Full wwPDB X-ray Structure Validation Report ⓘ

Mar 3, 2025 – 12:39 pm GMT

PDB ID	:	9H3D
Title	:	F-ENA exosporium anchoring complex between ExsF and a peptide derived from the N-terminus of F-Anchor
Authors	:	Sogues, A.; Sleutel, M.; Remaut, H.
Deposited on	:	2024-10-16
Resolution	:	1.92 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:

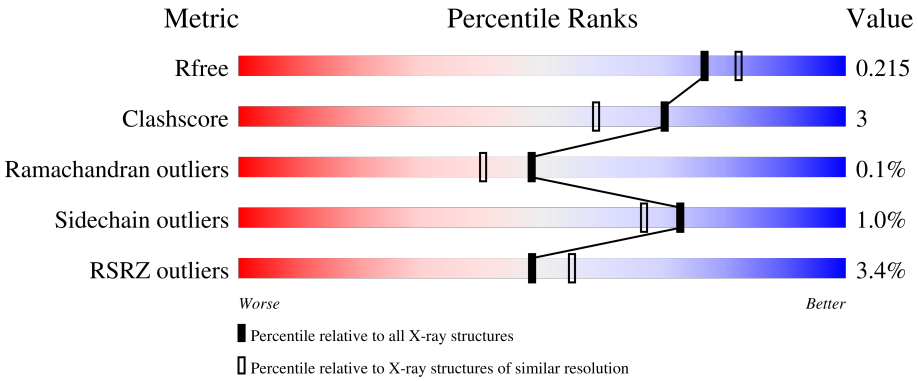
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.41

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 1.92 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}	164625	1028 (1.92-1.92)
Clashscore	180529	1100 (1.92-1.92)
Ramachandran outliers	177936	1087 (1.92-1.92)
Sidechain outliers	177891	1087 (1.92-1.92)
RSRZ outliers	164620	1028 (1.92-1.92)

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	21	5% 81% 10% 10%
1	B	21	5% 62% 38%
1	C	21	5% 81% 14% 5%
1	G	21	29% 52% 19% 29%
1	H	21	5% 43% 14% 43%

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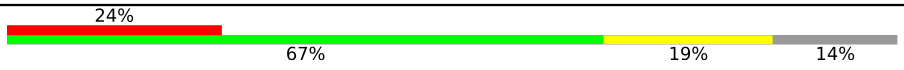
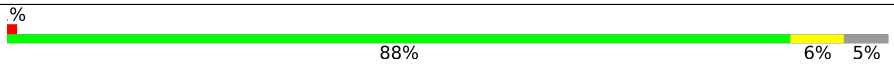
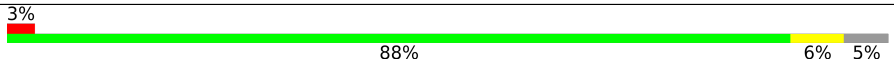
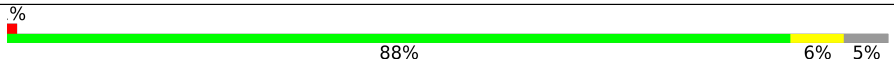
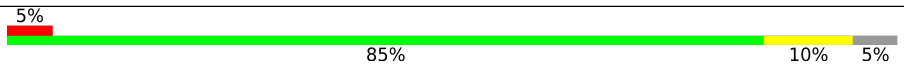
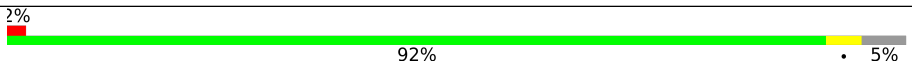
Mol	Chain	Length	Quality of chain
1	I	21	
2	D	155	
2	E	155	
2	F	155	
2	J	155	
2	K	155	
2	L	155	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7885 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 DUF4183 domain-containing protein.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	19	Total	C	N	O	0	0	0
			142	97	20	25			
1	B	13	Total	C	N	O	0	0	0
			93	61	14	18			
1	C	20	Total	C	N	O	0	0	0
			149	101	21	27			
1	G	15	Total	C	N	O	0	0	0
			107	71	16	20			
1	H	12	Total	C	N	O	0	0	0
			89	57	13	19			
1	I	18	Total	C	N	O	0	0	0
			139	94	19	26			

