Full wwPDB X-ray Structure Validation Report (i)

Dec 17, 2023 – 06:38 am GMT

PDB ID	:	4D1F
Title	:	Crystal structure of the fiber head domain of the Atadenovirus snake adenovirus 1, native, first P212121 crystal form
Authors	:	Singh, A.K.; van Raaij, M.J.
Deposited on	:	2014-05-01
Resolution	:	2.70 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 types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

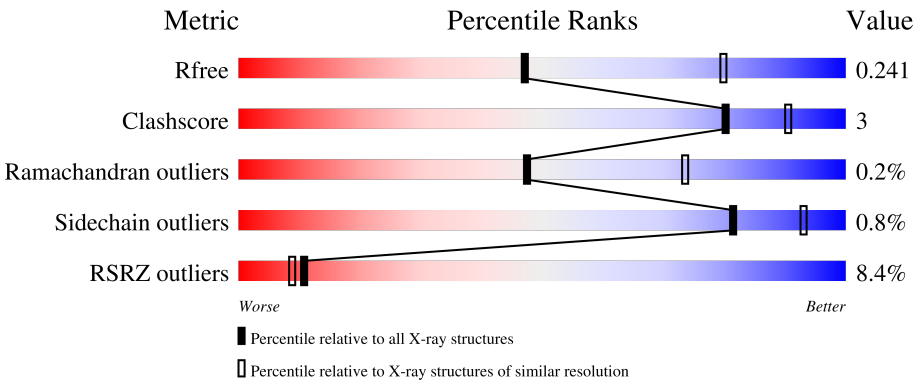
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.70 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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	145	7% 69% • 28%
1	B	145	4% 70% • 27%
1	C	145	3% 69% • 27%
1	D	145	12% 69% • 28%
1	E	145	5% 68% • 28%

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Mol	Chain	Length	Quality of chain
1	F	145	6% 71% 27%
1	G	145	6% 70% 28%
1	H	145	3% 68% 28%
1	I	145	4% 70% 28%
1	J	145	8% 68% 28%
1	K	145	7% 70% 26%
1	L	145	8% 70% 27%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 9799 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 FIBER PROTEIN.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
1	A	105	793	508	127	158	0	0	0
1	B	106	802	514	129	159	0	0	0
1	C	106	802	514	129	159	0	0	0
1	D	105	793	508	127	158	0	0	0
1	E	105	793	508	127	158	0	0	0
1	F	106	802	514	129	159	0	0	0
1	G	105	793	508	127	158	0	0	0
1	H	105	793	508	127	158	0	0	0
1	I	105	793	508	127	158	0	0	0
1	J	105	793	508	127	158	0	0	0
1	K	108	815	522	131	162	0	0	0
1	L	106	802	514	129	159	0	0	0

There are 468 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	201	GLY	-	expression tag	UNP A9CB96
A	202	SER	-	expression tag	UNP A9CB96
A	203	SER	-	expression tag	UNP A9CB96
A	204	HIS	-	expression tag	UNP A9CB96
A	205	HIS	-	expression tag	UNP A9CB96

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Chain	Residue	Modelled	Actual	Comment	Reference
A	206	HIS	-	expression tag	UNP A9CB96
A	207	HIS	-	expression tag	UNP A9CB96
A	208	HIS	-	expression tag	UNP A9CB96
A	209	HIS	-	expression tag	UNP A9CB96
A	210	SER	-	expression tag	UNP A9CB96
A	211	SER	-	expression tag	UNP A9CB96
A	212	GLY	-	expression tag	UNP A9CB96
A	213	LEU	-	expression tag	UNP A9CB96
A	214	VAL	-	expression tag	UNP A9CB96
A	215	PRO	-	expression tag	UNP A9CB96
A	216	ARG	-	expression tag	UNP A9CB96
A	217	GLY	-	expression tag	UNP A9CB96
A	218	SER	-	expression tag	UNP A9CB96
A	219	HIS	-	expression tag	UNP A9CB96
A	220	MET	-	expression tag	UNP A9CB96
A	221	ALA	-	expression tag	UNP A9CB96
A	222	SER	-	expression tag	UNP A9CB96
A	223	MET	-	expression tag	UNP A9CB96
A	224	THR	-	expression tag	UNP A9CB96
A	225	GLY	-	expression tag	UNP A9CB96
A	226	GLY	-	expression tag	UNP A9CB96
A	227	GLN	-	expression tag	UNP A9CB96
A	228	GLN	-	expression tag	UNP A9CB96
A	229	MET	-	expression tag	UNP A9CB96
A	230	GLY	-	expression tag	UNP A9CB96
A	231	ARG	-	expression tag	UNP A9CB96
A	232	GLY	-	expression tag	UNP A9CB96
A	233	SER	-	expression tag	UNP A9CB96
A	340	PHE	-	SEE REMARK 999	UNP A9CB96
A	341	TYR	-	SEE REMARK 999	UNP A9CB96
A	342	LEU	-	SEE REMARK 999	UNP A9CB96
A	343	THR	-	SEE REMARK 999	UNP A9CB96
A	344	GLU	-	SEE REMARK 999	UNP A9CB96
A	345	LYS	-	SEE REMARK 999	UNP A9CB96
B	201	GLY	-	expression tag	UNP A9CB96
B	202	SER	-	expression tag	UNP A9CB96
B	203	SER	-	expression tag	UNP A9CB96
B	204	HIS	-	expression tag	UNP A9CB96
B	205	HIS	-	expression tag	UNP A9CB96
B	206	HIS	-	expression tag	UNP A9CB96
B	207	HIS	-	expression tag	UNP A9CB96
B	208	HIS	-	expression tag	UNP A9CB96

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Chain	Residue	Modelled	Actual	Comment	Reference
B	209	HIS	-	expression tag	UNP A9CB96
B	210	SER	-	expression tag	UNP A9CB96
B	211	SER	-	expression tag	UNP A9CB96
B	212	GLY	-	expression tag	UNP A9CB96
B	213	LEU	-	expression tag	UNP A9CB96
B	214	VAL	-	expression tag	UNP A9CB96
B	215	PRO	-	expression tag	UNP A9CB96
B	216	ARG	-	expression tag	UNP A9CB96
B	217	GLY	-	expression tag	UNP A9CB96
B	218	SER	-	expression tag	UNP A9CB96
B	219	HIS	-	expression tag	UNP A9CB96
B	220	MET	-	expression tag	UNP A9CB96
B	221	ALA	-	expression tag	UNP A9CB96
B	222	SER	-	expression tag	UNP A9CB96
B	223	MET	-	expression tag	UNP A9CB96
B	224	THR	-	expression tag	UNP A9CB96
B	225	GLY	-	expression tag	UNP A9CB96
B	226	GLY	-	expression tag	UNP A9CB96
B	227	GLN	-	expression tag	UNP A9CB96
B	228	GLN	-	expression tag	UNP A9CB96
B	229	MET	-	expression tag	UNP A9CB96
B	230	GLY	-	expression tag	UNP A9CB96
B	231	ARG	-	expression tag	UNP A9CB96
B	232	GLY	-	expression tag	UNP A9CB96
B	233	SER	-	expression tag	UNP A9CB96
B	340	PHE	-	SEE REMARK 999	UNP A9CB96
B	341	TYR	-	SEE REMARK 999	UNP A9CB96
B	342	LEU	-	SEE REMARK 999	UNP A9CB96
B	343	THR	-	SEE REMARK 999	UNP A9CB96
B	344	GLU	-	SEE REMARK 999	UNP A9CB96
B	345	LYS	-	SEE REMARK 999	UNP A9CB96
C	201	GLY	-	expression tag	UNP A9CB96
C	202	SER	-	expression tag	UNP A9CB96
C	203	SER	-	expression tag	UNP A9CB96
C	204	HIS	-	expression tag	UNP A9CB96
C	205	HIS	-	expression tag	UNP A9CB96
C	206	HIS	-	expression tag	UNP A9CB96
C	207	HIS	-	expression tag	UNP A9CB96
C	208	HIS	-	expression tag	UNP A9CB96
C	209	HIS	-	expression tag	UNP A9CB96
C	210	SER	-	expression tag	UNP A9CB96
C	211	SER	-	expression tag	UNP A9CB96

