



Full wwPDB X-ray Structure Validation Report ⓘ

May 25, 2020 – 02:45 pm BST

PDB ID : 4D1G
Title : Crystal structure of the fiber head domain of the Atadenovirus snake adenovirus 1, native, second P212121 crystal form
Authors : Singh, A.K.; van Raaij, M.J.
Deposited on : 2014-05-01
Resolution : 1.90 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 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)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

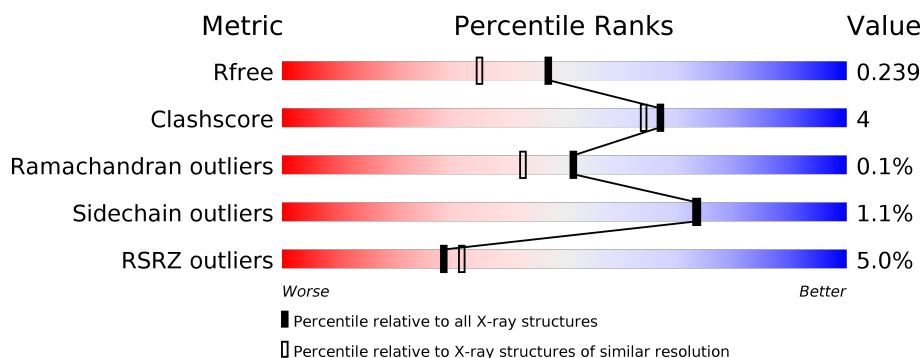
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	<div> <div>69%</div> <div>5%</div> <div>26%</div> </div>
1	B	145	<div> <div>69%</div> <div>5%</div> <div>26%</div> </div>
1	C	145	<div> <div>6%</div> <div>66%</div> <div>8%</div> <div>26%</div> </div>
1	D	145	<div> <div>4%</div> <div>72%</div> <div>26%</div> </div>
1	E	145	<div> <div>2%</div> <div>70%</div> <div>27%</div> </div>
1	F	145	<div> <div>4%</div> <div>73%</div> <div>26%</div> </div>

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Mol	Chain	Length	Quality of chain
1	G	145	
1	H	145	
1	I	145	
1	J	145	
1	K	145	
1	L	145	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10973 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
1	A	107	Total	C	N	O	0	2	0
			823	527	132	164			
1	B	108	Total	C	N	O	0	6	0
			838	536	134	168			
1	C	107	Total	C	N	O	0	5	0
			829	531	133	165			
1	D	107	Total	C	N	O	0	2	0
			814	521	130	163			
1	E	106	Total	C	N	O	0	3	0
			812	522	129	161			
1	F	107	Total	C	N	O	0	1	0
			812	520	130	162			
1	G	108	Total	C	N	O	0	8	0
			851	544	135	172			
1	H	107	Total	C	N	O	0	4	0
			825	527	133	165			
1	I	108	Total	C	N	O	0	7	0
			846	541	136	169			
1	J	106	Total	C	N	O	0	4	0
			820	527	129	164			
1	K	107	Total	C	N	O	0	3	0
			818	525	130	163			
1	L	107	Total	C	N	O	0	4	0
			823	526	133	164			

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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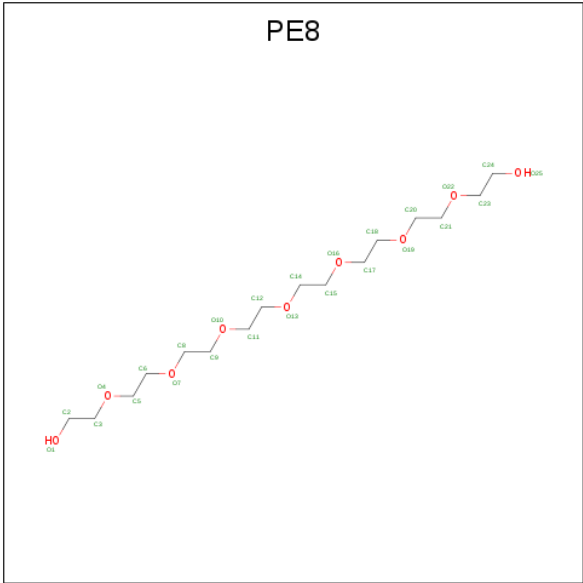
Chain	Residue	Modelled	Actual	Comment	Reference
K	342	LEU	-	SEE REMARK 999	UNP A9CB96
K	343	THR	-	SEE REMARK 999	UNP A9CB96
K	344	GLU	-	SEE REMARK 999	UNP A9CB96
K	345	LYS	-	SEE REMARK 999	UNP A9CB96
L	201	GLY	-	expression tag	UNP A9CB96
L	202	SER	-	expression tag	UNP A9CB96
L	203	SER	-	expression tag	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 3,6,9,12,15,18,21-HEPTAOXATRICOSANE-1,23-DIOL (three-letter code: PE8) (formula: C₁₆H₃₄O₉).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	C	O	0	0
			25	16	9		
2	C	1	Total	C	O	0	0
			25	16	9		
2	G	1	Total	C	O	0	0
			25	16	9		
2	J	1	Total	C	O	0	0
			25	16	9		
2	K	1	Total	C	O	0	0
			25	16	9		
2	L	1	Total	C	O	0	0
			25	16	9		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		
3	I	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	96	Total	O	0	0
			96	96		
4	B	98	Total	O	0	0
			98	98		
4	C	73	Total	O	0	0
			73	73		
4	D	75	Total	O	0	0
			75	75		
4	E	71	Total	O	0	0
			71	71		
4	F	70	Total	O	0	0
			70	70		
4	G	100	Total	O	0	0
			100	100		

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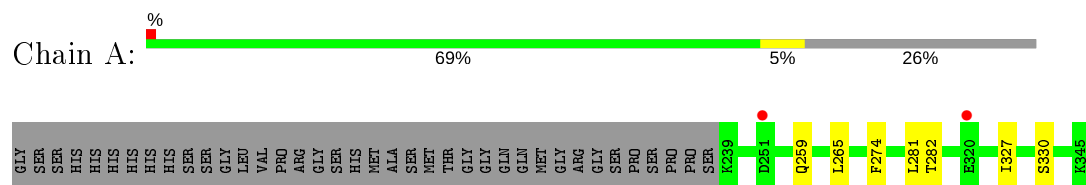
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	H	81	Total 81	O 81	0	0
4	I	62	Total 62	O 62	0	0
4	J	59	Total 59	O 59	0	0
4	K	64	Total 64	O 64	0	0
4	L	38	Total 38	O 38	0	0

