



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 7, 2023 – 12:09 PM JST

PDB ID : 8J0H
Title : Crystal structure of the fission yeast Rex1BD protein(C4H3.06)
Authors : Li, J.; Sun, W.; Chen, Y.
Deposited on : 2023-04-11
Resolution : 3.38 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 : 1.8.5 (274361), CSD as541be (2020)
Xtrriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

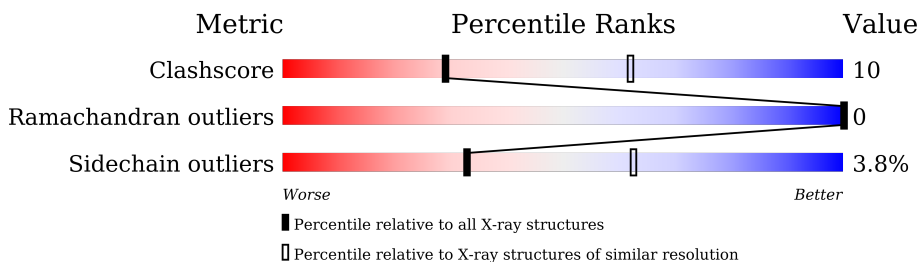
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.38 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))
Clashscore	141614	1762 (3.46-3.30)
Ramachandran outliers	138981	1732 (3.46-3.30)
Sidechain outliers	138945	1731 (3.46-3.30)

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 $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	142	69% 25% 6%
1	B	142	70% 23% 7%
1	C	142	71% 20% 8%
1	D	142	63% 26% 9%
1	E	142	70% 21% 8%
1	F	142	75% 14% 8%
1	G	142	71% 21% 8%
1	H	142	65% 22% 9%

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 8308 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 Uncharacterized protein C4H3.06.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	Se			
1	A	134	1063	657	181	222	3	0	0	0
1	B	132	1048	646	179	220	3	0	0	0
1	C	131	1040	640	178	219	3	0	0	0
1	D	129	1023	631	176	213	3	0	0	0
1	E	130	1032	636	177	216	3	0	0	0
1	F	131	1040	640	178	219	3	0	0	0
1	G	131	1040	640	178	219	3	0	0	0
1	H	129	1022	628	174	217	3	0	0	0

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	GLY	-	expression tag	UNP Q10214
A	-3	PRO	-	expression tag	UNP Q10214
A	-2	LEU	-	linker	UNP Q10214
A	-1	GLY	-	linker	UNP Q10214
A	0	SER	-	linker	UNP Q10214
B	-4	GLY	-	expression tag	UNP Q10214
B	-3	PRO	-	expression tag	UNP Q10214
B	-2	LEU	-	linker	UNP Q10214
B	-1	GLY	-	linker	UNP Q10214
B	0	SER	-	linker	UNP Q10214
C	-4	GLY	-	expression tag	UNP Q10214
C	-3	PRO	-	expression tag	UNP Q10214
C	-2	LEU	-	linker	UNP Q10214

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-1	GLY	-	linker	UNP Q10214
C	0	SER	-	linker	UNP Q10214
D	-4	GLY	-	expression tag	UNP Q10214
D	-3	PRO	-	expression tag	UNP Q10214
D	-2	LEU	-	linker	UNP Q10214
D	-1	GLY	-	linker	UNP Q10214
D	0	SER	-	linker	UNP Q10214
E	-4	GLY	-	expression tag	UNP Q10214
E	-3	PRO	-	expression tag	UNP Q10214
E	-2	LEU	-	linker	UNP Q10214
E	-1	GLY	-	linker	UNP Q10214
E	0	SER	-	linker	UNP Q10214
F	-4	GLY	-	expression tag	UNP Q10214
F	-3	PRO	-	expression tag	UNP Q10214
F	-2	LEU	-	linker	UNP Q10214
F	-1	GLY	-	linker	UNP Q10214
F	0	SER	-	linker	UNP Q10214
G	-4	GLY	-	expression tag	UNP Q10214
G	-3	PRO	-	expression tag	UNP Q10214
G	-2	LEU	-	linker	UNP Q10214
G	-1	GLY	-	linker	UNP Q10214
G	0	SER	-	linker	UNP Q10214
H	-4	GLY	-	expression tag	UNP Q10214
H	-3	PRO	-	expression tag	UNP Q10214
H	-2	LEU	-	linker	UNP Q10214
H	-1	GLY	-	linker	UNP Q10214
H	0	SER	-	linker	UNP Q10214