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Chain	Residue	Modelled	Actual	Comment	Reference
C	212	GLY	-	expression tag	UNP A9CB96
C	213	LEU	-	expression tag	UNP A9CB96
C	214	VAL	-	expression tag	UNP A9CB96
C	215	PRO	-	expression tag	UNP A9CB96
C	216	ARG	-	expression tag	UNP A9CB96
C	217	GLY	-	expression tag	UNP A9CB96
C	218	SER	-	expression tag	UNP A9CB96
C	219	HIS	-	expression tag	UNP A9CB96
C	220	MET	-	expression tag	UNP A9CB96
C	221	ALA	-	expression tag	UNP A9CB96
C	222	SER	-	expression tag	UNP A9CB96
C	223	MET	-	expression tag	UNP A9CB96
C	224	THR	-	expression tag	UNP A9CB96
C	225	GLY	-	expression tag	UNP A9CB96
C	226	GLY	-	expression tag	UNP A9CB96
C	227	GLN	-	expression tag	UNP A9CB96
C	228	GLN	-	expression tag	UNP A9CB96
C	229	MET	-	expression tag	UNP A9CB96
C	230	GLY	-	expression tag	UNP A9CB96
C	231	ARG	-	expression tag	UNP A9CB96
C	232	GLY	-	expression tag	UNP A9CB96
C	233	SER	-	expression tag	UNP A9CB96
C	340	PHE	-	SEE REMARK 999	UNP A9CB96
C	341	TYR	-	SEE REMARK 999	UNP A9CB96
C	342	LEU	-	SEE REMARK 999	UNP A9CB96
C	343	THR	-	SEE REMARK 999	UNP A9CB96
C	344	GLU	-	SEE REMARK 999	UNP A9CB96
C	345	LYS	-	SEE REMARK 999	UNP A9CB96
D	201	GLY	-	expression tag	UNP A9CB96
D	202	SER	-	expression tag	UNP A9CB96
D	203	SER	-	expression tag	UNP A9CB96
D	204	HIS	-	expression tag	UNP A9CB96
D	205	HIS	-	expression tag	UNP A9CB96
D	206	HIS	-	expression tag	UNP A9CB96
D	207	HIS	-	expression tag	UNP A9CB96
D	208	HIS	-	expression tag	UNP A9CB96
D	209	HIS	-	expression tag	UNP A9CB96
D	210	SER	-	expression tag	UNP A9CB96
D	211	SER	-	expression tag	UNP A9CB96
D	212	GLY	-	expression tag	UNP A9CB96
D	213	LEU	-	expression tag	UNP A9CB96
D	214	VAL	-	expression tag	UNP A9CB96

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Chain	Residue	Modelled	Actual	Comment	Reference
D	215	PRO	-	expression tag	UNP A9CB96
D	216	ARG	-	expression tag	UNP A9CB96
D	217	GLY	-	expression tag	UNP A9CB96
D	218	SER	-	expression tag	UNP A9CB96
D	219	HIS	-	expression tag	UNP A9CB96
D	220	MET	-	expression tag	UNP A9CB96
D	221	ALA	-	expression tag	UNP A9CB96
D	222	SER	-	expression tag	UNP A9CB96
D	223	MET	-	expression tag	UNP A9CB96
D	224	THR	-	expression tag	UNP A9CB96
D	225	GLY	-	expression tag	UNP A9CB96
D	226	GLY	-	expression tag	UNP A9CB96
D	227	GLN	-	expression tag	UNP A9CB96
D	228	GLN	-	expression tag	UNP A9CB96
D	229	MET	-	expression tag	UNP A9CB96
D	230	GLY	-	expression tag	UNP A9CB96
D	231	ARG	-	expression tag	UNP A9CB96
D	232	GLY	-	expression tag	UNP A9CB96
D	233	SER	-	expression tag	UNP A9CB96
D	340	PHE	-	SEE REMARK 999	UNP A9CB96
D	341	TYR	-	SEE REMARK 999	UNP A9CB96
D	342	LEU	-	SEE REMARK 999	UNP A9CB96
D	343	THR	-	SEE REMARK 999	UNP A9CB96
D	344	GLU	-	SEE REMARK 999	UNP A9CB96
D	345	LYS	-	SEE REMARK 999	UNP A9CB96
E	201	GLY	-	expression tag	UNP A9CB96
E	202	SER	-	expression tag	UNP A9CB96
E	203	SER	-	expression tag	UNP A9CB96
E	204	HIS	-	expression tag	UNP A9CB96
E	205	HIS	-	expression tag	UNP A9CB96
E	206	HIS	-	expression tag	UNP A9CB96
E	207	HIS	-	expression tag	UNP A9CB96
E	208	HIS	-	expression tag	UNP A9CB96
E	209	HIS	-	expression tag	UNP A9CB96
E	210	SER	-	expression tag	UNP A9CB96
E	211	SER	-	expression tag	UNP A9CB96
E	212	GLY	-	expression tag	UNP A9CB96
E	213	LEU	-	expression tag	UNP A9CB96
E	214	VAL	-	expression tag	UNP A9CB96
E	215	PRO	-	expression tag	UNP A9CB96
E	216	ARG	-	expression tag	UNP A9CB96
E	217	GLY	-	expression tag	UNP A9CB96

