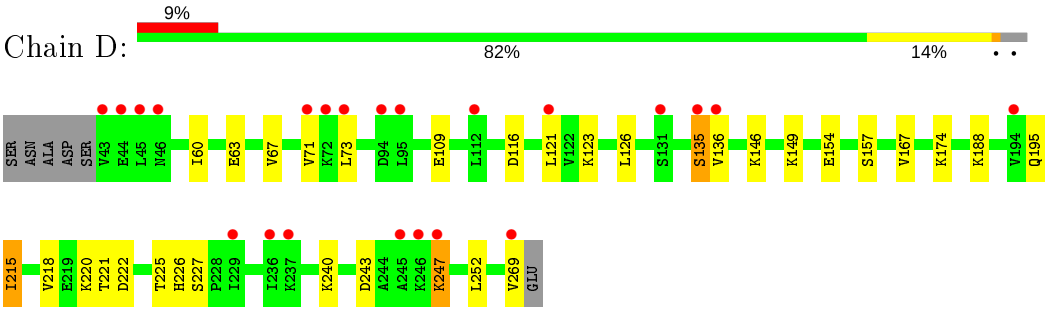


• Molecule 1: ABC-type transport system, molybdenum-specific extracellular solute-binding protein



• Molecule 1: ABC-type transport system, molybdenum-specific extracellular solute-binding protein

Chain D:


9%
82%
14%
SER ASN ALA ASP SER V43 E44 L45 N46 I60 E63 V67 V71 K72 L73 D94 L95 E109 L112 D116 L121 V122 K123 L126 S131 S135 V136 K146 K149 E154 S157 V167 K174 K188 V194 Q195 S196 G197 N198
I215 V218 E219 K220 T221 D222 T225 H226 S227 P228 I229 I236 K237 K240 D243 A244 A245 K246 K247 L252 V269 GLU

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	123.64Å 141.07Å 122.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.09 – 2.50 46.49 – 2.50	Depositor EDS
% Data completeness (in resolution range)	97.0 (34.09-2.50) 96.3 (46.49-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$< I/\sigma(I) >$ [1]	2.30 (at 2.51Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1227)	Depositor
R, R_{free}	0.204 , 0.259 0.204 , 0.259	Depositor DCC
R_{free} test set	2000 reflections (5.39%)	wwPDB-VP
Wilson B-factor (Å^2)	58.3	Xtriage
Anisotropy	0.224	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 44.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	7210	wwPDB-VP
Average B, all atoms (Å^2)	73.0	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 20.84 % 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 7.9624e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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

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

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	0.27	0/1786	0.45	0/2395
1	B	0.26	0/1777	0.43	0/2383
1	C	0.28	0/1818	0.44	0/2438
1	D	0.25	0/1777	0.42	0/2383
All	All	0.27	0/7158	0.44	0/9599

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

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	1770	0	1807	17	0
1	B	1761	0	1801	23	0
1	C	1802	0	1832	14	0
1	D	1761	0	1800	16	0
2	C	9	0	3	1	0
3	B	5	0	10	1	0
3	C	10	0	20	3	0
4	B	5	0	0	0	0
4	D	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	26	0	0	0	0
5	B	18	0	0	0	0
5	C	27	0	0	0	0
5	D	11	0	0	0	0
All	All	7210	0	7273	67	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 5.