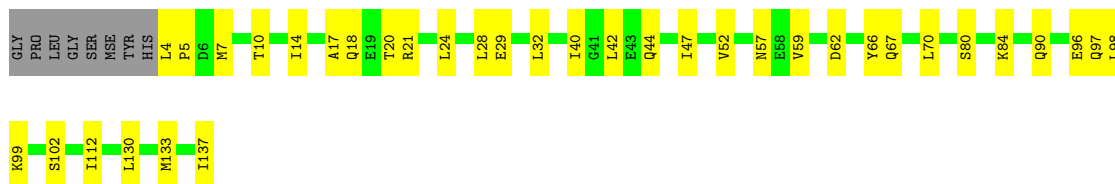
3 Residue-property plots [i](#)

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. 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. 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.

Note EDS was not executed.

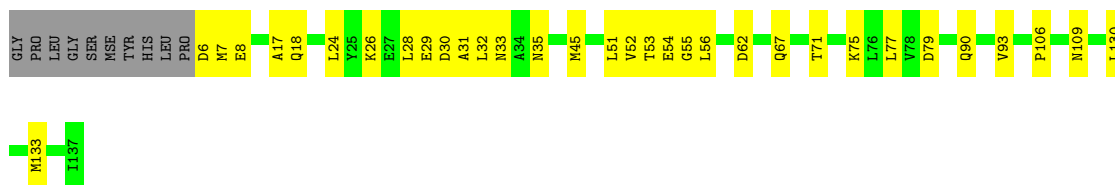
- Molecule 1: Uncharacterized protein C4H3.06

Chain A: 



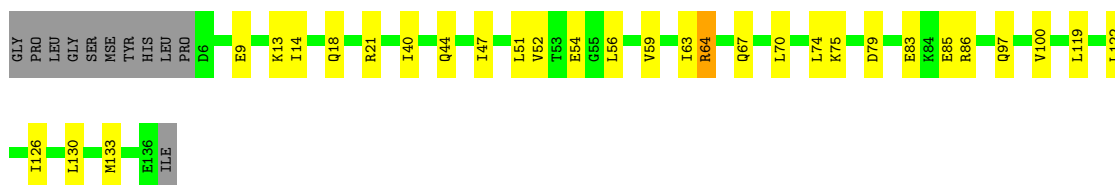
- Molecule 1: Uncharacterized protein C4H3.06

Chain B: 



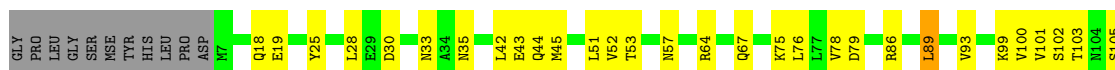
- Molecule 1: Uncharacterized protein C4H3.06

Chain C: 



- Molecule 1: Uncharacterized protein C4H3.06

Chain D: 





- Molecule 1: Uncharacterized protein C4H3.06

Chain E: 70% 21% 8%



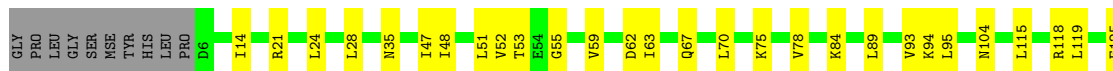
- Molecule 1: Uncharacterized protein C4H3.06

Chain F: 75% 14% 8%



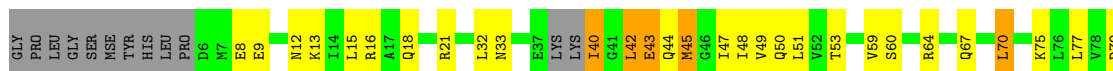
- Molecule 1: Uncharacterized protein C4H3.06

Chain G: 71% 21% 8%



- Molecule 1: Uncharacterized protein C4H3.06

Chain H: 65% 22% 9%



4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	159.01Å 138.48Å 50.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.47 – 3.38	Depositor
% Data completeness (in resolution range)	99.2 (48.47-3.38)	Depositor
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PHENIX (1.14_3260: ???)	Depositor
R, R_{free}	0.242 , 0.296	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	8308	wwPDB-VP
Average B, all atoms (Å ²)	92.0	wwPDB-VP

