Full wwPDB X-ray Structure Validation Report ⓘ

Jun 17, 2024 – 10:05 AM EDT

PDB ID	:	3BE5
Title	:	Crystal structure of FitE (crystal form 1), a group III periplasmic siderophore binding protein
Authors	:	Shi, R.; Matte, A.; Cygler, M.; Montreal-Kingston Bacterial Structural Genomics Initiative (BSGI)
Deposited on	:	2007-11-16
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:

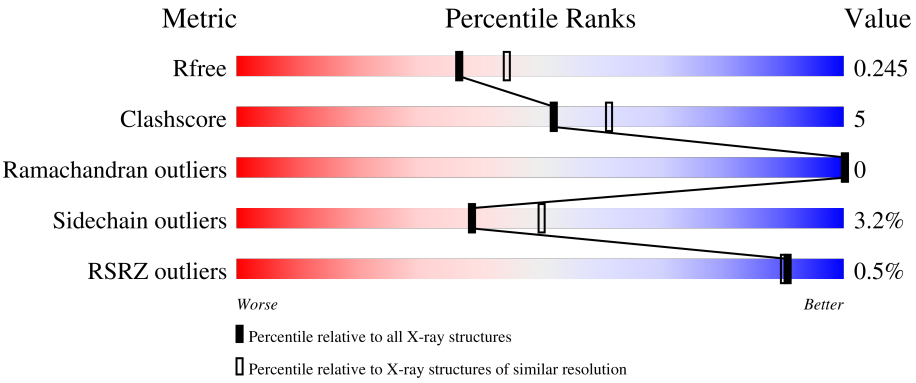
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance (i)

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 <=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	297	87% 10%
1	B	297	% 83% 15%
1	C	297	87% 11%
1	D	297	% 86% 12%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 9668 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 Putative iron compound-binding protein of ABC transporter family.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	294	Total	C	N	O	S	Se	0	2	0
			2264	1431	399	427	2	5			
1	B	294	Total	C	N	O	S	Se	0	2	0
			2265	1432	400	425	2	6			
1	C	294	Total	C	N	O	S	Se	0	3	0
			2272	1437	400	427	2	6			
1	D	294	Total	C	N	O	S	Se	0	0	0
			2256	1424	400	425	2	5			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	259	THR	ALA	SEE REMARK 999	UNP Q8XBR1
B	259	THR	ALA	SEE REMARK 999	UNP Q8XBR1
C	259	THR	ALA	SEE REMARK 999	UNP Q8XBR1
D	259	THR	ALA	SEE REMARK 999	UNP Q8XBR1

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	2	Total	Cl	0	0
			2	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	145	Total	O	0	0
			145	145		
3	B	121	Total	O	0	0
			121	121		

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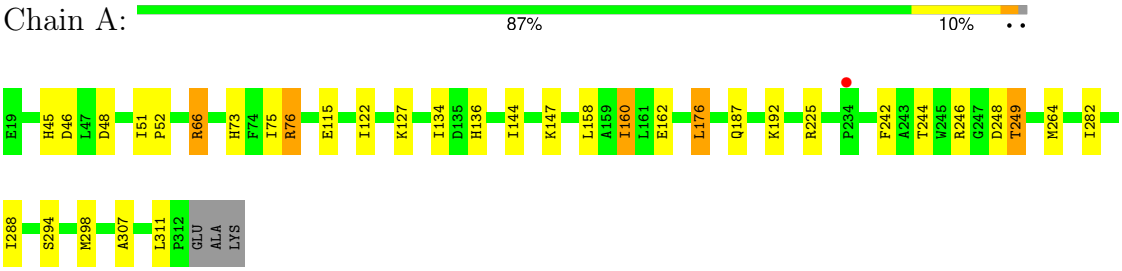
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	C	160	Total O 160 160	0	0
3	D	183	Total O 183 183	0	0

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.