All (67) 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:C:101:GLN:H	3:C:302:SBT:H2	1.56	0.69
1:A:135:SER:HB2	1:A:146:LYS:HE2	1.76	0.66
1:B:94:ASP:HA	1:B:239:SER:HB3	1.79	0.65
1:A:47:ILE:HB	1:A:75:VAL:HG22	1.79	0.65
1:D:136:VAL:HG12	1:D:218:VAL:HG11	1.79	0.64
1:B:97:ILE:HG12	1:B:233:VAL:HG23	1.79	0.63
1:D:121:LEU:HD11	1:D:252:LEU:HB3	1.83	0.61
1:D:196:SER:OG	1:D:198:ASN:ND2	2.34	0.60
1:B:207:SER:HA	1:B:265:GLY:HA3	1.85	0.58
1:B:46:ASN:N	1:B:94:ASP:OD2	2.34	0.57
1:C:65:LYS:NZ	1:C:69:SER:O	2.37	0.56
1:B:128:LEU:HD22	1:B:139:MSE:HE3	1.88	0.56
1:A:122:VAL:HG12	1:A:231:TYR:HB2	1.90	0.54
1:C:112:LEU:HB3	2:C:303:FMT:H	1.90	0.54
1:A:115:SER:HB2	1:D:188:LYS:HG3	1.88	0.54
1:B:212:ASN:HD22	1:B:215:ILE:HG12	1.74	0.53
1:D:195:GLN:HG3	1:D:215:ILE:HG23	1.91	0.53
1:C:173:LEU:HB3	1:C:177:LEU:HD22	1.91	0.53
1:C:63:GLU:HG2	1:C:260:ILE:HD11	1.91	0.52
1:B:48:SER:HB2	1:B:83:LEU:HD13	1.92	0.52
1:D:167:VAL:HG21	1:D:221:THR:HG21	1.91	0.52
1:A:59:LYS:HE2	1:A:264:PHE:CE2	2.45	0.52
1:A:109:GLU:HB2	1:D:157:SER:O	2.12	0.50
1:B:121:LEU:HD11	1:B:252:LEU:HB3	1.94	0.50
1:B:60:ILE:HD13	1:B:260:ILE:HD12	1.94	0.50
1:C:144:THR:HB	3:C:304:SBT:H32	1.95	0.49
1:A:127:VAL:HG12	1:A:220:LYS:HG3	1.95	0.49
1:B:127:VAL:HG12	1:B:220:LYS:HG2	1.94	0.49
1:A:195:GLN:HG2	1:A:215:ILE:HG22	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:222:ASP:O	1:D:225:THR:OG1	2.30	0.48
1:D:247:LYS:HD3	1:D:247:LYS:HA	1.64	0.47
1:B:101:GLN:HG3	3:B:301:SBT:H13	1.97	0.47
1:A:54:LYS:HA	1:A:77:TYR:CE1	2.50	0.47
1:A:51:ALA:HA	1:A:77:TYR:HB3	1.97	0.47
1:C:100:GLY:HA3	3:C:302:SBT:H42	1.96	0.47
1:C:204:VAL:HG13	1:C:205:TYR:O	2.14	0.47
1:D:135:SER:OG	1:D:146:LYS:HD3	2.15	0.46
1:D:63:GLU:O	1:D:67:VAL:HG23	2.14	0.46
1:C:47:ILE:HG13	1:C:95:LEU:HB3	1.96	0.46
1:D:226:HIS:HD2	1:D:227:SER:O	2.00	0.45
1:A:222:ASP:HB3	1:A:225:THR:HG23	1.99	0.45
1:A:184:ALA:HB1	1:A:189:GLU:HB3	1.97	0.45
1:C:121:LEU:HD11	1:C:252:LEU:HB3	1.99	0.45
1:A:237:LYS:HB2	1:A:237:LYS:HE2	1.78	0.44
1:B:146:LYS:HE3	1:B:146:LYS:HB2	1.76	0.44
1:C:238:ALA:HA	1:B:54:LYS:HE3	1.99	0.44
1:B:212:ASN:ND2	1:B:215:ILE:HG12	2.31	0.44
1:C:148:LYS:N	1:C:200:ASP:OD2	2.28	0.44
1:B:226:HIS:HD2	1:B:227:SER:O	2.02	0.43
1:B:250:GLU:O	1:B:254:SER:N	2.52	0.42
1:C:268:LYS:HG3	1:C:269:VAL:N	2.34	0.42
1:D:220:LYS:HE2	1:D:220:LYS:HB3	1.72	0.42
1:A:54:LYS:HG3	1:A:77:TYR:CE2	2.55	0.42
1:A:205:TYR:CE1	1:A:229:ILE:HD13	2.55	0.42
1:B:121:LEU:HD12	1:B:253:LEU:HD23	2.01	0.42
1:D:60:ILE:HG21	1:D:252:LEU:HD21	2.02	0.41
1:B:120:ASP:HB2	1:B:269:VAL:HG11	2.02	0.41
1:B:60:ILE:HG23	1:B:251:PHE:HE2	1.85	0.41
1:A:167:VAL:HG21	1:A:221:THR:HG21	2.02	0.41
1:A:48:SER:HB2	1:A:83:LEU:HD22	2.02	0.41
1:B:246:LYS:HA	1:B:249:GLU:HB3	2.03	0.41
1:D:149:LYS:HD2	1:D:198:ASN:O	2.20	0.41
1:B:126:LEU:HD23	1:B:126:LEU:HA	1.93	0.41
1:B:150:ILE:HB	1:B:181:LEU:HD23	2.02	0.41
1:B:216:LYS:HB3	1:B:216:LYS:HE2	1.86	0.40
1:D:123:LYS:HB3	1:D:269:VAL:HG22	2.02	0.40
1:C:184:ALA:HB1	1:C:189:GLU:HB3	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	228/233 (98%)	226 (99%)	2 (1%)	0	100	100
1	B	227/233 (97%)	223 (98%)	4 (2%)	0	100	100
1	C	232/233 (100%)	226 (97%)	6 (3%)	0	100	100
1	D	227/233 (97%)	222 (98%)	5 (2%)	0	100	100
All	All	914/932 (98%)	897 (98%)	17 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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	200/198 (101%)	180 (90%)	20 (10%)	7	15
1	B	199/198 (100%)	180 (90%)	19 (10%)	8	17
1	C	204/198 (103%)	188 (92%)	16 (8%)	12	24
1	D	199/198 (100%)	187 (94%)	12 (6%)	19	37
All	All	802/792 (101%)	735 (92%)	67 (8%)	11	21