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.22	0/1063	0.38	0/1424
1	B	0.22	0/1047	0.36	0/1401
1	C	0.23	0/1039	0.40	0/1390
1	D	0.27	0/1023	0.39	0/1370
1	E	0.23	0/1032	0.38	0/1382
1	F	0.27	0/1039	0.38	0/1390
1	G	0.22	0/1039	0.37	0/1390
1	H	0.27	0/1020	0.43	0/1365
All	All	0.24	0/8302	0.39	0/11112

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	1063	0	1101	25	0
1	B	1048	0	1083	24	0
1	C	1040	0	1072	23	0
1	D	1023	0	1062	21	0
1	E	1032	0	1068	24	0
1	F	1040	0	1072	18	0
1	G	1040	0	1072	20	0
1	H	1022	0	1045	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	8308	0	8575	162	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 10.

All (162) 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:H:12:ASN:HB3	1:H:16:ARG:NH1	1.75	0.99
1:G:47:ILE:O	1:G:51:LEU:HD22	1.73	0.86
1:H:12:ASN:HB3	1:H:16:ARG:HH11	1.38	0.86
1:E:78:VAL:HG22	1:E:133:MSE:CE	2.07	0.85
1:H:32:LEU:HD23	1:H:45:MSE:SE	2.28	0.84
1:D:28:LEU:HB2	1:D:52:VAL:HG11	1.63	0.81
1:H:70:LEU:HD12	1:H:75:LYS:HB2	1.64	0.78
1:E:78:VAL:HG22	1:E:133:MSE:HE3	1.66	0.76
1:H:32:LEU:HA	1:H:45:MSE:SE	2.35	0.75
1:E:78:VAL:CG2	1:E:133:MSE:HE3	2.17	0.74
1:F:32:LEU:HA	1:F:45:MSE:HE2	1.69	0.74
1:D:100:VAL:HG12	1:D:101:VAL:HG23	1.70	0.73
1:E:28:LEU:HB2	1:E:52:VAL:HG11	1.69	0.73
1:A:42:LEU:HD12	1:D:43:GLU:HB3	1.71	0.72
1:E:21:ARG:HB2	1:E:59:VAL:HG11	1.72	0.72
1:A:28:LEU:O	1:A:32:LEU:HD22	1.89	0.71
1:C:67:GLN:NE2	1:C:79:ASP:OD1	2.23	0.71
1:A:32:LEU:HB3	1:A:96:GLU:HG3	1.74	0.70
1:A:14:ILE:HG21	1:A:133:MSE:HE1	1.74	0.69
1:C:21:ARG:HH22	1:C:63:ILE:HD12	1.59	0.68
1:C:21:ARG:HB2	1:C:59:VAL:HG11	1.77	0.66
1:F:21:ARG:HB2	1:F:59:VAL:HG11	1.77	0.66
1:C:18:GLN:OE1	1:C:21:ARG:NH1	2.29	0.65
1:F:94:LYS:O	1:F:97:GLN:HG2	1.97	0.65
1:A:137:ILE:HD13	1:G:118:ARG:HB2	1.79	0.64
1:A:90:GLN:HG2	1:D:51:LEU:HD12	1.81	0.63
1:B:53:THR:HB	1:C:54:GLU:HG3	1.80	0.62
1:A:28:LEU:HB2	1:A:52:VAL:HG11	1.80	0.62
1:B:31:ALA:O	1:B:35:ASN:ND2	2.32	0.62
1:C:67:GLN:HE21	1:C:75:LYS:HG3	1.64	0.62
1:B:45:MSE:HE3	1:C:47:ILE:HD13	1.84	0.60
1:D:67:GLN:O	1:D:75:LYS:NZ	2.35	0.59
1:H:40:ILE:HG22	1:H:44:GLN:HB2	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:67:GLN:NE2	1:B:79:ASP:OD1	2.27	0.58
1:H:67:GLN:O	1:H:70:LEU:HB3	2.03	0.58
1:A:44:GLN:O	1:A:47:ILE:HG12	2.04	0.57
1:E:71:THR:HG22	1:E:74:LEU:HB2	1.86	0.57