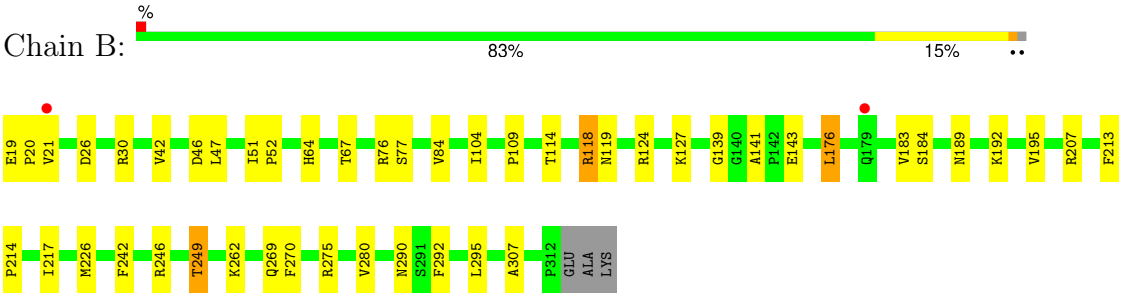
• Molecule 1: Putative iron compound-binding protein of ABC transporter family

Chain A:



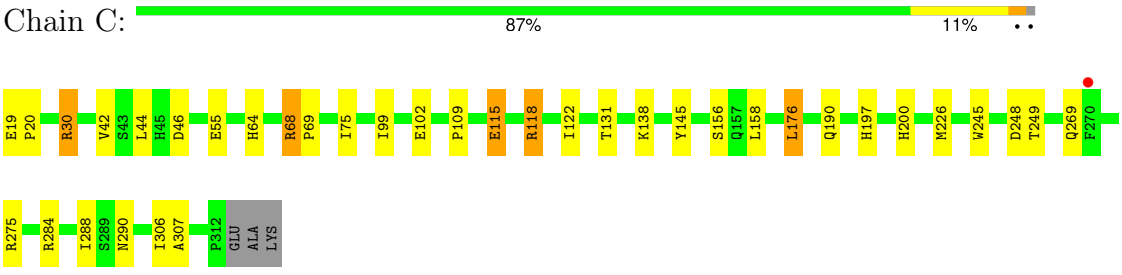
• Molecule 1: Putative iron compound-binding protein of ABC transporter family

Chain B:



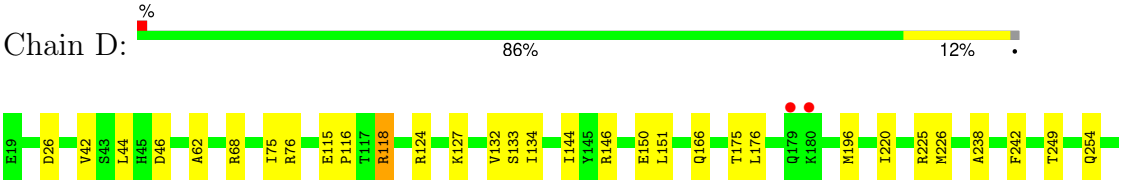
• Molecule 1: Putative iron compound-binding protein of ABC transporter family

Chain C:



• Molecule 1: Putative iron compound-binding protein of ABC transporter family

Chain D:




M264
P265
T272
A273
C274
R275
I282
A307
P312
GLU
ALA
LYS

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	51.66Å 113.63Å 224.52Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.04 – 2.20 47.03 – 2.20	Depositor EDS
% Data completeness (in resolution range)	87.7 (47.04-2.20) 87.7 (47.03-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	4.79 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.187 , 0.245 0.186 , 0.245	Depositor DCC
R_{free} test set	3042 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å^2)	24.2	Xtriage
Anisotropy	1.107	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 38.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	9668	wwPDB-VP
Average B, all atoms (Å^2)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.98% of the height of the origin peak. No significant pseudotranslation is detected.*

[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: CL

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	0.50	0/2309	0.59	0/3129
1	B	0.51	0/2310	0.62	0/3130
1	C	0.55	0/2320	0.67	2/3144 (0.1%)
1	D	0.55	0/2295	0.61	0/3109
All	All	0.53	0/9234	0.62	2/12512 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	30	ARG	NE-CZ-NH2	-8.21	116.19	120.30
1	C	30	ARG	NE-CZ-NH1	6.91	123.75	120.30