All (67) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	55[A]	GLU
1	C	55[B]	GLU

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Mol	Chain	Res	Type
1	C	62	GLU
1	C	98	SER
1	C	103	GLN
1	C	116	ASP
1	C	123	LYS
1	C	126	LEU
1	C	140	LYS
1	C	143	THR
1	C	145	ASP
1	C	177	LEU
1	C	181	LEU
1	C	204	VAL
1	C	215	ILE
1	C	268	LYS
1	A	53	LEU
1	A	55	GLU
1	A	109	GLU
1	A	122	VAL
1	A	126	LEU
1	A	131	SER
1	A	133	ASP
1	A	135	SER
1	A	137	SER
1	A	140	LYS
1	A	145	ASP
1	A	173	LEU
1	A	201	VAL
1	A	215	ILE
1	A	216	LYS
1	A	237	LYS
1	A	255	GLU
1	A	267	LYS
1	A	268	LYS
1	A	270	GLU
1	B	42	SER
1	B	44	GLU
1	B	45	LEU
1	B	53	LEU
1	B	66	LYS
1	B	95	LEU
1	B	116	ASP
1	B	119	LYS

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Mol	Chain	Res	Type
1	B	124	ASN
1	B	126	LEU
1	B	139	MSE
1	B	149	LYS
1	B	154	GLU
1	B	211	ASN
1	B	241	ASN
1	B	249	GLU
1	B	253	LEU
1	B	256	SER
1	B	267	LYS
1	D	71	VAL
1	D	73	LEU
1	D	109	GLU
1	D	116	ASP
1	D	126	LEU
1	D	135	SER
1	D	154	GLU
1	D	174	LYS
1	D	215	ILE
1	D	240	LYS
1	D	243	ASP
1	D	247	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	85	GLN
1	C	101	GLN
1	C	103	GLN
1	C	226	HIS
1	A	70	ASN
1	A	195	GLN
1	A	198	ASN
1	B	211	ASN
1	B	212	ASN
1	B	226	HIS
1	B	258	GLN
1	D	84	GLN
1	D	101	GLN
1	D	198	ASN
1	D	226	HIS