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Chain	Residue	Modelled	Actual	Comment	Reference
E	218	SER	-	expression tag	UNP A9CB96
E	219	HIS	-	expression tag	UNP A9CB96
E	220	MET	-	expression tag	UNP A9CB96
E	221	ALA	-	expression tag	UNP A9CB96
E	222	SER	-	expression tag	UNP A9CB96
E	223	MET	-	expression tag	UNP A9CB96
E	224	THR	-	expression tag	UNP A9CB96
E	225	GLY	-	expression tag	UNP A9CB96
E	226	GLY	-	expression tag	UNP A9CB96
E	227	GLN	-	expression tag	UNP A9CB96
E	228	GLN	-	expression tag	UNP A9CB96
E	229	MET	-	expression tag	UNP A9CB96
E	230	GLY	-	expression tag	UNP A9CB96
E	231	ARG	-	expression tag	UNP A9CB96
E	232	GLY	-	expression tag	UNP A9CB96
E	233	SER	-	expression tag	UNP A9CB96
E	340	PHE	-	SEE REMARK 999	UNP A9CB96
E	341	TYR	-	SEE REMARK 999	UNP A9CB96
E	342	LEU	-	SEE REMARK 999	UNP A9CB96
E	343	THR	-	SEE REMARK 999	UNP A9CB96
E	344	GLU	-	SEE REMARK 999	UNP A9CB96
E	345	LYS	-	SEE REMARK 999	UNP A9CB96
F	201	GLY	-	expression tag	UNP A9CB96
F	202	SER	-	expression tag	UNP A9CB96
F	203	SER	-	expression tag	UNP A9CB96
F	204	HIS	-	expression tag	UNP A9CB96
F	205	HIS	-	expression tag	UNP A9CB96
F	206	HIS	-	expression tag	UNP A9CB96
F	207	HIS	-	expression tag	UNP A9CB96
F	208	HIS	-	expression tag	UNP A9CB96
F	209	HIS	-	expression tag	UNP A9CB96
F	210	SER	-	expression tag	UNP A9CB96
F	211	SER	-	expression tag	UNP A9CB96
F	212	GLY	-	expression tag	UNP A9CB96
F	213	LEU	-	expression tag	UNP A9CB96
F	214	VAL	-	expression tag	UNP A9CB96
F	215	PRO	-	expression tag	UNP A9CB96
F	216	ARG	-	expression tag	UNP A9CB96
F	217	GLY	-	expression tag	UNP A9CB96
F	218	SER	-	expression tag	UNP A9CB96
F	219	HIS	-	expression tag	UNP A9CB96
F	220	MET	-	expression tag	UNP A9CB96

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Chain	Residue	Modelled	Actual	Comment	Reference
F	221	ALA	-	expression tag	UNP A9CB96
F	222	SER	-	expression tag	UNP A9CB96
F	223	MET	-	expression tag	UNP A9CB96
F	224	THR	-	expression tag	UNP A9CB96
F	225	GLY	-	expression tag	UNP A9CB96
F	226	GLY	-	expression tag	UNP A9CB96
F	227	GLN	-	expression tag	UNP A9CB96
F	228	GLN	-	expression tag	UNP A9CB96
F	229	MET	-	expression tag	UNP A9CB96
F	230	GLY	-	expression tag	UNP A9CB96
F	231	ARG	-	expression tag	UNP A9CB96
F	232	GLY	-	expression tag	UNP A9CB96
F	233	SER	-	expression tag	UNP A9CB96
F	340	PHE	-	SEE REMARK 999	UNP A9CB96
F	341	TYR	-	SEE REMARK 999	UNP A9CB96
F	342	LEU	-	SEE REMARK 999	UNP A9CB96
F	343	THR	-	SEE REMARK 999	UNP A9CB96
F	344	GLU	-	SEE REMARK 999	UNP A9CB96
F	345	LYS	-	SEE REMARK 999	UNP A9CB96
G	201	GLY	-	expression tag	UNP A9CB96
G	202	SER	-	expression tag	UNP A9CB96
G	203	SER	-	expression tag	UNP A9CB96
G	204	HIS	-	expression tag	UNP A9CB96
G	205	HIS	-	expression tag	UNP A9CB96
G	206	HIS	-	expression tag	UNP A9CB96
G	207	HIS	-	expression tag	UNP A9CB96
G	208	HIS	-	expression tag	UNP A9CB96
G	209	HIS	-	expression tag	UNP A9CB96
G	210	SER	-	expression tag	UNP A9CB96
G	211	SER	-	expression tag	UNP A9CB96
G	212	GLY	-	expression tag	UNP A9CB96
G	213	LEU	-	expression tag	UNP A9CB96
G	214	VAL	-	expression tag	UNP A9CB96
G	215	PRO	-	expression tag	UNP A9CB96
G	216	ARG	-	expression tag	UNP A9CB96
G	217	GLY	-	expression tag	UNP A9CB96
G	218	SER	-	expression tag	UNP A9CB96
G	219	HIS	-	expression tag	UNP A9CB96
G	220	MET	-	expression tag	UNP A9CB96
G	221	ALA	-	expression tag	UNP A9CB96
G	222	SER	-	expression tag	UNP A9CB96
G	223	MET	-	expression tag	UNP A9CB96

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Chain	Residue	Modelled	Actual	Comment	Reference
G	224	THR	-	expression tag	UNP A9CB96
G	225	GLY	-	expression tag	UNP A9CB96
G	226	GLY	-	expression tag	UNP A9CB96
G	227	GLN	-	expression tag	UNP A9CB96
G	228	GLN	-	expression tag	UNP A9CB96
G	229	MET	-	expression tag	UNP A9CB96
G	230	GLY	-	expression tag	UNP A9CB96
G	231	ARG	-	expression tag	UNP A9CB96
G	232	GLY	-	expression tag	UNP A9CB96
G	233	SER	-	expression tag	UNP A9CB96
G	340	PHE	-	SEE REMARK 999	UNP A9CB96
G	341	TYR	-	SEE REMARK 999	UNP A9CB96
G	342	LEU	-	SEE REMARK 999	UNP A9CB96
G	343	THR	-	SEE REMARK 999	UNP A9CB96
G	344	GLU	-	SEE REMARK 999	UNP A9CB96
G	345	LYS	-	SEE REMARK 999	UNP A9CB96
H	201	GLY	-	expression tag	UNP A9CB96
H	202	SER	-	expression tag	UNP A9CB96
H	203	SER	-	expression tag	UNP A9CB96
H	204	HIS	-	expression tag	UNP A9CB96
H	205	HIS	-	expression tag	UNP A9CB96
H	206	HIS	-	expression tag	UNP A9CB96
H	207	HIS	-	expression tag	UNP A9CB96
H	208	HIS	-	expression tag	UNP A9CB96
H	209	HIS	-	expression tag	UNP A9CB96
H	210	SER	-	expression tag	UNP A9CB96
H	211	SER	-	expression tag	UNP A9CB96
H	212	GLY	-	expression tag	UNP A9CB96
H	213	LEU	-	expression tag	UNP A9CB96
H	214	VAL	-	expression tag	UNP A9CB96
H	215	PRO	-	expression tag	UNP A9CB96
H	216	ARG	-	expression tag	UNP A9CB96
H	217	GLY	-	expression tag	UNP A9CB96
H	218	SER	-	expression tag	UNP A9CB96
H	219	HIS	-	expression tag	UNP A9CB96
H	220	MET	-	expression tag	UNP A9CB96
H	221	ALA	-	expression tag	UNP A9CB96
H	222	SER	-	expression tag	UNP A9CB96
H	223	MET	-	expression tag	UNP A9CB96
H	224	THR	-	expression tag	UNP A9CB96
H	225	GLY	-	expression tag	UNP A9CB96
H	226	GLY	-	expression tag	UNP A9CB96