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	2264	0	2295	24	0
1	B	2265	0	2305	32	0
1	C	2272	0	2313	24	0
1	D	2256	0	2287	24	0
2	C	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	145	0	0	4	0
3	B	121	0	0	4	0
3	C	160	0	0	1	0
3	D	183	0	0	1	0
All	All	9668	0	9200	100	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 (100) 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:220:ILE:HG12	1:D:226:MSE:HE3	1.44	0.99
1:C:30:ARG:NH2	1:C:131:THR:O	2.07	0.85
1:B:114:THR:OG1	1:B:118:ARG:HD3	1.79	0.82
1:B:242:PHE:CD1	1:B:280[A]:VAL:CG2	2.64	0.80
1:C:46:ASP:H	1:C:64:HIS:HD2	1.29	0.80
1:B:242:PHE:CE1	1:B:280[A]:VAL:HG21	2.16	0.80
1:B:46:ASP:H	1:B:64:HIS:HD2	1.32	0.78
1:B:242:PHE:CD1	1:B:280[A]:VAL:HG21	2.21	0.74
1:A:45:HIS:HD2	1:A:48:ASP:H	1.34	0.74
1:C:245:TRP:CH2	1:D:175:THR:HG21	2.23	0.73
1:B:19:GLU:N	1:B:20:PRO:HD3	2.04	0.72
3:B:403:HOH:O	1:C:226:MSE:CE	2.38	0.71
1:A:76:ARG:HH12	1:A:288:ILE:HD11	1.58	0.68
1:A:176:LEU:HD23	1:A:307:ALA:HB2	1.75	0.68
1:A:311:LEU:HD23	3:B:535:HOH:O	1.94	0.66
1:B:19:GLU:N	1:B:20:PRO:CD	2.58	0.66
1:D:132:VAL:HG21	1:D:151:LEU:HD11	1.78	0.66
1:C:68:ARG:HB2	1:C:69:PRO:HD2	1.79	0.65
1:D:166:GLN:HG3	3:D:592:HOH:O	1.97	0.65
1:A:136:HIS:HB3	1:A:144:ILE:HD11	1.79	0.64
1:C:176[B]:LEU:HD13	1:C:307:ALA:HB2	1.78	0.64
1:B:42:VAL:HG23	1:B:109:PRO:HB3	1.80	0.64
1:D:115:GLU:OE2	1:D:118:ARG:HG2	1.98	0.63
1:D:176:LEU:HD21	1:D:307:ALA:HB2	1.80	0.62
1:B:195:VAL:HG11	1:B:217:ILE:HG12	1.81	0.61
3:B:403:HOH:O	1:C:226:MSE:HE3	2.00	0.60
1:B:46:ASP:H	1:B:64:HIS:CD2	2.17	0.59
1:A:187:GLN:CD	3:A:928:HOH:O	2.40	0.59
1:B:139:GLY:HA3	1:B:143:GLU:HG3	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:264:MSE:HE3	1:D:265:PRO:HD2	1.84	0.58
1:B:246:ARG:HH12	1:B:249:THR:CG2	2.17	0.57
1:C:68:ARG:HB2	1:C:69:PRO:CD	2.36	0.56
1:B:246:ARG:HH12	1:B:249:THR:HG22	1.71	0.55
1:C:176[B]:LEU:HD21	1:C:306:ILE:CG2	2.36	0.55
1:A:249:THR:O	1:A:249:THR:HG23	2.07	0.54
1:A:136:HIS:CB	1:A:144:ILE:HD11	2.38	0.54
1:B:249:THR:O	1:B:249:THR:HG23	2.07	0.54
1:D:272:THR:HG22	1:D:275:ARG:HH21	1.72	0.53
1:B:242:PHE:CD1	1:B:280[A]:VAL:HG23	2.42	0.53
1:C:176[B]:LEU:HD21	1:C:306:ILE:HG21	1.91	0.53
1:B:183:VAL:O	1:B:214:PRO:HD3	2.10	0.52
1:D:146:ARG:O	1:D:150:GLU:HG2	2.10	0.52
1:A:76:ARG:NH1	1:A:288:ILE:HD11	2.25	0.51
1:C:145:TYR:HB3	1:C:158:LEU:HD13	1.92	0.51
1:D:124:ARG:HA	1:D:127:LYS:HE3	1.92	0.51
1:B:51:ILE:HB	1:B:52:PRO:HD3	1.94	0.50
1:B:67:THR:HG21	1:C:102:GLU:HG3	1.93	0.50
1:A:249:THR:O	1:A:249:THR:CG2	2.60	0.50
1:D:42:VAL:HG22	1:D:62:ALA:HB3	1.94	0.49
1:B:207:ARG:HG2	1:B:213:PHE:CE2	2.47	0.49
1:C:46:ASP:HB2	1:C:75:ILE:HG23	1.94	0.49