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

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

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

8 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	SO4	D	300	-	4,4,4	0.15	0	6,6,6	0.09	0
3	SBT	B	301	-	4,4,4	0.22	0	4,4,4	0.20	0
3	SBT	C	304	-	4,4,4	0.25	0	4,4,4	0.18	0
2	FMT	C	301	-	0,2,2	0.00	-	0,1,1	0.00	-
4	SO4	B	302	-	4,4,4	0.14	0	6,6,6	0.06	0
2	FMT	C	303	-	0,2,2	0.00	-	0,1,1	0.00	-
3	SBT	C	302	-	4,4,4	0.23	0	4,4,4	0.24	0
2	FMT	C	300	-	0,2,2	0.00	-	0,1,1	0.00	-

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
3	SBT	C	302	-	-	2/2/2/2	-
3	SBT	B	301	-	-	0/2/2/2	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	SBT	C	304	-	-	0/2/2/2	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	302	SBT	OH-C2-C3-C4
3	C	302	SBT	C1-C2-C3-C4

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	301	SBT	1	0
3	C	304	SBT	1	0
2	C	303	FMT	1	0
3	C	302	SBT	2	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

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, 95^{th} 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	225/233 (96%)	0.20	5 (2%)	62	65	43, 67, 98, 118	3 (1%)
1	B	224/233 (96%)	0.46	13 (5%)	23	24	47, 80, 116, 132	10 (4%)
1	C	225/233 (96%)	0.17	5 (2%)	62	65	39, 60, 89, 113	2 (0%)
1	D	223/233 (95%)	0.56	22 (9%)	7	7	50, 79, 110, 143	8 (3%)
All	All	897/932 (96%)	0.35	45 (5%)	28	30	39, 70, 108, 143	23 (2%)

All (45) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	69	SER	4.6
1	D	73	LEU	4.5
1	B	70	ASN	4.3
1	D	45	LEU	3.9
1	B	146	LYS	3.7
1	D	247	LYS	3.6
1	A	136	VAL	3.6
1	D	136	VAL	3.5
1	D	194	VAL	3.4
1	A	194	VAL	3.3
1	D	44	GLU	3.2
1	D	43	VAL	3.1
1	C	145	ASP	3.1
1	D	72	LYS	3.0
1	D	121	LEU	3.0
1	B	74	THR	3.0
1	D	236	ILE	2.8
1	D	246	LYS	2.8
1	D	237	LYS	2.7
1	B	133	ASP	2.7
1	A	132	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	134	SER	2.6
1	C	146	LYS	2.5
1	D	71	VAL	2.5
1	A	213	ASP	2.5
1	D	95	LEU	2.5
1	B	95	LEU	2.4
1	D	245	ALA	2.4
1	B	77	TYR	2.4
1	C	110	GLU	2.4
1	D	131	SER	2.4
1	B	149	LYS	2.3
1	D	269	VAL	2.3
1	B	71	VAL	2.2
1	D	112	LEU	2.2
1	A	146	LYS	2.2
1	B	92	PRO	2.1
1	C	96	PHE	2.1
1	D	94	ASP	2.1
1	D	229	ILE	2.0
1	B	258	GLN	2.0
1	D	46	ASN	2.0
1	B	136	VAL	2.0
1	D	135	SER	2.0
1	C	112	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 carbohydrates 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, 95^{th} 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	FMT	C	303	3/3	0.64	0.95	72,72,80,82	0
2	FMT	C	300	3/3	0.69	0.28	88,88,91,91	0
4	SO4	B	302	5/5	0.86	0.24	132,134,134,136	0
4	SO4	D	300	5/5	0.87	0.33	127,127,130,134	0
3	SBT	B	301	5/5	0.88	0.20	58,59,65,66	0
3	SBT	C	304	5/5	0.91	0.40	66,68,73,77	0
3	SBT	C	302	5/5	0.94	0.18	44,49,53,61	0
2	FMT	C	301	3/3	0.94	0.13	65,65,70,70	0

6.5 Other polymers

There are no such residues in this entry.