- Molecule 2 is a protein called Exosporium protein ExsF.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	D	148	Total	C	N	O	0	0	0
			1075	693	177	205			
2	E	147	Total	C	N	O	0	0	0
			1067	689	176	202			
2	F	147	Total	C	N	O	0	0	0
			1067	689	176	202			
2	J	147	Total	C	N	O	0	0	0
			1068	689	176	203			
2	K	148	Total	C	N	O	0	0	0
			1074	693	177	204			
2	L	148	Total	C	N	O	0	0	0
			1074	693	177	204			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	13	MET	-	initiating methionine	UNP A0AAP5G885

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Chain	Residue	Modelled	Actual	Comment	Reference
D	14	HIS	-	expression tag	UNP A0AAP5G885
D	15	HIS	-	expression tag	UNP A0AAP5G885
D	16	HIS	-	expression tag	UNP A0AAP5G885
D	17	HIS	-	expression tag	UNP A0AAP5G885
D	18	HIS	-	expression tag	UNP A0AAP5G885
D	19	HIS	-	expression tag	UNP A0AAP5G885
E	13	MET	-	initiating methionine	UNP A0AAP5G885
E	14	HIS	-	expression tag	UNP A0AAP5G885
E	15	HIS	-	expression tag	UNP A0AAP5G885
E	16	HIS	-	expression tag	UNP A0AAP5G885
E	17	HIS	-	expression tag	UNP A0AAP5G885
E	18	HIS	-	expression tag	UNP A0AAP5G885
E	19	HIS	-	expression tag	UNP A0AAP5G885
F	13	MET	-	initiating methionine	UNP A0AAP5G885
F	14	HIS	-	expression tag	UNP A0AAP5G885
F	15	HIS	-	expression tag	UNP A0AAP5G885
F	16	HIS	-	expression tag	UNP A0AAP5G885
F	17	HIS	-	expression tag	UNP A0AAP5G885
F	18	HIS	-	expression tag	UNP A0AAP5G885
F	19	HIS	-	expression tag	UNP A0AAP5G885
J	13	MET	-	initiating methionine	UNP A0AAP5G885
J	14	HIS	-	expression tag	UNP A0AAP5G885
J	15	HIS	-	expression tag	UNP A0AAP5G885
J	16	HIS	-	expression tag	UNP A0AAP5G885
J	17	HIS	-	expression tag	UNP A0AAP5G885
J	18	HIS	-	expression tag	UNP A0AAP5G885
J	19	HIS	-	expression tag	UNP A0AAP5G885
K	13	MET	-	initiating methionine	UNP A0AAP5G885
K	14	HIS	-	expression tag	UNP A0AAP5G885
K	15	HIS	-	expression tag	UNP A0AAP5G885
K	16	HIS	-	expression tag	UNP A0AAP5G885
K	17	HIS	-	expression tag	UNP A0AAP5G885
K	18	HIS	-	expression tag	UNP A0AAP5G885
K	19	HIS	-	expression tag	UNP A0AAP5G885
L	13	MET	-	initiating methionine	UNP A0AAP5G885
L	14	HIS	-	expression tag	UNP A0AAP5G885
L	15	HIS	-	expression tag	UNP A0AAP5G885
L	16	HIS	-	expression tag	UNP A0AAP5G885
L	17	HIS	-	expression tag	UNP A0AAP5G885
L	18	HIS	-	expression tag	UNP A0AAP5G885
L	19	HIS	-	expression tag	UNP A0AAP5G885

- Molecule 3 is water.

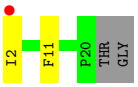
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	15	Total O 15 15	0	0
3	B	11	Total O 11 11	0	0
3	C	20	Total O 20 20	0	0
3	D	133	Total O 133 133	0	0
3	E	151	Total O 151 151	0	0
3	F	128	Total O 128 128	0	0
3	G	6	Total O 6 6	0	0
3	H	7	Total O 7 7	0	0
3	I	7	Total O 7 7	0	0
3	J	73	Total O 73 73	0	0
3	K	83	Total O 83 83	0	0
3	L	107	Total O 107 107	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.