1:A:20:THR:HG21	1:C:86:ARG:HD3	1.86	0.56
1:D:18:GLN:HG2	1:D:130:LEU:HD11	1.87	0.56
1:B:6:ASP:N	1:B:6:ASP:OD1	2.38	0.56
1:B:28:LEU:HB2	1:B:52:VAL:HG11	1.86	0.56
1:A:97:GLN:HG3	1:D:44:GLN:HE22	1.71	0.56
1:E:54:GLU:HG3	1:G:53:THR:HB	1.87	0.56
1:F:45:MSE:SE	1:G:47:ILE:HD13	2.56	0.55
1:C:79:ASP:O	1:C:83:GLU:HG3	2.07	0.55
1:A:17:ALA:HB1	1:A:59:VAL:HG13	1.88	0.55
1:A:24:LEU:HG	1:A:52:VAL:HG13	1.87	0.55
1:E:81:LEU:HD12	1:E:133:MSE:SE	2.57	0.55
1:D:106:PRO:O	1:D:110:THR:HG23	2.07	0.55
1:D:78:VAL:HG22	1:D:133:MSE:CE	2.36	0.54
1:E:103:THR:OG1	1:E:108:GLU:OE2	2.25	0.54
1:G:67:GLN:NE2	1:G:75:LYS:O	2.41	0.53
1:A:29:GLU:HA	1:A:32:LEU:HD23	1.91	0.53
1:D:42:LEU:HA	1:D:45:MSE:HG2	1.91	0.53
1:G:28:LEU:HB2	1:G:52:VAL:HG11	1.90	0.52
1:A:18:GLN:OE1	1:A:21:ARG:NH1	2.43	0.52
1:H:12:ASN:HB3	1:H:16:ARG:HH12	1.70	0.52
1:D:89:LEU:O	1:D:93:VAL:HG22	2.09	0.52
1:A:40:ILE:HD11	1:C:100:VAL:HG13	1.92	0.51
1:F:97:GLN:HG3	1:F:98:LEU:HD13	1.91	0.51
1:D:33:ASN:OD1	1:D:99:LYS:NZ	2.43	0.51
1:H:95:LEU:HD11	1:H:116:GLU:HG2	1.92	0.51
1:C:14:ILE:HG21	1:C:133:MSE:HE1	1.93	0.51
1:H:15:LEU:HG	1:H:130:LEU:HD12	1.94	0.50
1:B:93:VAL:HG22	1:C:51:LEU:HB3	1.93	0.49
1:C:21:ARG:NH2	1:C:63:ILE:HD12	2.27	0.49
1:D:102:SER:HB3	1:D:108:GLU:OE2	2.11	0.49
1:A:67:GLN:HA	1:A:70:LEU:HD12	1.93	0.49
1:D:78:VAL:HG22	1:D:133:MSE:HE1	1.94	0.49
1:H:21:ARG:HB2	1:H:59:VAL:HG11	1.95	0.49
1:G:47:ILE:HG13	1:G:48:ILE:N	2.28	0.49
1:H:47:ILE:O	1:H:48:ILE:C	2.51	0.48
1:E:42:LEU:HB2	1:H:43:GLU:HG3	1.94	0.48
1:F:97:GLN:O	1:F:101:VAL:HG23	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:67:GLN:NE2	1:C:75:LYS:HG3	2.28	0.47
1:H:45:MSE:HA	1:H:48:ILE:HD12	1.95	0.47
1:D:122:LEU:HA	1:D:125:GLU:HG3	1.95	0.47
1:A:10:THR:HG22	1:A:66:TYR:HB3	1.95	0.47
1:E:78:VAL:HG22	1:E:133:MSE:HE1	1.92	0.46
1:A:18:GLN:HG2	1:A:130:LEU:HD11	1.98	0.46
1:G:21:ARG:HB2	1:G:59:VAL:HG11	1.97	0.46
1:B:29:GLU:O	1:B:33:ASN:ND2	2.48	0.46
1:C:64:ARG:HH22	1:C:79:ASP:HA	1.80	0.46
1:C:21:ARG:HD2	1:C:85:GLU:OE2	2.16	0.46
1:B:35:ASN:OD1	1:B:45:MSE:HB2	2.16	0.46
1:E:78:VAL:CG2	1:E:133:MSE:CE	2.82	0.46
1:H:47:ILE:O	1:H:50:GLN:N	2.49	0.45
1:B:7:MSE:SE	1:B:71:THR:HG23	2.67	0.45
1:G:125:GLU:O	1:G:129:ILE:HG12	2.16	0.45
1:G:67:GLN:HA	1:G:70:LEU:HD12	1.98	0.45
1:A:57:ASN:ND2	1:D:57:ASN:OD1	2.36	0.45
1:E:93:VAL:HG13	1:H:51:LEU:HB3	1.97	0.45