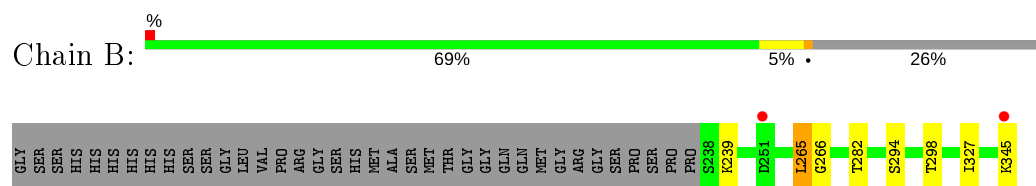
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

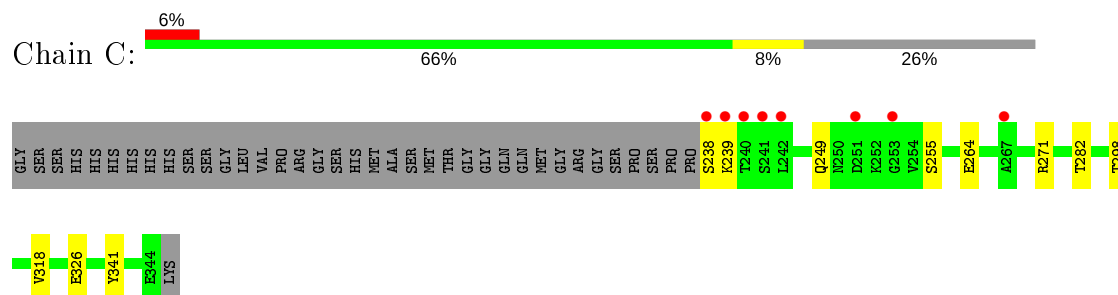
• Molecule 1: FIBER PROTEIN



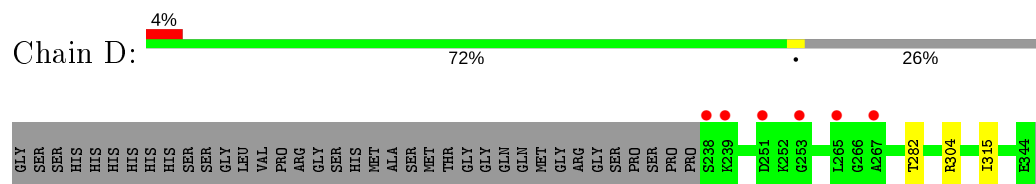
• Molecule 1: FIBER PROTEIN



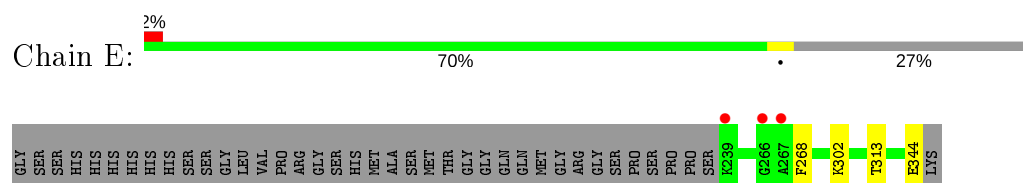
• Molecule 1: FIBER PROTEIN




• Molecule 1: FIBER PROTEIN

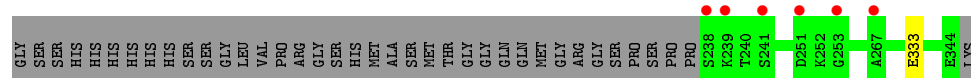


• Molecule 1: FIBER PROTEIN



- Molecule 1: FIBER PROTEIN

Chain F: 



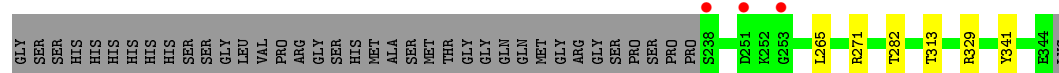
- Molecule 1: FIBER PROTEIN

Chain G: 



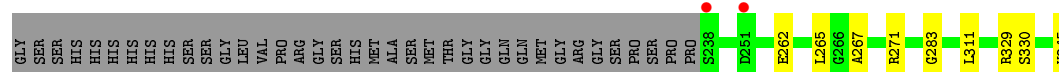
- Molecule 1: FIBER PROTEIN

Chain H: 



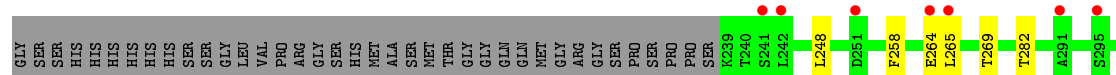
- Molecule 1: FIBER PROTEIN

Chain I: 



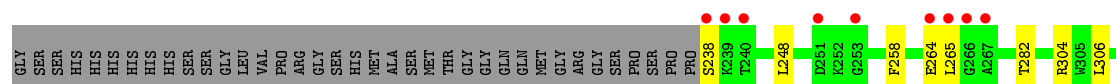
- Molecule 1: FIBER PROTEIN

Chain J: 

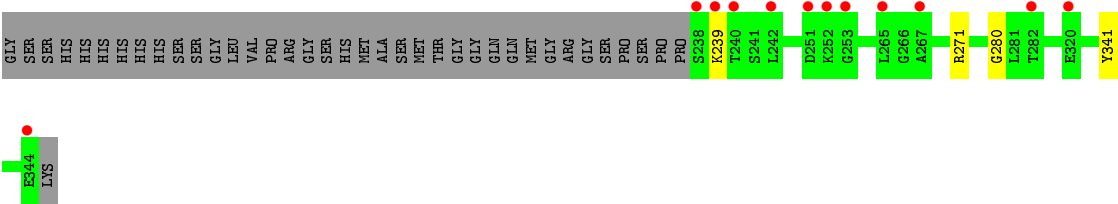


- Molecule 1: FIBER PROTEIN

Chain K: 



● Molecule 1: FIBER PROTEIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	96.77Å 96.75Å 153.29Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.73 – 1.90 29.73 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.8 (29.73-1.90) 99.8 (29.73-1.90)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.43 (at 1.91Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.173 , 0.239 0.174 , 0.239	Depositor DCC
R_{free} test set	2004 reflections (1.76%)	wwPDB-VP
Wilson B-factor (Å ²)	26.3	Xtriage
Anisotropy	0.219	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 50.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.018 for k,h,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	10973	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.12% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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: PE8, SO4