1:B:141:ALA:HB2	1:B:290:ASN:HB3	1.94	0.49
1:A:242:PHE:HD1	1:A:282:ILE:CD1	2.27	0.48
1:A:158:LEU:O	1:A:162:GLU:HG3	2.14	0.47
1:C:248:ASP:HB3	1:C:249:THR:HG23	1.96	0.47
1:C:200:HIS:HA	1:C:290:ASN:HD21	1.79	0.47
1:A:294:SER:O	1:A:298:MSE:HG2	2.14	0.47
1:D:134:ILE:HG22	1:D:144:ILE:HD12	1.97	0.47
1:B:189:ASN:O	1:B:192:LYS:HG2	2.15	0.47
1:D:196:MSE:HG2	1:D:225:ARG:HB3	1.97	0.47
1:A:136:HIS:CE1	3:A:999:HOH:O	2.68	0.47
1:C:245:TRP:CH2	1:D:175:THR:CG2	2.96	0.46
1:C:44:LEU:HD22	1:C:99:ILE:HG12	1.98	0.46
1:A:134:ILE:HD12	1:A:147:LYS:HD3	1.97	0.46
1:D:242:PHE:HD1	1:D:282:ILE:HD12	1.80	0.46
1:A:160[A]:ILE:HD12	1:B:84:VAL:HG23	1.98	0.45
1:C:19:GLU:N	1:C:20:PRO:CD	2.80	0.45
1:D:134:ILE:CG2	1:D:144:ILE:HD12	2.46	0.45
1:C:42:VAL:HG23	1:C:109:PRO:HB3	1.99	0.45
1:D:44:LEU:O	1:D:118:ARG:HD2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:26:ASP:OD2	1:B:30:ARG:NH2	2.50	0.44
1:B:262:LYS:HB2	1:B:262:LYS:HE2	1.89	0.44
1:D:26:ASP:HB2	1:D:133:SER:O	2.18	0.44
1:B:104:ILE:O	1:B:109:PRO:HD3	2.18	0.44
1:A:51:ILE:HB	1:A:52:PRO:HD3	2.00	0.44
1:A:46:ASP:HB2	1:A:75:ILE:HG23	2.00	0.43
1:B:118:ARG:HG2	1:B:119:ASN:N	2.33	0.43
1:A:244:THR:HA	1:A:282:ILE:O	2.19	0.43
1:C:55:GLU:OE1	1:C:145:TYR:OH	2.25	0.43
1:C:115[B]:GLU:HG3	1:C:118:ARG:HD3	2.00	0.43
1:D:115:GLU:HB2	1:D:116:PRO:HD2	2.01	0.43
1:B:76:ARG:O	1:B:77:SER:HB2	2.20	0.42
1:D:118:ARG:HH11	1:D:118:ARG:HA	1.85	0.42
1:C:269:GLN:HA	1:C:275:ARG:HD3	2.02	0.42
1:D:46:ASP:HB2	1:D:75:ILE:HG23	2.02	0.41
1:A:66:ARG:O	1:A:73:HIS:HA	2.20	0.41
1:B:47:LEU:HD21	1:B:76:ARG:HG2	2.02	0.41
1:C:284:ARG:HG2	1:C:288:ILE:HD13	2.03	0.41
1:A:246:ARG:HE	1:A:246:ARG:HB3	1.74	0.41
1:D:238:ALA:O	1:D:273:ALA:HB2	2.21	0.41
1:B:226:MSE:HE1	3:B:554:HOH:O	2.21	0.41
1:D:254:GLN:CD	1:D:254:GLN:H	2.24	0.41
1:B:292:PHE:HA	1:B:295:LEU:HD12	2.01	0.41
1:A:136:HIS:HE1	3:A:999:HOH:O	2.03	0.40
1:A:242:PHE:HD1	1:A:282:ILE:HD13	1.85	0.40
1:A:225:ARG:HD2	3:A:624:HOH:O	2.20	0.40
1:C:197:HIS:HD2	3:C:536:HOH:O	2.03	0.40
1:B:176:LEU:HD23	1:B:307:ALA:HB2	2.02	0.40
1:D:242:PHE:HD1	1:D:282:ILE:CD1	2.34	0.40
1:B:269:GLN:OE1	1:B:275:ARG:HD3	2.21	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	294/297 (99%)	286 (97%)	8 (3%)	0	100	100
1	B	294/297 (99%)	288 (98%)	6 (2%)	0	100	100
1	C	295/297 (99%)	288 (98%)	7 (2%)	0	100	100
1	D	292/297 (98%)	288 (99%)	4 (1%)	0	100	100
All	All	1175/1188 (99%)	1150 (98%)	25 (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	246/242 (102%)	234 (95%)	12 (5%)	25	31
1	B	247/242 (102%)	239 (97%)	8 (3%)	39	50
1	C	248/242 (102%)	238 (96%)	10 (4%)	31	40
1	D	245/242 (101%)	241 (98%)	4 (2%)	62	76
All	All	986/968 (102%)	952 (97%)	34 (3%)	39	47