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Chain	Residue	Modelled	Actual	Comment	Reference
H	227	GLN	-	expression tag	UNP A9CB96
H	228	GLN	-	expression tag	UNP A9CB96
H	229	MET	-	expression tag	UNP A9CB96
H	230	GLY	-	expression tag	UNP A9CB96
H	231	ARG	-	expression tag	UNP A9CB96
H	232	GLY	-	expression tag	UNP A9CB96
H	233	SER	-	expression tag	UNP A9CB96
H	340	PHE	-	SEE REMARK 999	UNP A9CB96
H	341	TYR	-	SEE REMARK 999	UNP A9CB96
H	342	LEU	-	SEE REMARK 999	UNP A9CB96
H	343	THR	-	SEE REMARK 999	UNP A9CB96
H	344	GLU	-	SEE REMARK 999	UNP A9CB96
H	345	LYS	-	SEE REMARK 999	UNP A9CB96
I	201	GLY	-	expression tag	UNP A9CB96
I	202	SER	-	expression tag	UNP A9CB96
I	203	SER	-	expression tag	UNP A9CB96
I	204	HIS	-	expression tag	UNP A9CB96
I	205	HIS	-	expression tag	UNP A9CB96
I	206	HIS	-	expression tag	UNP A9CB96
I	207	HIS	-	expression tag	UNP A9CB96
I	208	HIS	-	expression tag	UNP A9CB96
I	209	HIS	-	expression tag	UNP A9CB96
I	210	SER	-	expression tag	UNP A9CB96
I	211	SER	-	expression tag	UNP A9CB96
I	212	GLY	-	expression tag	UNP A9CB96
I	213	LEU	-	expression tag	UNP A9CB96
I	214	VAL	-	expression tag	UNP A9CB96
I	215	PRO	-	expression tag	UNP A9CB96
I	216	ARG	-	expression tag	UNP A9CB96
I	217	GLY	-	expression tag	UNP A9CB96
I	218	SER	-	expression tag	UNP A9CB96
I	219	HIS	-	expression tag	UNP A9CB96
I	220	MET	-	expression tag	UNP A9CB96
I	221	ALA	-	expression tag	UNP A9CB96
I	222	SER	-	expression tag	UNP A9CB96
I	223	MET	-	expression tag	UNP A9CB96
I	224	THR	-	expression tag	UNP A9CB96
I	225	GLY	-	expression tag	UNP A9CB96
I	226	GLY	-	expression tag	UNP A9CB96
I	227	GLN	-	expression tag	UNP A9CB96
I	228	GLN	-	expression tag	UNP A9CB96
I	229	MET	-	expression tag	UNP A9CB96

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Chain	Residue	Modelled	Actual	Comment	Reference
I	230	GLY	-	expression tag	UNP A9CB96
I	231	ARG	-	expression tag	UNP A9CB96
I	232	GLY	-	expression tag	UNP A9CB96
I	233	SER	-	expression tag	UNP A9CB96
I	340	PHE	-	SEE REMARK 999	UNP A9CB96
I	341	TYR	-	SEE REMARK 999	UNP A9CB96
I	342	LEU	-	SEE REMARK 999	UNP A9CB96
I	343	THR	-	SEE REMARK 999	UNP A9CB96
I	344	GLU	-	SEE REMARK 999	UNP A9CB96
I	345	LYS	-	SEE REMARK 999	UNP A9CB96
J	201	GLY	-	expression tag	UNP A9CB96
J	202	SER	-	expression tag	UNP A9CB96
J	203	SER	-	expression tag	UNP A9CB96
J	204	HIS	-	expression tag	UNP A9CB96
J	205	HIS	-	expression tag	UNP A9CB96
J	206	HIS	-	expression tag	UNP A9CB96
J	207	HIS	-	expression tag	UNP A9CB96
J	208	HIS	-	expression tag	UNP A9CB96
J	209	HIS	-	expression tag	UNP A9CB96
J	210	SER	-	expression tag	UNP A9CB96
J	211	SER	-	expression tag	UNP A9CB96
J	212	GLY	-	expression tag	UNP A9CB96
J	213	LEU	-	expression tag	UNP A9CB96
J	214	VAL	-	expression tag	UNP A9CB96
J	215	PRO	-	expression tag	UNP A9CB96
J	216	ARG	-	expression tag	UNP A9CB96
J	217	GLY	-	expression tag	UNP A9CB96
J	218	SER	-	expression tag	UNP A9CB96
J	219	HIS	-	expression tag	UNP A9CB96
J	220	MET	-	expression tag	UNP A9CB96
J	221	ALA	-	expression tag	UNP A9CB96
J	222	SER	-	expression tag	UNP A9CB96
J	223	MET	-	expression tag	UNP A9CB96
J	224	THR	-	expression tag	UNP A9CB96
J	225	GLY	-	expression tag	UNP A9CB96
J	226	GLY	-	expression tag	UNP A9CB96
J	227	GLN	-	expression tag	UNP A9CB96
J	228	GLN	-	expression tag	UNP A9CB96
J	229	MET	-	expression tag	UNP A9CB96
J	230	GLY	-	expression tag	UNP A9CB96
J	231	ARG	-	expression tag	UNP A9CB96
J	232	GLY	-	expression tag	UNP A9CB96

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Chain	Residue	Modelled	Actual	Comment	Reference
J	233	SER	-	expression tag	UNP A9CB96
J	340	PHE	-	SEE REMARK 999	UNP A9CB96
J	341	TYR	-	SEE REMARK 999	UNP A9CB96
J	342	LEU	-	SEE REMARK 999	UNP A9CB96
J	343	THR	-	SEE REMARK 999	UNP A9CB96
J	344	GLU	-	SEE REMARK 999	UNP A9CB96
J	345	LYS	-	SEE REMARK 999	UNP A9CB96
K	201	GLY	-	expression tag	UNP A9CB96
K	202	SER	-	expression tag	UNP A9CB96
K	203	SER	-	expression tag	UNP A9CB96
K	204	HIS	-	expression tag	UNP A9CB96
K	205	HIS	-	expression tag	UNP A9CB96
K	206	HIS	-	expression tag	UNP A9CB96
K	207	HIS	-	expression tag	UNP A9CB96
K	208	HIS	-	expression tag	UNP A9CB96
K	209	HIS	-	expression tag	UNP A9CB96
K	210	SER	-	expression tag	UNP A9CB96
K	211	SER	-	expression tag	UNP A9CB96
K	212	GLY	-	expression tag	UNP A9CB96
K	213	LEU	-	expression tag	UNP A9CB96
K	214	VAL	-	expression tag	UNP A9CB96
K	215	PRO	-	expression tag	UNP A9CB96
K	216	ARG	-	expression tag	UNP A9CB96
K	217	GLY	-	expression tag	UNP A9CB96
K	218	SER	-	expression tag	UNP A9CB96
K	219	HIS	-	expression tag	UNP A9CB96
K	220	MET	-	expression tag	UNP A9CB96
K	221	ALA	-	expression tag	UNP A9CB96
K	222	SER	-	expression tag	UNP A9CB96
K	223	MET	-	expression tag	UNP A9CB96
K	224	THR	-	expression tag	UNP A9CB96
K	225	GLY	-	expression tag	UNP A9CB96
K	226	GLY	-	expression tag	UNP A9CB96
K	227	GLN	-	expression tag	UNP A9CB96
K	228	GLN	-	expression tag	UNP A9CB96
K	229	MET	-	expression tag	UNP A9CB96
K	230	GLY	-	expression tag	UNP A9CB96
K	231	ARG	-	expression tag	UNP A9CB96
K	232	GLY	-	expression tag	UNP A9CB96
K	233	SER	-	expression tag	UNP A9CB96
K	340	PHE	-	SEE REMARK 999	UNP A9CB96
K	341	TYR	-	SEE REMARK 999	UNP A9CB96