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	0.65	0/843	0.70	0/1139
1	B	0.69	0/874	0.70	1/1179 (0.1%)
1	C	0.70	0/863	0.68	0/1168
1	D	0.64	0/838	0.66	0/1134
1	E	0.63	0/840	0.61	0/1137
1	F	0.63	0/832	0.65	0/1126
1	G	0.68	0/887	0.65	0/1199
1	H	0.60	0/861	0.64	0/1164
1	I	0.66	0/884	0.65	0/1194
1	J	0.61	0/853	0.64	0/1156
1	K	0.64	0/846	0.61	0/1145
1	L	0.59	0/855	0.61	0/1156
All	All	0.64	0/10276	0.65	1/13897 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	265	LEU	CA-CB-CG	5.98	129.04	115.30

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	823	0	815	8	0
1	B	838	0	830	4	0
1	C	829	0	825	13	0
1	D	814	0	802	3	0
1	E	812	0	804	6	0
1	F	812	0	801	1	0
1	G	851	0	839	11	0
1	H	825	0	815	6	0
1	I	846	0	843	6	0
1	J	820	0	818	7	0
1	K	818	0	809	8	0
1	L	823	0	812	2	0
2	B	25	0	34	4	0
2	C	25	0	34	6	0
2	G	25	0	34	1	0
2	J	25	0	34	2	0
2	K	25	0	34	5	0
2	L	25	0	34	3	0
3	B	5	0	0	0	0
3	C	5	0	0	0	0
3	E	5	0	0	0	0
3	H	5	0	0	1	0
3	I	5	0	0	0	0
4	A	96	0	0	1	0
4	B	98	0	0	3	0
4	C	73	0	0	3	0
4	D	75	0	0	0	0
4	E	71	0	0	3	0
4	F	70	0	0	0	0
4	G	100	0	0	0	0
4	H	81	0	0	2	0
4	I	62	0	0	2	0
4	J	59	0	0	2	0
4	K	64	0	0	0	0
4	L	38	0	0	0	0
All	All	10973	0	10017	78	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 4.

All (78) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:282[B]:THR:CG2	1:G:282[B]:THR:HG21	1.61	1.29
1:C:282[B]:THR:HG22	1:G:282[B]:THR:CG2	1.66	1.26
2:C:1345:PE8:H241	2:C:1345:PE8:H82	1.31	1.04
1:H:282:THR:HG21	4:J:2023:HOH:O	1.60	0.99
2:K:1345:PE8:H242	2:K:1345:PE8:H92	1.53	0.89
2:C:1345:PE8:H241	2:C:1345:PE8:C8	2.08	0.83
1:C:282[B]:THR:HG22	1:G:282[B]:THR:HG21	0.80	0.76
3:H:1345:SO4:O1	4:H:2081:HOH:O	2.02	0.76
2:B:1346:PE8:H21	4:B:2079:HOH:O	1.85	0.76
2:J:1345:PE8:H241	2:J:1345:PE8:H81	1.68	0.75
1:C:282[B]:THR:CG2	1:G:282[B]:THR:CG2	2.43	0.75
1:K:315[A]:ILE:HD12	2:K:1345:PE8:H121	1.74	0.69
1:C:249:GLN:HG2	1:C:255:SER:HB3	1.77	0.67
2:G:1346:PE8:H81	2:G:1346:PE8:H241	1.78	0.64
1:A:282[A]:THR:HG23	1:A:330:SER:OG	1.99	0.61
1:C:271:ARG:HD2	1:C:341:TYR:OH	2.00	0.61
1:I:329[B]:ARG:NH2	4:I:2053:HOH:O	2.34	0.57
1:J:313[B]:THR:HG23	2:J:1345:PE8:H111	1.86	0.56
1:E:268:PHE:CZ	1:E:344:GLU:HG3	2.41	0.55
1:I:311:LEU:O	1:I:329[A]:ARG:HD3	2.07	0.55
2:C:1345:PE8:H22	2:C:1345:PE8:H171	1.89	0.55
1:I:267:ALA:O	1:I:345:LYS:N	2.31	0.55
2:B:1346:PE8:H211	1:D:315:ILE:CD1	2.36	0.54
1:E:268:PHE:CE2	1:E:344:GLU:HG3	2.43	0.54
1:G:282[B]:THR:HG22	1:G:330[B]:SER:HB3	1.89	0.53
1:D:282:THR:HG22	1:G:282[B]:THR:HB	1.89	0.53
1:C:239:LYS:HG3	1:C:264:GLU:HB2	1.91	0.53
1:B:266:GLY:O	1:B:345:LYS:HE3	2.09	0.52
1:G:294:SER:O	1:G:298:THR:HG23	2.09	0.52
1:H:329[B]:ARG:HG3	1:J:329:ARG:NH2	2.25	0.51
1:L:271[A]:ARG:HD2	1:L:341:TYR:OH	2.11	0.51
1:E:313[B]:THR:HB	4:E:2050:HOH:O	2.11	0.51
1:K:238:SER:HA	1:K:264:GLU:O	2.11	0.50
1:K:304:ARG:HD3	1:K:315[B]:ILE:HD12	1.93	0.50
1:C:326:GLU:OE1	2:C:1345:PE8:H111	2.11	0.50
1:H:271:ARG:HD3	4:H:2045:HOH:O	2.11	0.50
1:J:282:THR:HG23	1:J:330[B]:SER:OG	2.11	0.50
1:J:248:LEU:HD13	1:J:258:PHE:HD2	1.77	0.50
1:A:281:LEU:HB3	1:A:327:ILE:HD13	1.94	0.49
1:A:330:SER:HG	1:I:330[B]:SER:HB2	1.75	0.49
1:A:282[A]:THR:O	1:A:282[A]:THR:HG22	2.13	0.49
1:C:271:ARG:HD3	4:C:2035:HOH:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:264:GLU:HG3	1:J:269[B]:THR:HG22	1.96	0.48
2:L:1345:PE8:H171	2:L:1345:PE8:O1	2.13	0.48
2:L:1345:PE8:H81	2:L:1345:PE8:H241	1.96	0.48
1:A:282[A]:THR:HG23	1:A:330:SER:CB	2.43	0.48
1:H:271:ARG:HD2	1:H:341:TYR:CZ	2.49	0.48
4:A:2042:HOH:O	1:L:280:GLY:HA3	2.13	0.48
1:C:298[B]:THR:HG23	1:C:318:VAL:CG1	2.44	0.48
1:B:294:SER:O	1:B:298:THR:HG23	2.14	0.47
1:H:271:ARG:HD2	1:H:341:TYR:OH	2.14	0.47
1:H:282:THR:O	1:J:332:PRO:HA	2.16	0.46
1:K:315[A]:ILE:HG13	2:K:1345:PE8:H51	1.97	0.46
1:E:313[B]:THR:HG22	4:E:2051:HOH:O	2.17	0.45
2:B:1346:PE8:H242	4:B:2062:HOH:O	2.17	0.44
1:C:271:ARG:HD2	1:C:341:TYR:CZ	2.52	0.44
2:K:1345:PE8:H242	2:K:1345:PE8:C9	2.37	0.44
1:E:313[B]:THR:CG2	4:E:2051:HOH:O	2.65	0.44
1:C:282[B]:THR:HG21	1:G:282[B]:THR:OG1	2.17	0.44
2:C:1345:PE8:H61	4:C:2072:HOH:O	2.18	0.44
1:B:282:THR:OG1	1:K:282:THR:HG23	2.18	0.44
1:B:327:ILE:HG12	4:B:2041:HOH:O	2.18	0.43
2:C:1345:PE8:H21	4:C:2071:HOH:O	2.18	0.43
1:C:282[A]:THR:HG23	1:G:282[A]:THR:OG1	2.18	0.43
1:K:311:LEU:O	1:K:329:ARG:NH1	2.48	0.43
1:E:302:LYS:HE2	1:F:333:GLU:OE2	2.18	0.42
2:B:1346:PE8:C21	1:D:315:ILE:CD1	2.97	0.42
1:A:259:GLN:HB3	1:A:274:PHE:HB2	2.02	0.42
1:I:262:GLU:HG3	1:I:271:ARG:HD3	2.01	0.42
1:K:306:LEU:CD1	2:K:1345:PE8:H31	2.49	0.41
1:J:313[B]:THR:CG2	4:J:2041:HOH:O	2.69	0.41
1:K:248:LEU:HD13	1:K:258:PHE:HD1	1.86	0.41
1:I:283:GLY:N	4:I:2023:HOH:O	2.47	0.41
1:A:282[A]:THR:HG23	1:A:330:SER:HB2	2.03	0.40
2:L:1345:PE8:H172	2:L:1345:PE8:H202	1.77	0.40
1:G:238:SER:HA	1:G:264:GLU:O	2.21	0.40
1:A:282[B]:THR:O	1:A:282[B]:THR:OG1	2.37	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	107/145 (74%)	107 (100%)	0	0	100	100
1	B	112/145 (77%)	110 (98%)	2 (2%)	0	100	100
1	C	110/145 (76%)	110 (100%)	0	0	100	100
1	D	107/145 (74%)	105 (98%)	2 (2%)	0	100	100
1	E	107/145 (74%)	106 (99%)	1 (1%)	0	100	100
1	F	106/145 (73%)	105 (99%)	1 (1%)	0	100	100
1	G	114/145 (79%)	113 (99%)	1 (1%)	0	100	100
1	H	110/145 (76%)	108 (98%)	2 (2%)	0	100	100
1	I	113/145 (78%)	112 (99%)	1 (1%)	0	100	100
1	J	109/145 (75%)	105 (96%)	4 (4%)	0	100	100
1	K	108/145 (74%)	106 (98%)	2 (2%)	0	100	100
1	L	109/145 (75%)	106 (97%)	2 (2%)	1 (1%)	17	7
All	All	1312/1740 (75%)	1293 (99%)	18 (1%)	1 (0%)	51	43