1:A:98:LEU:O	1:A:102:SER:HB3	2.17	0.45
1:E:40:ILE:HD12	1:E:40:ILE:HA	1.86	0.44
1:F:18:GLN:HG2	1:F:130:LEU:HD21	1.99	0.44
1:H:60:SER:HB2	1:H:64:ARG:HH21	1.82	0.44
1:B:18:GLN:HG2	1:B:130:LEU:HD21	1.97	0.44
1:A:99:LYS:HG2	1:A:112:ILE:HG12	1.99	0.44
1:F:106:PRO:O	1:F:110:THR:HG23	2.18	0.44
1:E:84:LYS:HA	1:E:84:LYS:HD2	1.83	0.44
1:E:118:ARG:O	1:E:122:LEU:HB2	2.17	0.44
1:C:18:GLN:HG2	1:C:130:LEU:HD21	1.98	0.44
1:B:24:LEU:HD21	1:B:55:GLY:HA3	1.99	0.44
1:E:17:ALA:HB3	1:E:63:ILE:HD11	2.00	0.44
1:B:6:ASP:N	1:B:8:GLU:OE1	2.51	0.44
1:G:24:LEU:HD21	1:G:55:GLY:HA3	1.99	0.44
1:H:32:LEU:HD23	1:H:32:LEU:HA	1.86	0.44
1:A:7:MSE:HG3	1:G:125:GLU:HG3	2.00	0.43
1:B:77:LEU:HD23	1:B:133:MSE:CG	2.48	0.43
1:C:122:LEU:O	1:C:126:ILE:HG13	2.18	0.43
1:F:18:GLN:OE1	1:F:21:ARG:NH1	2.51	0.43
1:E:72:LYS:HA	1:E:72:LYS:HD2	1.79	0.43
1:F:6:ASP:N	1:F:6:ASP:OD1	2.51	0.43
1:G:94:LYS:HB3	1:G:115:LEU:HD11	2.00	0.43
1:F:7:MSE:HE3	1:F:71:THR:HG23	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:42:LEU:HD12	1:H:42:LEU:HA	1.84	0.43
1:B:26:LYS:O	1:B:30:ASP:HB2	2.19	0.43
1:A:80:SER:O	1:A:84:LYS:HG2	2.19	0.43
1:A:28:LEU:HG	1:A:32:LEU:HD21	1.99	0.43
1:F:18:GLN:HG2	1:F:130:LEU:HD11	1.99	0.43
1:F:21:ARG:NH1	1:F:85:GLU:HG3	2.33	0.43
1:B:17:ALA:HA	1:D:86:ARG:NH2	2.34	0.42
1:G:78:VAL:HG22	1:G:133:MSE:CE	2.49	0.42
1:B:51:LEU:HB3	1:D:93:VAL:HG12	2.01	0.42
1:E:70:LEU:O	1:E:75:LYS:NZ	2.36	0.42
1:E:92:THR:HG23	1:E:119:LEU:HD21	2.00	0.42
1:H:9:GLU:O	1:H:13:LYS:HG2	2.19	0.42
1:G:14:ILE:HG23	1:G:63:ILE:HG23	2.01	0.42
1:B:77:LEU:HD23	1:B:133:MSE:HG2	2.02	0.42
1:G:89:LEU:O	1:G:93:VAL:HG23	2.20	0.42
1:F:26:LYS:HA	1:F:26:LYS:HD2	1.78	0.42
1:H:67:GLN:NE2	1:H:79:ASP:OD1	2.52	0.42
1:G:95:LEU:HD23	1:G:95:LEU:HA	1.87	0.42
1:C:9:GLU:HG2	1:C:13:LYS:HE3	2.02	0.41
1:C:40:ILE:HG12	1:C:44:GLN:HB2	2.01	0.41
1:E:77:LEU:HD23	1:E:77:LEU:HA	1.93	0.41
1:E:88:LYS:HE2	1:E:123:SER:HB2	2.02	0.41
1:F:95:LEU:HD12	1:F:115:LEU:HB3	2.02	0.41
1:G:119:LEU:HD23	1:G:119:LEU:HA	1.95	0.41
1:B:24:LEU:HD23	1:B:56:LEU:HD23	2.03	0.41
1:B:28:LEU:O	1:B:32:LEU:HB2	2.21	0.41
1:B:54:GLU:HG3	1:D:53:THR:HB	2.02	0.41
1:C:119:LEU:HD23	1:C:119:LEU:HA	1.87	0.41
1:G:47:ILE:O	1:G:51:LEU:CD2	2.57	0.41
1:B:24:LEU:HD12	1:B:24:LEU:HA	1.87	0.41
1:B:62:ASP:OD1	1:D:64:ARG:NE	2.52	0.41
1:D:76:LEU:HA	1:D:79:ASP:HB2	2.03	0.41