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	66	ARG
1	A	76	ARG
1	A	115	GLU
1	A	122	ILE
1	A	127	LYS
1	A	160[A]	ILE
1	A	160[B]	ILE
1	A	176	LEU
1	A	192	LYS
1	A	248	ASP

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Mol	Chain	Res	Type
1	A	249	THR
1	A	264	MSE
1	B	21	VAL
1	B	118	ARG
1	B	124	ARG
1	B	127	LYS
1	B	176	LEU
1	B	184	SER
1	B	249	THR
1	B	270	PHE
1	C	68	ARG
1	C	115[A]	GLU
1	C	115[B]	GLU
1	C	118	ARG
1	C	122	ILE
1	C	138	LYS
1	C	156	SER
1	C	176[A]	LEU
1	C	176[B]	LEU
1	C	190	GLN
1	D	68	ARG
1	D	76	ARG
1	D	118	ARG
1	D	249	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	45	HIS
1	A	136	HIS
1	A	168	GLN
1	A	170	ASN
1	A	190	GLN
1	B	22	GLN
1	B	64	HIS
1	B	73	HIS
1	B	168	GLN
1	B	170	ASN
1	B	197	HIS
1	C	64	HIS
1	C	170	ASN
1	C	197	HIS

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Mol	Chain	Res	Type
1	C	290	ASN
1	D	22	GLN
1	D	73	HIS
1	D	303	GLN

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 monosaccharides in this entry.

5.6 Ligand geometry

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	289/297 (97%)	-0.35	1 (0%)	94	93	23, 32, 44, 49	0
1	B	289/297 (97%)	-0.26	2 (0%)	87	86	21, 30, 45, 55	0
1	C	289/297 (97%)	-0.36	1 (0%)	94	93	18, 26, 36, 51	0
1	D	289/297 (97%)	-0.45	2 (0%)	87	86	20, 29, 38, 45	0
All	All	1156/1188 (97%)	-0.36	6 (0%)	91	90	18, 29, 42, 55	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	179	GLN	4.2
1	B	21	VAL	2.3
1	D	180	LYS	2.1
1	A	234	PRO	2.1
1	C	270	PHE	2.1
1	B	179	GLN	2.0

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

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

6.3 Carbohydrates

There are no monosaccharides 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, 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	CL	C	402	1/1	0.96	0.07	41,41,41,41	0
2	CL	C	401	1/1	0.98	0.06	30,30,30,30	0

6.5 Other polymers (i)

There are no such residues in this entry.