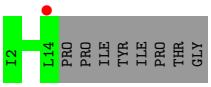
• Molecule 1: DUF4183 domain-containing protein

Chain A:



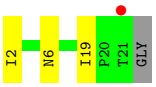
• Molecule 1: DUF4183 domain-containing protein

Chain B:



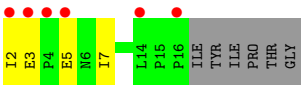
• Molecule 1: DUF4183 domain-containing protein

Chain C:



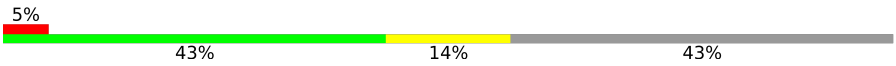
• Molecule 1: DUF4183 domain-containing protein

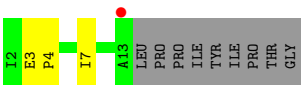
Chain G:



• Molecule 1: DUF4183 domain-containing protein

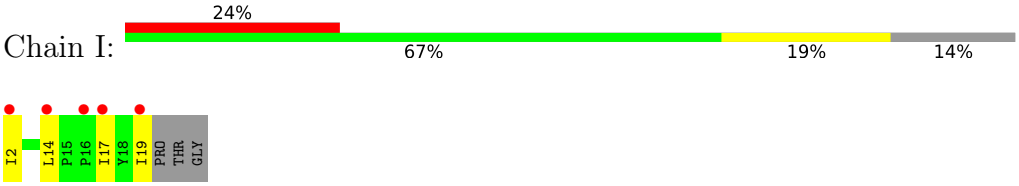
Chain H:





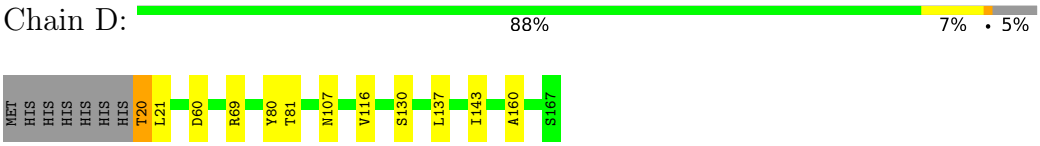
• Molecule 1: DUF4183 domain-containing protein

Chain I:



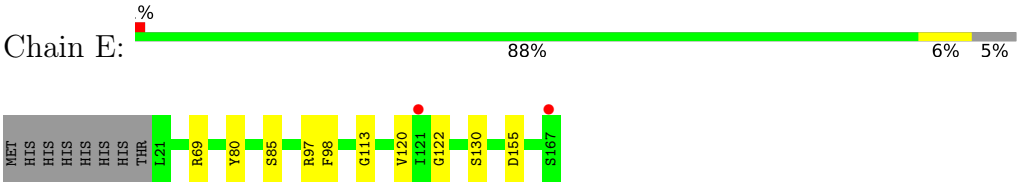
• Molecule 2: Exosporium protein ExsF

Chain D:



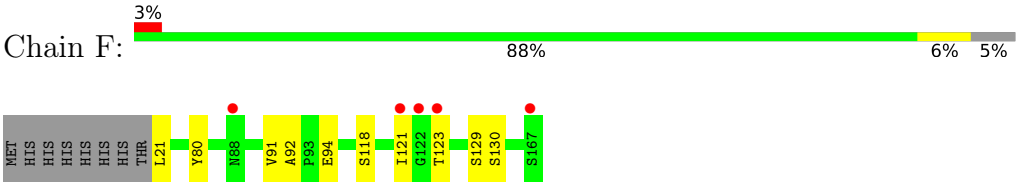
• Molecule 2: Exosporium protein ExsF

Chain E:



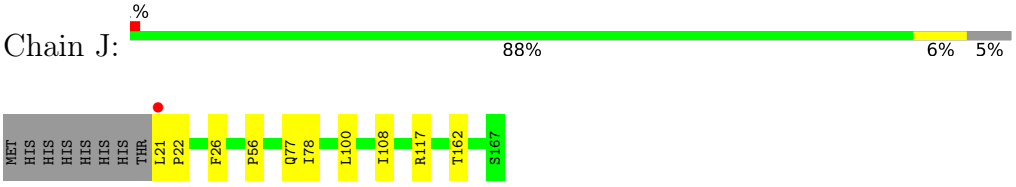
• Molecule 2: Exosporium protein ExsF

Chain F:



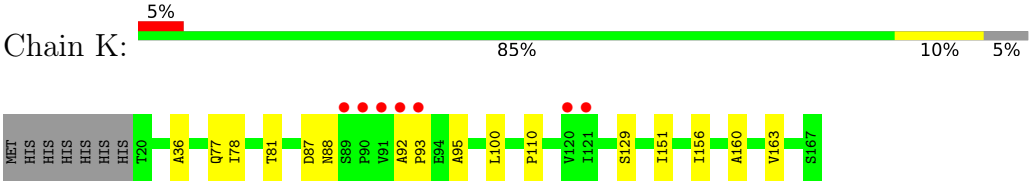
• Molecule 2: Exosporium protein ExsF

Chain J:



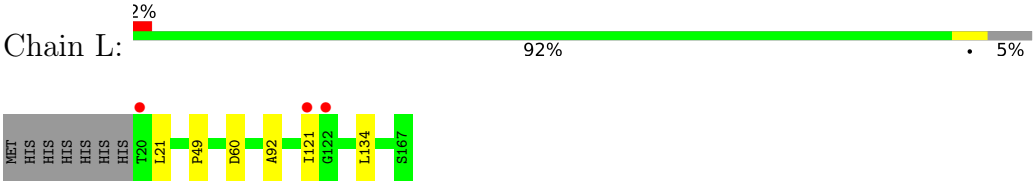
• Molecule 2: Exosporium protein ExsF

Chain K:



• Molecule 2: Exosporium protein ExsF

Chain L:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	51.29Å 91.81Å 99.93Å 90.00° 101.57° 90.00°	Depositor
Resolution (Å)	50.25 – 1.92 50.25 – 1.92	Depositor EDS
% Data completeness (in resolution range)	98.8 (50.25-1.92) 98.8 (50.25-1.92)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.37 (at 1.92Å)	Xtriage
Refinement program	PHENIX 1.21_5207	Depositor
R, R_{free}	0.184 , 0.216 0.184 , 0.215	Depositor DCC
R_{free} test set	3407 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å^2)	22.9	Xtriage
Anisotropy	0.636	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 48.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	7885	wwPDB-VP
Average B, all atoms (Å^2)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.44% 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

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	0.35	0/148	0.44	0/206
1	B	0.36	0/95	0.47	0/130
1	C	0.34	0/155	0.53	0/216
1	G	0.32	0/111	0.48	0/154
1	H	0.33	0/91	0.43	0/124
1	I	0.36	0/144	0.49	0/199
2	D	0.40	0/1097	0.63	0/1509
2	E	0.39	0/1089	0.60	0/1499
2	F	0.38	0/1089	0.58	0/1499
2	J	0.34	0/1090	0.56	0/1499
2	K	0.35	0/1096	0.58	0/1509
2	L	0.36	0/1096	0.61	0/1508
All	All	0.37	0/7301	0.58	0/10052

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	142	0	141	2	0
1	B	93	0	89	0	0
1	C	149	0	148	3	0
1	G	107	0	103	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	H	89	0	82	3	0
1	I	139	0	138	2	0
2	D	1075	0	1109	6	0
2	E	1067	0	1102	6	0
2	F	1067	0	1102	7	0
2	J	1068	0	1102	8	0
2	K	1074	0	1109	11	0
2	L	1074	0	1106	4	0
3	A	15	0	0	1	0
3	B	11	0	0	0	0
3	C	20	0	0	2	1
3	D	133	0	0	2	2
3	E	151	0	0	1	4
3	F	128	0	0	3	1
3	G	6	0	0	0	0
3	H	7	0	0	1	0
3	I	7	0	0	1	0
3	J	73	0	0	1	0
3	K	83	0	0	2	0
3	L	107	0	0	1	0
All	All	7885	0	7331	48	4

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 3.