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	L	239	LYS

5.3.2 Protein sidechains

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	88/116 (76%)	87 (99%)	1 (1%)	73	73
1	B	92/116 (79%)	90 (98%)	2 (2%)	52	47
1	C	91/116 (78%)	90 (99%)	1 (1%)	73	73
1	D	88/116 (76%)	87 (99%)	1 (1%)	73	73
1	E	88/116 (76%)	88 (100%)	0	100	100
1	F	87/116 (75%)	87 (100%)	0	100	100
1	G	93/116 (80%)	92 (99%)	1 (1%)	73	73
1	H	91/116 (78%)	88 (97%)	3 (3%)	38	29
1	I	93/116 (80%)	92 (99%)	1 (1%)	73	73
1	J	90/116 (78%)	89 (99%)	1 (1%)	73	73
1	K	89/116 (77%)	88 (99%)	1 (1%)	73	73
1	L	90/116 (78%)	90 (100%)	0	100	100
All	All	1080/1392 (78%)	1068 (99%)	12 (1%)	73	73

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	265	LEU
1	B	239	LYS
1	B	265	LEU
1	C	238	SER
1	D	304	ARG
1	G	265	LEU
1	H	265	LEU
1	H	313[A]	THR
1	H	313[B]	THR
1	I	265	LEU
1	J	265	LEU
1	K	265	LEU

Some 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 [i](#)

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

11 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	PE8	C	1345	-	24,24,24	0.57	0	23,23,23	0.50	0
3	SO4	I	1346	-	4,4,4	0.32	0	6,6,6	0.43	0
3	SO4	C	1346	-	4,4,4	0.16	0	6,6,6	0.19	0
2	PE8	B	1346	-	24,24,24	0.42	0	23,23,23	0.51	0
2	PE8	L	1345	-	24,24,24	0.48	0	23,23,23	0.40	0
3	SO4	E	1345	-	4,4,4	0.15	0	6,6,6	0.13	0
3	SO4	H	1345	-	4,4,4	0.26	0	6,6,6	0.31	0
2	PE8	G	1346	-	24,24,24	0.50	0	23,23,23	0.54	0
2	PE8	J	1345	-	24,24,24	0.56	0	23,23,23	0.39	0
3	SO4	B	1347	-	4,4,4	0.10	0	6,6,6	0.05	0
2	PE8	K	1345	-	24,24,24	0.61	0	23,23,23	0.52	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	PE8	C	1345	-	-	7/22/22/22	-
2	PE8	B	1346	-	-	7/22/22/22	-
2	PE8	G	1346	-	-	8/22/22/22	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PE8	L	1345	-	-	8/22/22/22	-
2	PE8	J	1345	-	-	6/22/22/22	-
2	PE8	K	1345	-	-	7/22/22/22	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (43) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	L	1345	PE8	C17-C18-O19-C20
2	C	1345	PE8	O7-C8-C9-O10
2	G	1346	PE8	O13-C14-C15-O16
2	L	1345	PE8	O16-C17-C18-O19
2	G	1346	PE8	O16-C17-C18-O19
2	C	1345	PE8	O4-C5-C6-O7
2	L	1345	PE8	O19-C20-C21-O22
2	L	1345	PE8	O22-C23-C24-O25
2	K	1345	PE8	O13-C14-C15-O16
2	K	1345	PE8	O4-C5-C6-O7
2	G	1346	PE8	O1-C2-C3-O4
2	J	1345	PE8	O22-C23-C24-O25
2	C	1345	PE8	C9-C8-O7-C6
2	B	1346	PE8	O10-C11-C12-O13
2	C	1345	PE8	O13-C14-C15-O16
2	K	1345	PE8	O1-C2-C3-O4
2	G	1346	PE8	O4-C5-C6-O7
2	G	1346	PE8	O19-C20-C21-O22
2	C	1345	PE8	O16-C17-C18-O19
2	L	1345	PE8	C20-C21-O22-C23
2	B	1346	PE8	C24-C23-O22-C21
2	B	1346	PE8	C8-C9-O10-C11
2	B	1346	PE8	O1-C2-C3-O4
2	L	1345	PE8	C15-C14-O13-C12
2	J	1345	PE8	C6-C5-O4-C3
2	K	1345	PE8	C2-C3-O4-C5
2	L	1345	PE8	C8-C9-O10-C11
2	L	1345	PE8	O7-C8-C9-O10
2	B	1346	PE8	C2-C3-O4-C5
2	G	1346	PE8	C18-C17-O16-C15