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Chain	Residue	Modelled	Actual	Comment	Reference
K	342	LEU	-	SEE REMARK 999	UNP A9CB96
K	343	THR	-	SEE REMARK 999	UNP A9CB96
K	344	GLU	-	SEE REMARK 999	UNP A9CB96
K	345	LYS	-	SEE REMARK 999	UNP A9CB96
L	201	GLY	-	expression tag	UNP A9CB96
L	202	SER	-	expression tag	UNP A9CB96
L	203	SER	-	expression tag	UNP A9CB96
L	204	HIS	-	expression tag	UNP A9CB96
L	205	HIS	-	expression tag	UNP A9CB96
L	206	HIS	-	expression tag	UNP A9CB96
L	207	HIS	-	expression tag	UNP A9CB96
L	208	HIS	-	expression tag	UNP A9CB96
L	209	HIS	-	expression tag	UNP A9CB96
L	210	SER	-	expression tag	UNP A9CB96
L	211	SER	-	expression tag	UNP A9CB96
L	212	GLY	-	expression tag	UNP A9CB96
L	213	LEU	-	expression tag	UNP A9CB96
L	214	VAL	-	expression tag	UNP A9CB96
L	215	PRO	-	expression tag	UNP A9CB96
L	216	ARG	-	expression tag	UNP A9CB96
L	217	GLY	-	expression tag	UNP A9CB96
L	218	SER	-	expression tag	UNP A9CB96
L	219	HIS	-	expression tag	UNP A9CB96
L	220	MET	-	expression tag	UNP A9CB96
L	221	ALA	-	expression tag	UNP A9CB96
L	222	SER	-	expression tag	UNP A9CB96
L	223	MET	-	expression tag	UNP A9CB96
L	224	THR	-	expression tag	UNP A9CB96
L	225	GLY	-	expression tag	UNP A9CB96
L	226	GLY	-	expression tag	UNP A9CB96
L	227	GLN	-	expression tag	UNP A9CB96
L	228	GLN	-	expression tag	UNP A9CB96
L	229	MET	-	expression tag	UNP A9CB96
L	230	GLY	-	expression tag	UNP A9CB96
L	231	ARG	-	expression tag	UNP A9CB96
L	232	GLY	-	expression tag	UNP A9CB96
L	233	SER	-	expression tag	UNP A9CB96
L	340	PHE	-	SEE REMARK 999	UNP A9CB96
L	341	TYR	-	SEE REMARK 999	UNP A9CB96
L	342	LEU	-	SEE REMARK 999	UNP A9CB96
L	343	THR	-	SEE REMARK 999	UNP A9CB96
L	344	GLU	-	SEE REMARK 999	UNP A9CB96

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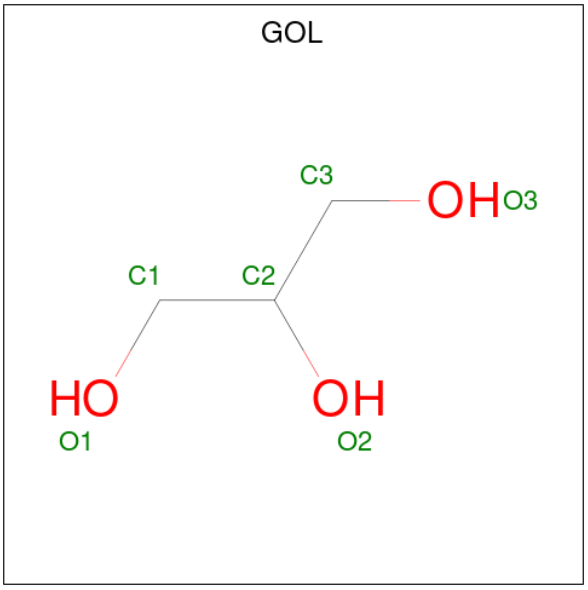
Chain	Residue	Modelled	Actual	Comment	Reference
L	345	LYS	-	SEE REMARK 999	UNP A9CB96

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	D	1	6	3	3	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	29	29	29	0	0
3	B	25	25	25	0	0
3	C	20	20	20	0	0
3	D	23	23	23	0	0
3	E	22	22	22	0	0
3	F	21	21	21	0	0
3	G	19	19	19	0	0
3	H	19	19	19	0	0

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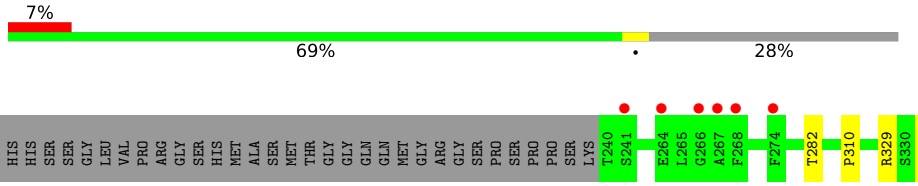
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	I	14	14	14	0	0
			Total	O		
3	J	10	10	10	0	0
			Total	O		
3	K	8	8	8	0	0
			Total	O		
3	L	9	9	9	0	0

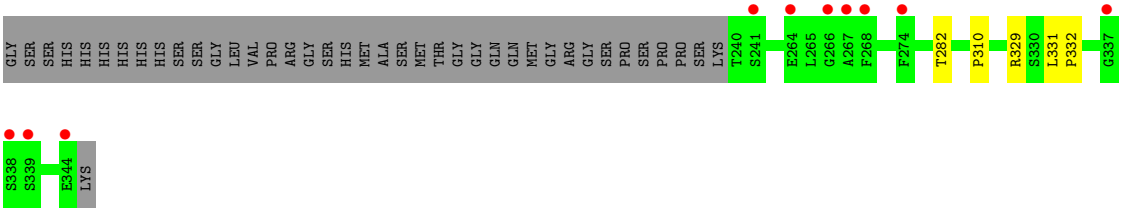
3 Residue-property plots (i)