1:H:77:LEU:HD22	1:H:129:ILE:HG23	2.03	0.41
1:H:77:LEU:HB3	1:H:133:MSE:HE2	2.02	0.41
1:C:70:LEU:HD13	1:C:74:LEU:HB3	2.02	0.41
1:H:49:VAL:O	1:H:53:THR:HG23	2.20	0.41
1:H:32:LEU:O	1:H:45:MSE:HE1	2.21	0.40
1:B:106:PRO:HA	1:B:109:ASN:HB2	2.03	0.40
1:G:84:LYS:HA	1:G:84:LYS:HD3	1.89	0.40
1:E:14:ILE:HG23	1:E:63:ILE:HD12	2.03	0.40
1:E:119:LEU:HD23	1:E:119:LEU:HA	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:50:GLN:HG2	1:H:50:GLN:HA	2.04	0.40
1:F:94:LYS:O	1:F:98:LEU:HD22	2.21	0.40
1:A:4:LEU:N	1:A:5:PRO:HD3	2.36	0.40
1:C:52:VAL:O	1:C:56:LEU:HG	2.21	0.40
1:F:25:TYR:OH	1:F:89:LEU:HD22	2.21	0.40
1:H:18:GLN:NE2	1:H:85:GLU:OE1	2.55	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	132/142 (93%)	130 (98%)	2 (2%)	0	100	100
1	B	130/142 (92%)	130 (100%)	0	0	100	100
1	C	129/142 (91%)	128 (99%)	1 (1%)	0	100	100
1	D	127/142 (89%)	126 (99%)	1 (1%)	0	100	100
1	E	128/142 (90%)	128 (100%)	0	0	100	100
1	F	129/142 (91%)	127 (98%)	2 (2%)	0	100	100
1	G	129/142 (91%)	128 (99%)	1 (1%)	0	100	100
1	H	125/142 (88%)	123 (98%)	2 (2%)	0	100	100
All	All	1029/1136 (91%)	1020 (99%)	9 (1%)	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	124/126 (98%)	123 (99%)	1 (1%)	81	91
1	B	122/126 (97%)	120 (98%)	2 (2%)	62	81
1	C	121/126 (96%)	119 (98%)	2 (2%)	60	80
1	D	119/126 (94%)	109 (92%)	10 (8%)	11	37
1	E	120/126 (95%)	117 (98%)	3 (2%)	47	73
1	F	121/126 (96%)	113 (93%)	8 (7%)	16	47
1	G	121/126 (96%)	118 (98%)	3 (2%)	47	73
1	H	119/126 (94%)	111 (93%)	8 (7%)	16	47
All	All	967/1008 (96%)	930 (96%)	37 (4%)	33	62

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	62	ASP
1	B	75	LYS
1	B	90	GLN
1	C	64	ARG
1	C	97	GLN
1	D	19	GLU
1	D	25	TYR
1	D	30	ASP
1	D	35	ASN
1	D	89	LEU
1	D	103	THR
1	D	105	SER
1	D	107	VAL
1	D	108	GLU
1	D	132	ASN
1	E	13	LYS
1	E	79	ASP
1	E	122	LEU
1	F	25	TYR
1	F	26	LYS
1	F	94	LYS
1	F	98	LEU
1	F	101	VAL
1	F	105	SER

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Mol	Chain	Res	Type
1	F	131	GLN
1	F	135	ASP
1	G	35	ASN
1	G	62	ASP
1	G	104	ASN
1	H	8	GLU
1	H	33	ASN
1	H	40	ILE
1	H	42	LEU
1	H	43	GLU
1	H	45	MSE
1	H	70	LEU
1	H	90	GLN

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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

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](#)

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.