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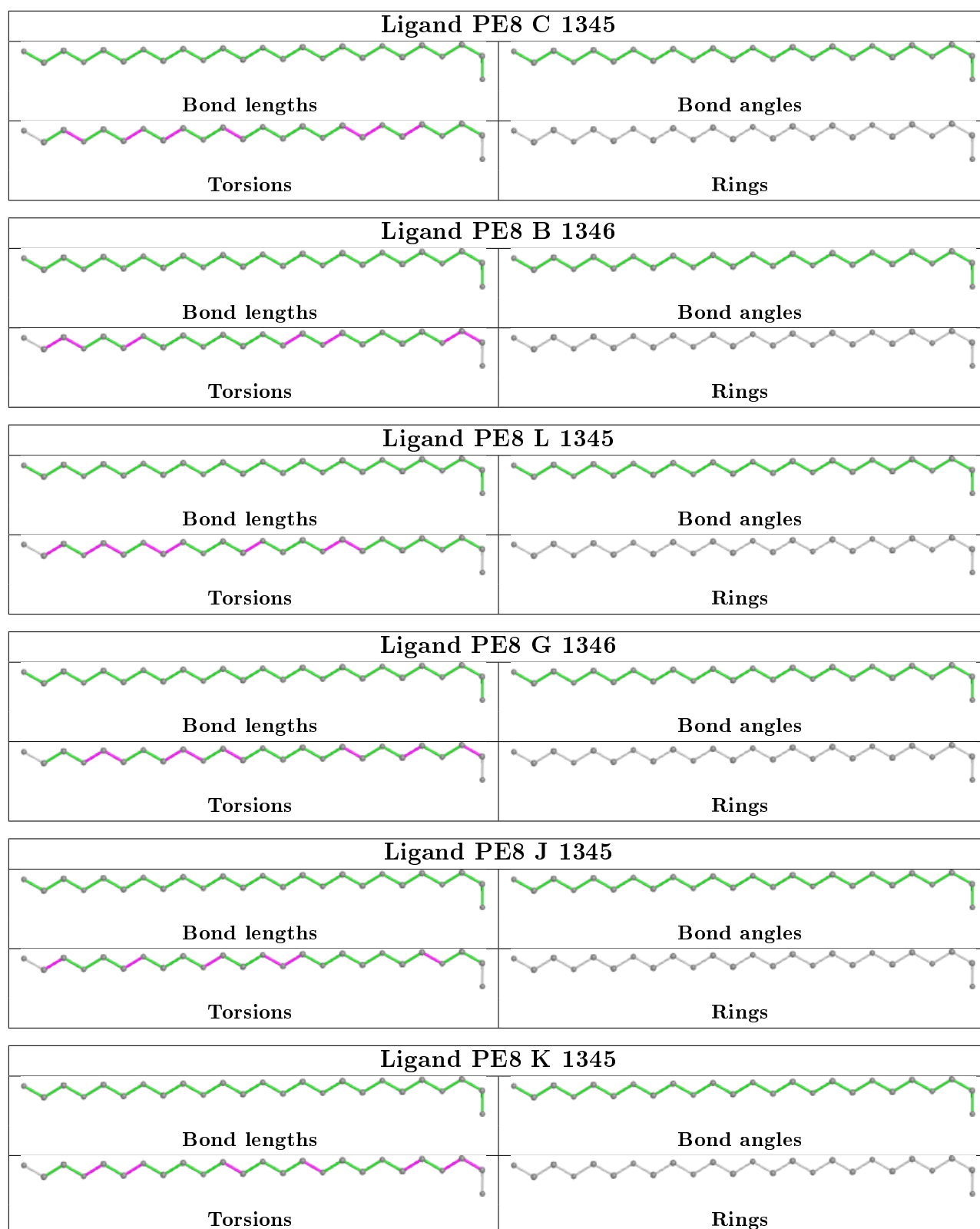
Mol	Chain	Res	Type	Atoms
2	J	1345	PE8	C14-C15-O16-C17
2	C	1345	PE8	C21-C20-O19-C18
2	K	1345	PE8	C20-C21-O22-C23
2	K	1345	PE8	C21-C20-O19-C18
2	J	1345	PE8	C21-C20-O19-C18
2	B	1346	PE8	C21-C20-O19-C18
2	K	1345	PE8	C12-C11-O10-C9
2	B	1346	PE8	O22-C23-C24-O25
2	J	1345	PE8	C11-C12-O13-C14
2	J	1345	PE8	O10-C11-C12-O13
2	G	1346	PE8	O7-C8-C9-O10
2	G	1346	PE8	C20-C21-O22-C23
2	C	1345	PE8	C24-C23-O22-C21

There are no ring outliers.

7 monomers are involved in 22 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	1345	PE8	6	0
2	B	1346	PE8	4	0
2	L	1345	PE8	3	0
3	H	1345	SO4	1	0
2	G	1346	PE8	1	0
2	J	1345	PE8	2	0
2	K	1345	PE8	5	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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, 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	107/145 (73%)	-0.05	2 (1%) 66 69	16, 28, 45, 53	0
1	B	108/145 (74%)	-0.18	2 (1%) 66 69	15, 24, 47, 54	0
1	C	107/145 (73%)	-0.02	8 (7%) 14 15	14, 24, 50, 66	0
1	D	107/145 (73%)	-0.04	6 (5%) 24 27	16, 25, 51, 66	0
1	E	106/145 (73%)	0.11	3 (2%) 53 56	17, 30, 49, 63	0
1	F	107/145 (73%)	-0.02	6 (5%) 24 27	17, 26, 49, 64	0
1	G	108/145 (74%)	-0.13	3 (2%) 53 56	16, 25, 46, 59	0
1	H	107/145 (73%)	0.02	3 (2%) 53 56	17, 31, 49, 62	0
1	I	108/145 (74%)	-0.04	2 (1%) 66 69	17, 28, 48, 60	0
1	J	106/145 (73%)	0.38	8 (7%) 14 15	20, 35, 57, 72	0
1	K	107/145 (73%)	0.26	9 (8%) 11 12	19, 29, 60, 81	0
1	L	107/145 (73%)	0.65	12 (11%) 5 6	21, 39, 65, 84	0
All	All	1285/1740 (73%)	0.08	64 (4%) 28 32	14, 28, 54, 84	0