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: FIBER PROTEIN

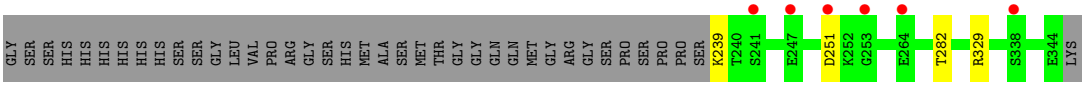
Chain A:





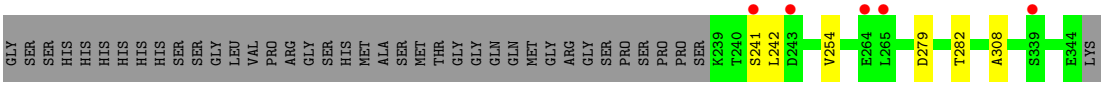
• Molecule 1: FIBER PROTEIN

Chain B:



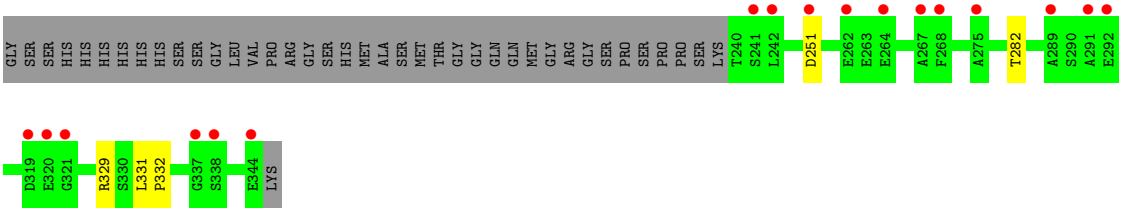
• Molecule 1: FIBER PROTEIN

Chain C:



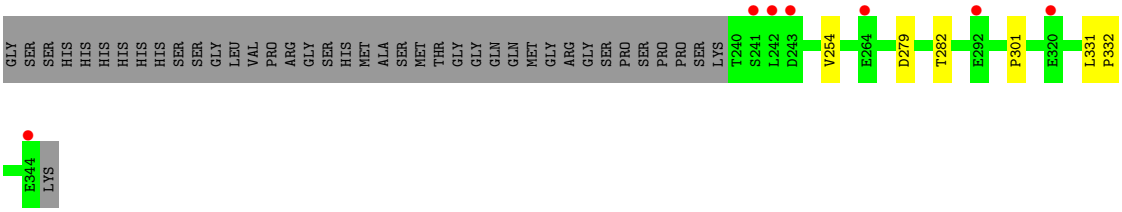
• Molecule 1: FIBER PROTEIN

Chain D:



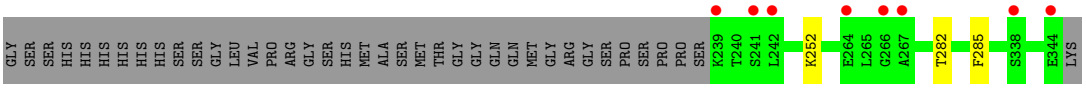
• Molecule 1: FIBER PROTEIN

Chain E:



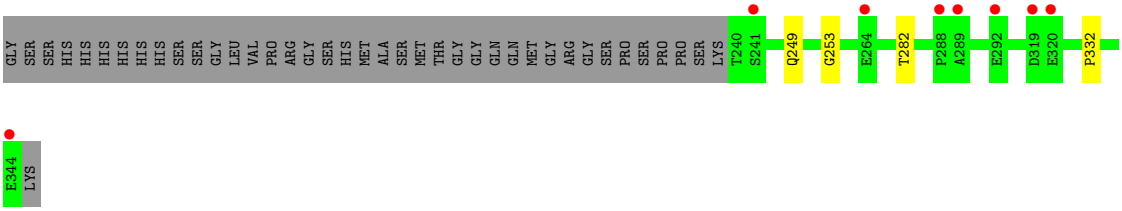
- Molecule 1: FIBER PROTEIN

Chain F:



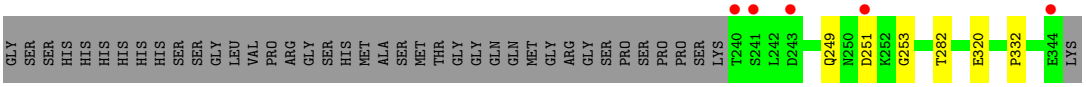
- Molecule 1: FIBER PROTEIN

Chain G:



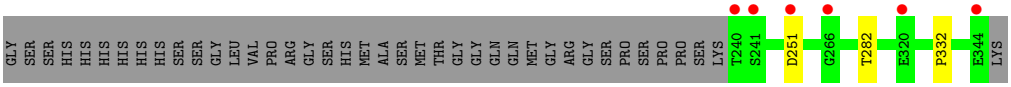
- Molecule 1: FIBER PROTEIN

Chain H:



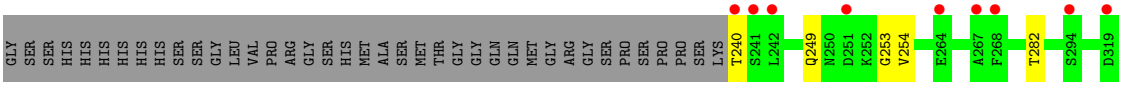
- Molecule 1: FIBER PROTEIN

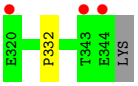
Chain I:



- Molecule 1: FIBER PROTEIN

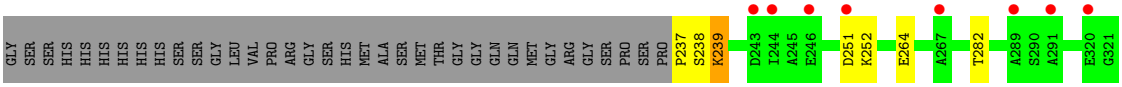
Chain J:

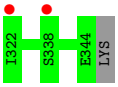




• Molecule 1: FIBER PROTEIN

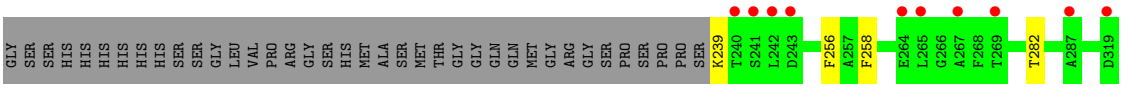
Chain K:

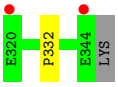




• Molecule 1: FIBER PROTEIN

Chain L:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	79.66Å 122.45Å 133.73Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.89 – 2.70 29.89 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.5 (29.89-2.70) 95.4 (29.89-2.70)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.95 (at 2.68Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.212 , 0.247 0.210 , 0.241	Depositor DCC
R_{free} test set	2064 reflections (5.89%)	wwPDB-VP
Wilson B-factor (Å^2)	51.7	Xtriage
Anisotropy	0.656	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 52.3	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	0.94	EDS
Total number of atoms	9799	wwPDB-VP
Average B, all atoms (Å^2)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.84% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL

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	0.82	0/810	0.63	0/1097
1	B	0.78	0/819	0.63	0/1108
1	C	0.80	0/819	0.60	0/1108
1	D	0.80	0/810	0.61	0/1097
1	E	0.80	0/810	0.63	0/1097
1	F	0.79	0/819	0.62	0/1108
1	G	0.76	0/810	0.59	0/1097
1	H	0.79	0/810	0.60	0/1097
1	I	0.78	0/810	0.60	0/1097
1	J	0.83	0/810	0.60	0/1097
1	K	0.83	0/833	0.64	0/1127
1	L	0.78	0/819	0.61	0/1108
All	All	0.80	0/9779	0.61	0/13238

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	793	0	776	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	802	0	789	5	0
1	C	802	0	789	7	0
1	D	793	0	776	5	0
1	E	793	0	776	12	0
1	F	802	0	789	6	0
1	G	793	0	776	4	0
1	H	793	0	776	6	0
1	I	793	0	776	4	0
1	J	793	0	776	7	0
1	K	815	0	802	4	0
1	L	802	0	789	8	0
2	D	6	0	8	2	0
3	A	29	0	0	3	0
3	B	25	0	0	1	0
3	C	20	0	0	0	0
3	D	23	0	0	0	0
3	E	22	0	0	0	0
3	F	21	0	0	2	0
3	G	19	0	0	0	0
3	H	19	0	0	1	0
3	I	14	0	0	0	0
3	J	10	0	0	1	0
3	K	8	0	0	0	0
3	L	9	0	0	0	0
All	All	9799	0	9398	52	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 3.

All (52) 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:A:282:THR:HG21	1:E:282:THR:HG21	1.45	0.95
1:E:282:THR:HG21	1:L:282:THR:HG21	1.57	0.86
1:C:282:THR:HG21	1:H:282:THR:HG21	1.68	0.73
1:A:282:THR:O	1:E:332:PRO:HA	1.90	0.71
1:A:329:ARG:HD2	3:A:2021:HOH:O	1.90	0.71
1:A:282:THR:HG21	1:E:282:THR:CG2	2.21	0.70
1:A:329:ARG:CD	3:A:2021:HOH:O	2.41	0.69
1:H:320:GLU:HG3	3:H:2013:HOH:O	1.92	0.67
1:H:282:THR:HG21	1:J:282:THR:HG21	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:282:THR:HG21	1:I:282:THR:HG21	1.80	0.64
1:F:282:THR:HG21	1:K:282:THR:HG21	1.81	0.62
1:F:285:PHE:HA	3:F:2002:HOH:O	2.02	0.59
1:E:282:THR:HB	1:L:282:THR:HG22	1.87	0.56
1:E:254:VAL:HG13	1:E:279:ASP:HB2	1.88	0.55
1:G:249:GLN:HE21	1:G:253:GLY:HA2	1.73	0.54
1:B:282:THR:HG21	1:D:282:THR:HG21	1.89	0.53
1:B:282:THR:HG21	1:I:282:THR:HG21	1.90	0.53
1:A:282:THR:HG21	1:L:282:THR:HG21	1.90	0.53
1:C:282:THR:HG21	1:J:282:THR:HG21	1.90	0.52
1:G:282:THR:HG21	1:K:282:THR:HG21	1.92	0.51
1:E:282:THR:O	1:L:332:PRO:HA	2.11	0.50
1:A:310:PRO:HA	1:C:308:ALA:HB2	1.94	0.49
1:D:332:PRO:HA	1:I:282:THR:O	2.13	0.49
1:A:282:THR:HB	1:E:282:THR:HG22	1.95	0.48
1:C:282:THR:O	1:J:332:PRO:HA	2.12	0.48
1:A:282:THR:CG2	1:E:282:THR:CG2	2.91	0.48
1:E:282:THR:HG21	1:L:282:THR:CG2	2.35	0.48
1:F:282:THR:HG21	1:G:282:THR:HG21	1.96	0.47
1:J:240:THR:N	3:J:2001:HOH:O	2.47	0.47
1:A:282:THR:CG2	1:E:282:THR:HG21	2.30	0.47
1:A:332:PRO:HA	1:L:282:THR:O	2.14	0.46
1:B:282:THR:O	1:I:332:PRO:HA	2.16	0.46
1:L:256:PHE:HB3	1:L:258:PHE:CE2	2.51	0.45
1:B:239:LYS:HB2	3:B:2001:HOH:O	2.16	0.45
1:C:282:THR:HG22	1:H:282:THR:HB	1.98	0.45
1:A:329:ARG:HD3	3:A:2021:HOH:O	2.13	0.44
1:D:329:ARG:HB2	2:D:1345:GOL:H31	2.00	0.44
1:H:249:GLN:HE21	1:H:253:GLY:HA2	1.83	0.44
1:H:332:PRO:HA	1:J:282:THR:O	2.18	0.44
1:J:249:GLN:HE21	1:J:253:GLY:HA2	1.83	0.44
1:K:239:LYS:HB2	1:K:264:GLU:HB2	1.99	0.44
1:C:254:VAL:HG13	1:C:279:ASP:HB2	1.99	0.43
1:F:282:THR:HG22	1:K:282:THR:HB	2.00	0.43
1:F:282:THR:O	1:G:332:PRO:HB3	2.19	0.42
1:F:252:LYS:HE3	3:F:2004:HOH:O	2.20	0.42
1:C:241:SER:O	1:C:242:LEU:HB2	2.20	0.42
1:A:331:LEU:HA	1:A:332:PRO:HD2	1.94	0.41
1:B:329:ARG:HD3	2:D:1345:GOL:H11	2.02	0.41
1:E:331:LEU:HA	1:E:332:PRO:HD2	1.96	0.41
1:J:249:GLN:HA	1:J:254:VAL:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:239:LYS:HE3	1:L:239:LYS:HB3	1.80	0.41
1:D:331:LEU:HA	1:D:332:PRO:HD2	1.95	0.41

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	103/145 (71%)	101 (98%)	2 (2%)	0	100	100
1	B	104/145 (72%)	100 (96%)	3 (3%)	1 (1%)	15	37
1	C	104/145 (72%)	102 (98%)	2 (2%)	0	100	100
1	D	103/145 (71%)	100 (97%)	3 (3%)	0	100	100
1	E	103/145 (71%)	100 (97%)	3 (3%)	0	100	100
1	F	104/145 (72%)	99 (95%)	5 (5%)	0	100	100
1	G	103/145 (71%)	101 (98%)	2 (2%)	0	100	100
1	H	103/145 (71%)	101 (98%)	2 (2%)	0	100	100
1	I	103/145 (71%)	101 (98%)	2 (2%)	0	100	100
1	J	103/145 (71%)	100 (97%)	3 (3%)	0	100	100
1	K	106/145 (73%)	100 (94%)	5 (5%)	1 (1%)	17	40
1	L	104/145 (72%)	101 (97%)	3 (3%)	0	100	100
All	All	1243/1740 (71%)	1206 (97%)	35 (3%)	2 (0%)	47	73