All (48) 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)
2:D:107:ASN:ND2	3:D:201:HOH:O	1.95	0.99
1:I:2:ILE:O	3:I:101:HOH:O	1.88	0.92
2:K:88:ASN:O	3:K:201:HOH:O	1.90	0.90
1:A:2:ILE:O	3:A:101:HOH:O	2.04	0.75
2:D:69:ARG:HD3	3:D:255:HOH:O	1.88	0.73
1:G:2:ILE:HB	1:G:7:ILE:HD11	1.69	0.73
2:K:36:ALA:HB2	2:K:156:ILE:HD11	1.70	0.73
1:C:6:ASN:O	3:C:101:HOH:O	2.10	0.68
2:F:129:SER:O	3:F:201:HOH:O	2.14	0.65
2:E:69:ARG:HD3	3:E:253:HOH:O	1.96	0.64
2:J:56:PRO:O	3:J:201:HOH:O	2.16	0.59
2:D:20:THR:HG23	2:D:21:LEU:H	1.68	0.58
1:H:7:ILE:HD12	2:J:108:ILE:HD11	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2:ILE:HG13	3:C:103:HOH:O	2.07	0.53
2:L:121:ILE:HG12	3:L:272:HOH:O	2.09	0.52
2:J:117:ARG:NH2	2:K:87:ASP:OD2	2.45	0.50
2:E:85:SER:HB3	2:E:155:ASP:HB3	1.94	0.49
2:D:81:THR:HG22	2:D:160:ALA:HB3	1.94	0.49
1:C:19:ILE:HG12	2:F:91:VAL:HG12	1.96	0.47
2:F:129:SER:HB3	3:F:280:HOH:O	2.15	0.46
2:J:78:ILE:HA	2:J:162:THR:O	2.17	0.45
2:K:78:ILE:HG22	2:K:163:VAL:HG22	1.99	0.44
2:K:129:SER:O	3:K:202:HOH:O	2.20	0.44
2:D:137:LEU:HD13	2:D:143:ILE:HD11	1.99	0.44
1:H:3:GLU:HG3	1:H:4:PRO:HD2	1.99	0.44
2:F:80:TYR:CE2	2:F:130:SER:HB3	2.53	0.44
1:G:3:GLU:O	1:G:7:ILE:HG12	2.18	0.44
2:J:78:ILE:HD12	2:J:100:LEU:HD13	2.00	0.44
2:K:92:ALA:HB3	2:K:93:PRO:HD3	1.99	0.43
2:E:98:PHE:O	2:E:113:GLY:HA2	2.17	0.43
2:J:26:PHE:HB2	2:L:134:LEU:HB2	1.99	0.43
2:F:21:LEU:N	3:F:207:HOH:O	2.52	0.42
1:H:3:GLU:HG2	3:H:101:HOH:O	2.18	0.42
2:F:118:SER:CB	2:F:123:THR:HG1	2.32	0.42
2:D:80:TYR:CE1	2:D:130:SER:HB3	2.54	0.42
2:E:120:VAL:HG23	2:E:122:GLY:H	1.85	0.42
1:I:17:ILE:HA	2:L:92:ALA:O	2.19	0.42
2:K:77:GLN:O	2:K:77:GLN:HG3	2.20	0.42
1:A:11:PHE:CZ	2:E:97:ARG:HG3	2.56	0.41
1:G:2:ILE:HB	1:G:7:ILE:CD1	2.45	0.41
2:K:81:THR:HG22	2:K:160:ALA:HB3	2.03	0.41
2:K:110:PRO:HD2	2:L:49:PRO:O	2.20	0.41
2:F:92:ALA:HB2	2:F:121:ILE:HG23	2.02	0.41
2:E:80:TYR:CE2	2:E:130:SER:HB3	2.56	0.41
2:J:77:GLN:O	2:J:77:GLN:HG3	2.21	0.40
2:K:95:ALA:HB3	2:K:151:ILE:HB	2.02	0.40
2:J:21:LEU:N	2:J:22:PRO:HD2	2.37	0.40
2:K:78:ILE:HD12	2:K:100:LEU:HD13	2.04	0.40

All (4) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:293:HOH:O	3:E:271:HOH:O[2_646]	1.90	0.30

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:265:HOH:O	3:E:224:HOH:O[2_646]	2.07	0.13
3:E:331:HOH:O	3:F:302:HOH:O[1_455]	2.13	0.07
3:C:105:HOH:O	3:E:300:HOH:O[2_646]	2.17	0.03