All (64) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	K	238	SER	7.7
1	L	238	SER	7.4
1	F	238	SER	5.1
1	H	251	ASP	4.6
1	E	239	LYS	4.0
1	C	239	LYS	3.8
1	C	238	SER	3.8
1	K	239	LYS	3.7
1	H	238	SER	3.6
1	L	267	ALA	3.6
1	I	251	ASP	3.6

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Mol	Chain	Res	Type	RSRZ
1	D	238	SER	3.6
1	K	267	ALA	3.4
1	J	241	SER	3.4
1	J	251	ASP	3.4
1	D	239	LYS	3.4
1	L	252	LYS	3.3
1	J	265	LEU	3.3
1	K	240	THR	3.3
1	G	345	LYS	3.2
1	L	239	LYS	3.2
1	C	241	SER	3.2
1	K	251	ASP	3.2
1	F	239	LYS	3.1
1	L	251	ASP	3.0
1	L	320	GLU	2.9
1	G	238	SER	2.9
1	L	265	LEU	2.9
1	C	253	GLY	2.9
1	L	242	LEU	2.9
1	G	251	ASP	2.9
1	E	267	ALA	2.8
1	D	267	ALA	2.8
1	L	344	GLU	2.7
1	F	251	ASP	2.6
1	J	320	GLU	2.6
1	K	265	LEU	2.6
1	L	240	THR	2.6
1	I	238	SER	2.6
1	E	266	GLY	2.6
1	A	251	ASP	2.5
1	C	267	ALA	2.5
1	J	291	ALA	2.5
1	J	242	LEU	2.5
1	J	295	SER	2.5
1	F	241	SER	2.4
1	K	266	GLY	2.3
1	L	253	GLY	2.3
1	K	264	GLU	2.3
1	H	253	GLY	2.3
1	J	264	GLU	2.3
1	D	253	GLY	2.2
1	F	267	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	L	282	THR	2.2
1	C	251	ASP	2.2
1	A	320	GLU	2.2
1	B	251	ASP	2.1
1	K	253	GLY	2.1
1	C	242	LEU	2.1
1	D	265	LEU	2.1
1	B	345	LYS	2.1
1	D	251	ASP	2.1
1	F	253	GLY	2.1
1	C	240	THR	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 carbohydrates in this entry.

6.4 Ligands [i](#)

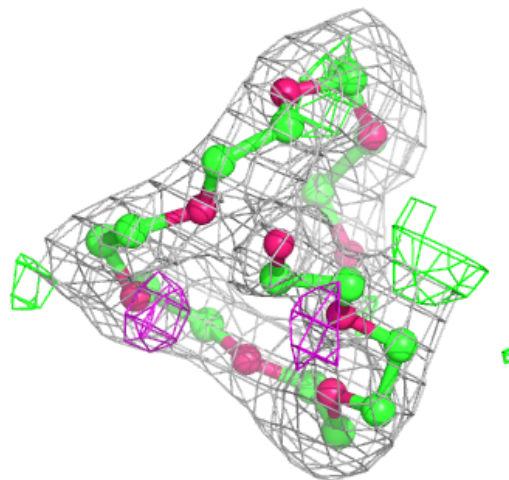
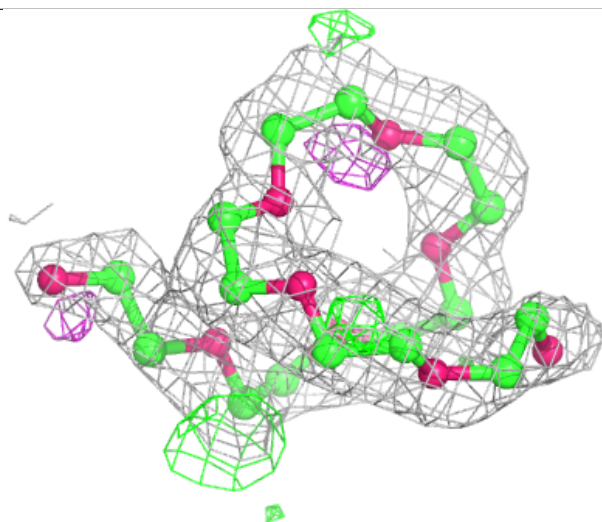
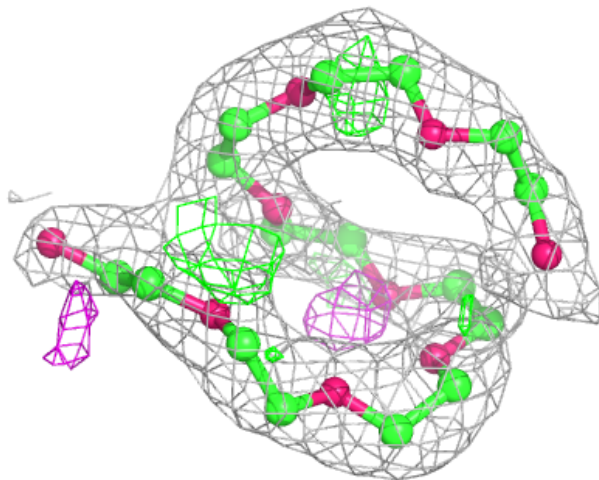
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	SO4	E	1345	5/5	0.57	0.31	115,116,119,119	0
2	PE8	K	1345	25/25	0.90	0.16	27,49,58,61	0
2	PE8	C	1345	25/25	0.91	0.16	24,45,55,59	0
2	PE8	J	1345	25/25	0.93	0.15	27,45,63,71	0
2	PE8	G	1346	25/25	0.93	0.12	27,43,54,65	0
2	PE8	B	1346	25/25	0.94	0.14	25,47,61,63	0
2	PE8	L	1345	25/25	0.94	0.12	24,48,57,61	0
3	SO4	H	1345	5/5	0.97	0.13	40,42,51,53	0
3	SO4	C	1346	5/5	0.98	0.16	45,45,47,53	0
3	SO4	B	1347	5/5	0.98	0.13	41,43,45,51	0
3	SO4	I	1346	5/5	0.98	0.18	29,31,39,45	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