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	K	239	LYS
1	B	251	ASP

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	84/116 (72%)	84 (100%)	0	100	100
1	B	85/116 (73%)	85 (100%)	0	100	100
1	C	85/116 (73%)	85 (100%)	0	100	100
1	D	84/116 (72%)	83 (99%)	1 (1%)	71	88
1	E	84/116 (72%)	83 (99%)	1 (1%)	71	88
1	F	85/116 (73%)	85 (100%)	0	100	100
1	G	84/116 (72%)	84 (100%)	0	100	100
1	H	84/116 (72%)	83 (99%)	1 (1%)	71	88
1	I	84/116 (72%)	83 (99%)	1 (1%)	71	88
1	J	84/116 (72%)	84 (100%)	0	100	100
1	K	87/116 (75%)	83 (95%)	4 (5%)	27	54
1	L	85/116 (73%)	85 (100%)	0	100	100
All	All	1015/1392 (73%)	1007 (99%)	8 (1%)	81	93

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

Mol	Chain	Res	Type
1	D	251	ASP
1	E	301	PRO
1	H	251	ASP
1	I	251	ASP
1	K	237	PRO
1	K	238	SER
1	K	251	ASP
1	K	252	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	G	249	GLN

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)

1 ligand is 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	$\#\|Z\| > 2$
2	GOL	D	1345	-	5,5,5	0.46	0	5,5,5	0.91	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
2	GOL	D	1345	-	-	2/4/4/4	-

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
2	D	1345	GOL	O1-C1-C2-C3
2	D	1345	GOL	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	1345	GOL	2	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

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	105/145 (72%)	0.45	10 (9%)	8	6	37, 48, 61, 69	0
1	B	106/145 (73%)	0.37	6 (5%)	23	22	37, 49, 64, 70	0
1	C	106/145 (73%)	0.32	5 (4%)	31	30	37, 49, 64, 74	0
1	D	105/145 (72%)	0.74	17 (16%)	1	1	37, 49, 62, 72	0
1	E	105/145 (72%)	0.41	7 (6%)	17	16	37, 49, 62, 69	0
1	F	106/145 (73%)	0.45	8 (7%)	14	12	37, 49, 62, 76	0
1	G	105/145 (72%)	0.30	8 (7%)	13	12	37, 49, 62, 73	0
1	H	105/145 (72%)	0.32	5 (4%)	30	28	37, 49, 62, 71	0
1	I	105/145 (72%)	0.46	6 (5%)	23	22	37, 49, 62, 72	0
1	J	105/145 (72%)	0.41	12 (11%)	5	4	37, 49, 62, 72	0
1	K	108/145 (74%)	0.47	10 (9%)	8	6	37, 50, 66, 80	0
1	L	106/145 (73%)	0.60	12 (11%)	5	4	37, 50, 64, 76	0
All	All	1267/1740 (72%)	0.44	106 (8%)	11	9	37, 49, 64, 80	0

All (106) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	L	241	SER	5.9
1	D	241	SER	4.8
1	E	241	SER	4.8
1	F	242	LEU	4.3
1	J	241	SER	4.2
1	H	241	SER	3.9
1	D	267	ALA	3.8
1	E	320	GLU	3.8
1	J	264	GLU	3.7
1	L	344	GLU	3.7
1	B	251	ASP	3.6

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Mol	Chain	Res	Type	RSRZ
1	C	241	SER	3.6
1	F	241	SER	3.6
1	F	264	GLU	3.5
1	I	320	GLU	3.4
1	E	242	LEU	3.4
1	I	241	SER	3.4
1	J	320	GLU	3.4
1	F	267	ALA	3.3
1	L	242	LEU	3.3
1	H	251	ASP	3.3
1	J	344	GLU	3.3
1	A	241	SER	3.2
1	A	267	ALA	3.2
1	I	251	ASP	3.2
1	K	243	ASP	3.1
1	L	319	ASP	3.1
1	L	320	GLU	3.1
1	H	344	GLU	3.1
1	C	264	GLU	3.1
1	K	244	ILE	3.1
1	E	344	GLU	3.1
1	J	319	ASP	3.0
1	K	320	GLU	3.0
1	I	344	GLU	3.0
1	A	338	SER	3.0
1	A	264	GLU	2.9
1	E	264	GLU	2.9
1	K	267	ALA	2.9
1	G	319	ASP	2.9
1	D	275	ALA	2.9
1	L	264	GLU	2.9
1	B	253	GLY	2.9
1	A	344	GLU	2.8
1	D	320	GLU	2.8
1	D	321	GLY	2.8
1	K	251	ASP	2.8
1	F	338	SER	2.7
1	D	344	GLU	2.7
1	B	241	SER	2.7
1	D	289	ALA	2.7
1	D	268	PHE	2.7
1	F	344	GLU	2.6

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Mol	Chain	Res	Type	RSRZ
1	D	338	SER	2.6
1	D	292	GLU	2.6
1	K	246	GLU	2.6
1	G	320	GLU	2.5
1	D	337	GLY	2.5
1	I	240	THR	2.5
1	F	266	GLY	2.5
1	C	265	LEU	2.5
1	D	291	ALA	2.5
1	H	240	THR	2.5
1	A	266	GLY	2.5
1	D	242	LEU	2.5
1	A	339	SER	2.5
1	A	268	PHE	2.4
1	L	240	THR	2.4
1	G	344	GLU	2.4
1	I	266	GLY	2.4
1	G	289	ALA	2.4
1	L	287	ALA	2.4
1	G	292	GLU	2.4
1	L	265	LEU	2.4
1	K	289	ALA	2.4
1	L	267	ALA	2.4
1	B	247	GLU	2.3
1	K	322	ILE	2.3
1	J	242	LEU	2.3
1	J	343	THR	2.3
1	D	319	ASP	2.3
1	B	264	GLU	2.3
1	J	267	ALA	2.3
1	D	262	GLU	2.2
1	A	337	GLY	2.2
1	D	264	GLU	2.2
1	H	243	ASP	2.2
1	K	291	ALA	2.2
1	J	294	SER	2.2
1	J	251	ASP	2.2
1	J	268	PHE	2.2
1	G	241	SER	2.2
1	L	269	THR	2.2
1	A	274	PHE	2.1
1	D	251	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	338	SER	2.1
1	G	288	PRO	2.1
1	E	243	ASP	2.1
1	K	338	SER	2.1
1	G	264	GLU	2.1
1	C	339	SER	2.1
1	L	243	ASP	2.1
1	C	243	ASP	2.0
1	J	240	THR	2.0
1	F	239	LYS	2.0
1	E	292	GLU	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 monosaccharides 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, 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
2	GOL	D	1345	6/6	0.85	0.29	50,58,68,71	0

6.5 Other polymers (i)

There are no such residues in this entry.