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	17/21 (81%)	17 (100%)	0	0	100	100
1	B	11/21 (52%)	11 (100%)	0	0	100	100
1	C	18/21 (86%)	18 (100%)	0	0	100	100
1	G	13/21 (62%)	12 (92%)	1 (8%)	0	100	100
1	H	10/21 (48%)	10 (100%)	0	0	100	100
1	I	16/21 (76%)	16 (100%)	0	0	100	100
2	D	146/155 (94%)	144 (99%)	2 (1%)	0	100	100
2	E	145/155 (94%)	140 (97%)	5 (3%)	0	100	100
2	F	145/155 (94%)	138 (95%)	7 (5%)	0	100	100
2	J	145/155 (94%)	141 (97%)	4 (3%)	0	100	100
2	K	146/155 (94%)	139 (95%)	7 (5%)	0	100	100
2	L	146/155 (94%)	140 (96%)	5 (3%)	1 (1%)	19	9
All	All	958/1056 (91%)	926 (97%)	31 (3%)	1 (0%)	48	40

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	L	21	LEU

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	16/18 (89%)	16 (100%)	0	100 100
1	B	10/18 (56%)	10 (100%)	0	100 100
1	C	17/18 (94%)	17 (100%)	0	100 100
1	G	12/18 (67%)	11 (92%)	1 (8%)	9 1
1	H	10/18 (56%)	10 (100%)	0	100 100
1	I	16/18 (89%)	14 (88%)	2 (12%)	3 0
2	D	121/128 (94%)	118 (98%)	3 (2%)	42 27
2	E	120/128 (94%)	120 (100%)	0	100 100
2	F	120/128 (94%)	119 (99%)	1 (1%)	79 74
2	J	120/128 (94%)	120 (100%)	0	100 100
2	K	121/128 (94%)	121 (100%)	0	100 100
2	L	120/128 (94%)	119 (99%)	1 (1%)	79 74
All	All	803/876 (92%)	795 (99%)	8 (1%)	73 67

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	20	THR
2	D	60	ASP
2	D	116	VAL
2	F	94	GLU
1	G	5	GLU
1	I	14	LEU
1	I	19	ILE
2	L	60	ASP

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

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 oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

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	19/21 (90%)	0.36	1 (5%) 33 38	22, 36, 55, 58	0
1	B	13/21 (61%)	0.39	1 (7%) 21 26	20, 31, 52, 57	0
1	C	20/21 (95%)	0.31	1 (5%) 35 40	21, 31, 47, 49	0
1	G	15/21 (71%)	1.83	6 (40%) 1 1	35, 56, 94, 102	0
1	H	12/21 (57%)	0.68	1 (8%) 19 23	42, 53, 69, 75	0
1	I	18/21 (85%)	1.12	5 (27%) 2 1	34, 50, 76, 78	0
2	D	148/155 (95%)	-0.40	0 100 100	18, 24, 31, 51	0
2	E	147/155 (94%)	-0.44	2 (1%) 73 79	18, 23, 30, 43	0
2	F	147/155 (94%)	-0.27	5 (3%) 48 55	18, 24, 31, 51	0
2	J	147/155 (94%)	0.10	1 (0%) 84 88	32, 42, 50, 53	0
2	K	148/155 (95%)	0.16	7 (4%) 37 43	26, 37, 65, 123	0
2	L	148/155 (95%)	-0.02	3 (2%) 64 70	27, 33, 45, 84	0
All	All	982/1056 (92%)	-0.05	33 (3%) 48 55	18, 30, 53, 123	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	2	ILE	4.7
1	I	19	ILE	4.1
2	F	122	GLY	3.9
1	G	4	PRO	3.8
1	G	16	PRO	3.8
2	E	121	ILE	3.7
2	K	91	VAL	3.6
2	F	121	ILE	3.6
1	G	3	GLU	3.3
1	B	14	LEU	3.1
2	K	90	PRO	3.1

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Mol	Chain	Res	Type	RSRZ
2	J	21	LEU	3.1
2	K	120	VAL	3.0
2	K	121	ILE	2.8
1	I	14	LEU	2.8
2	E	167	SER	2.8
2	K	93	PRO	2.7
2	L	20	THR	2.6
2	K	92	ALA	2.6
2	L	121	ILE	2.6
2	L	122	GLY	2.6
2	F	123	THR	2.6
1	G	14	LEU	2.5
1	G	5	GLU	2.5
2	K	89	SER	2.4
1	H	13	ALA	2.4
1	A	2	ILE	2.3
1	I	2	ILE	2.3
2	F	167	SER	2.2
1	C	21	THR	2.1
1	I	16	PRO	2.1
1	I	17	ILE	2.1
2	F	88	ASN	2.1

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)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.