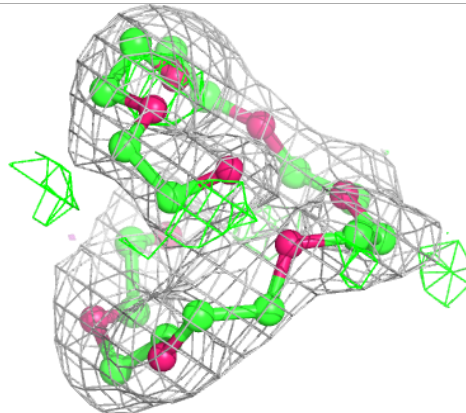
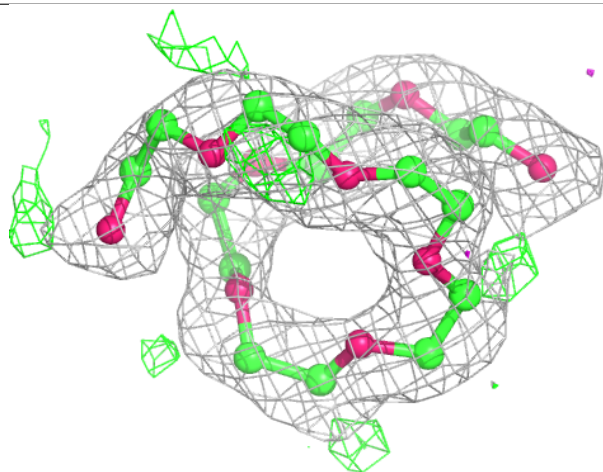
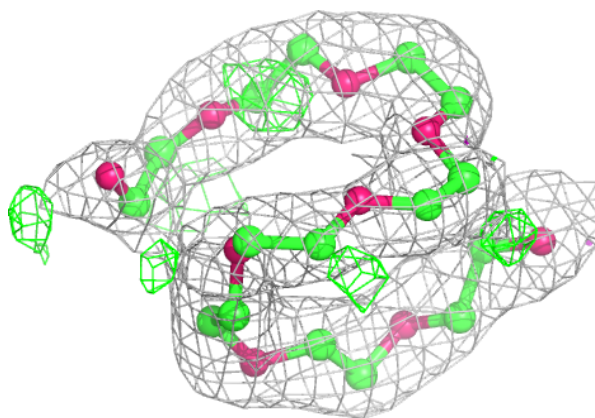
Electron density around PE8 K 1345:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



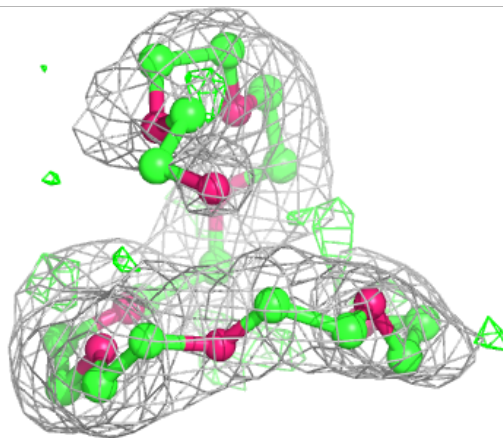
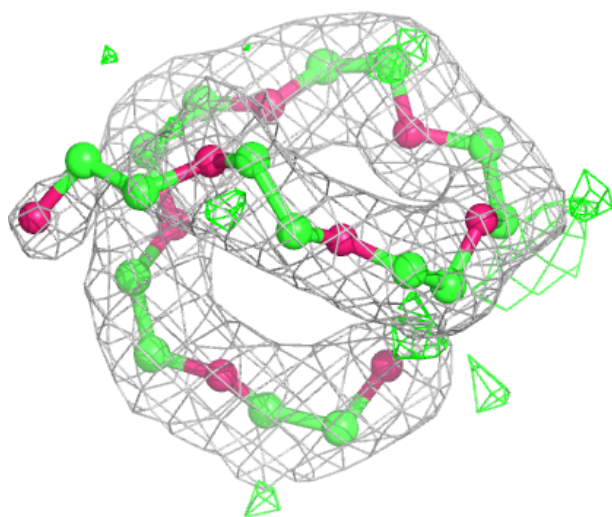
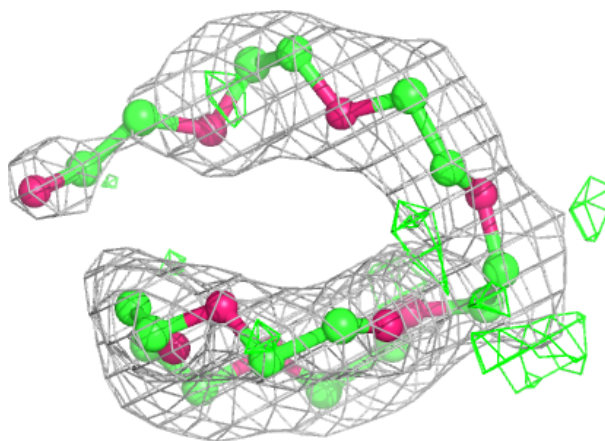
Electron density around PE8 C 1345:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



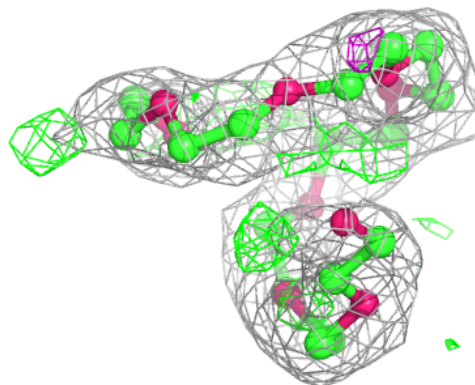
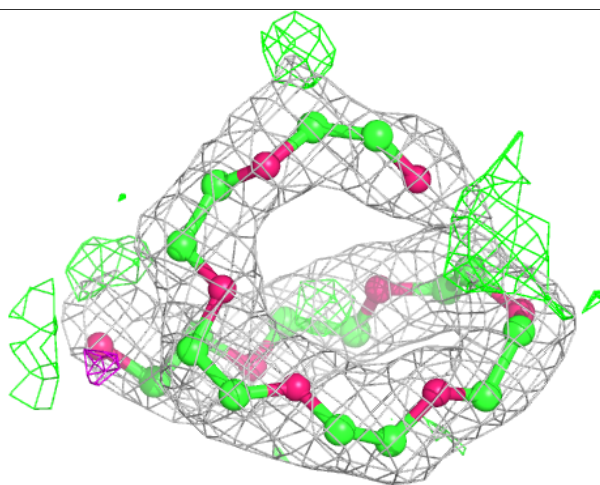
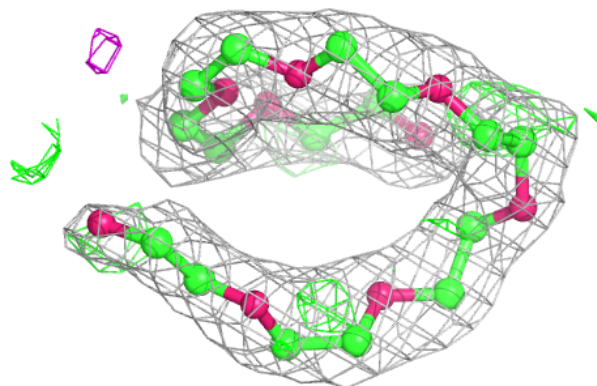
Electron density around PE8 J 1345:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



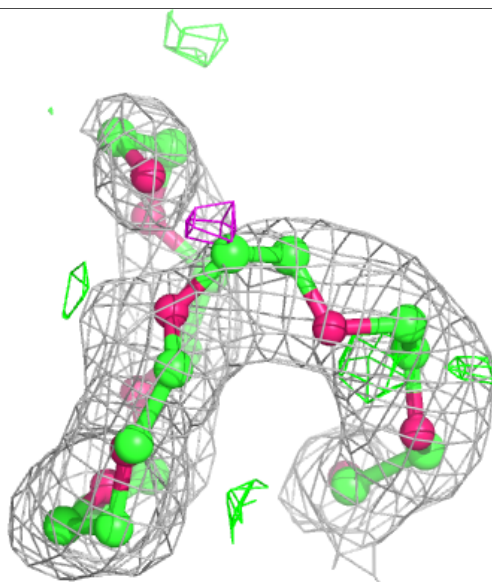
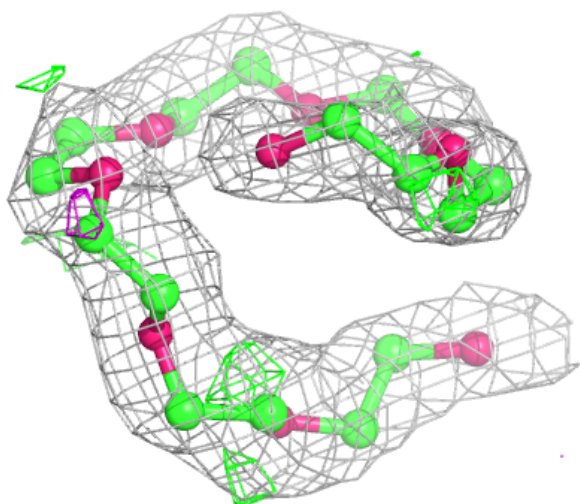
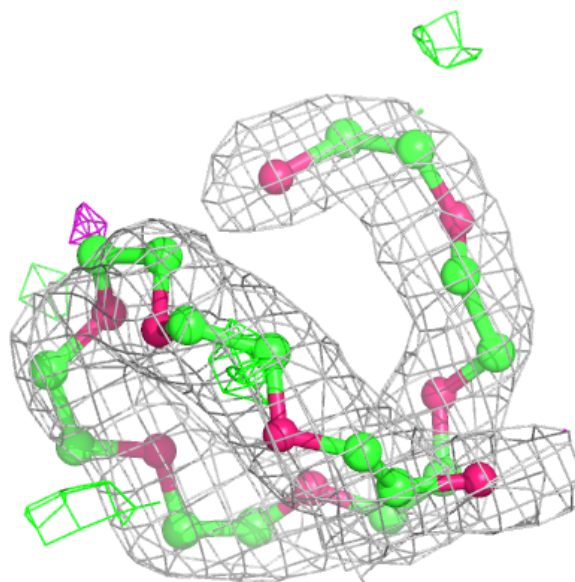
Electron density around PE8 G 1346:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



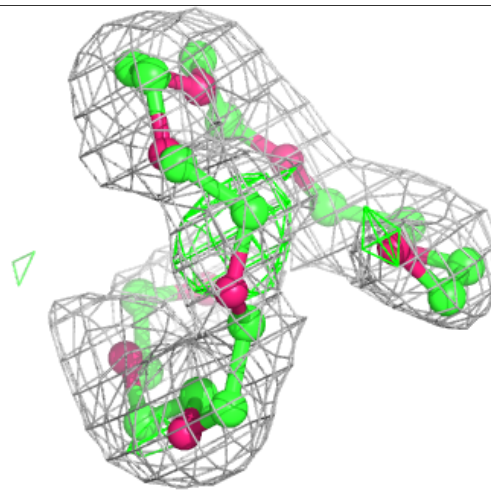
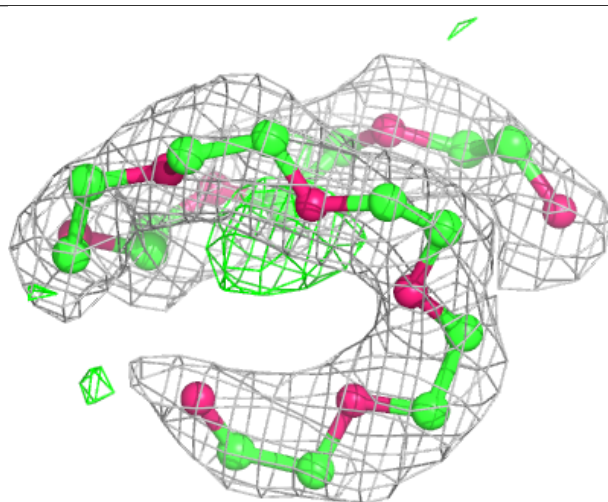
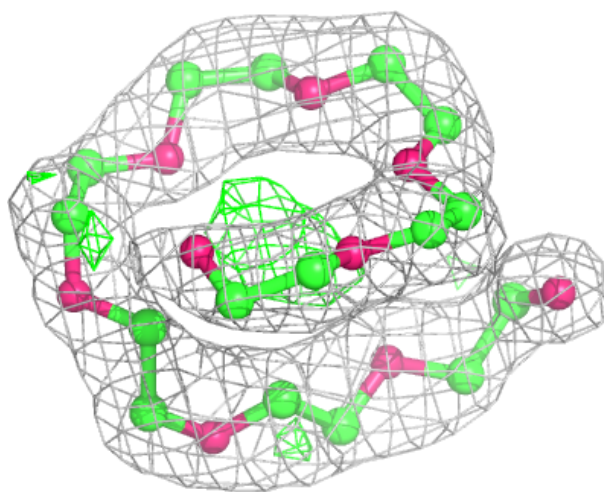
Electron density around PE8 B 1346:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around PE8 L 1345:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers ⓘ

There are no such residues in this entry.