



wwPDB X-ray Structure Validation Summary Report ⓘ

May 26, 2020 – 12:04 am BST

PDB ID : 4IND
Title : The Triple Jelly Roll Fold and Turret Assembly in an Archaeal Virus
Authors : Eilers, B.J.; Kraft, D.; Burgess, M.C.; Young, M.J.; Lawrence, C.M.
Deposited on : 2013-01-04
Resolution : 1.80 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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
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

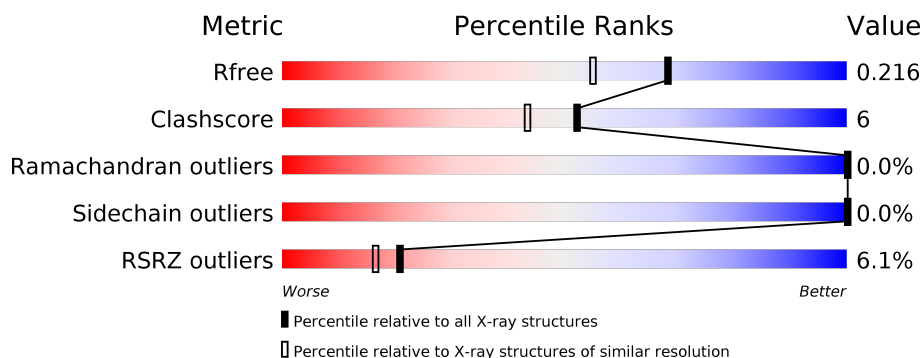
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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	387	<div> <div>7%</div> <div>88%</div> <div>9%</div> <div>.</div> </div>
1	B	387	<div> <div>5%</div> <div>89%</div> <div>8%</div> <div>.</div> </div>
1	C	387	<div> <div>7%</div> <div>90%</div> <div>7%</div> <div>.</div> </div>
1	D	387	<div> <div>6%</div> <div>88%</div> <div>9%</div> <div>.</div> </div>
1	E	387	<div> <div>4%</div> <div>87%</div> <div>11%</div> <div>.</div> </div>
1	F	387	<div> <div>5%</div> <div>87%</div> <div>11%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
1	G	387	
1	H	387	
1	I	387	
1	J	387	
1	K	387	
1	L	387	
1	M	387	
1	N	387	
1	O	387	
1	P	387	
1	Q	387	
1	R	387	
1	S	387	
1	T	387	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	2HP	A	401	-	-	X	-
2	2HP	B	403	-	-	X	-
2	2HP	C	401	-	-	X	-
2	2HP	F	401	-	-	X	-
2	2HP	F	403	-	-	X	-
2	2HP	G	401	-	-	X	-
2	2HP	P	402	-	-	X	-
2	2HP	R	401	-	-	X	-
2	2HP	S	401	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 64220 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 C381 turret protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	377	Total	C	N	O	S	0	6	0
			2970	1905	477	584	4			
1	B	377	Total	C	N	O	S	0	6	0
			2970	1905	477	584	4			
1	C	377	Total	C	N	O	S	0	6	0
			2970	1905	477	584	4			
1	D	377	Total	C	N	O	S	0	6	0
			2970	1905	477	584	4			
1	E	377	Total	C	N	O	S	0	6	0
			2970	1905	477	584	4			
1	F	377	Total	C	N	O	S	0	6	0
			2970	1905	477	584	4			
1	G	377	Total	C	N	O	S	0	6	0
			2970	1905	477	584	4			
1	H	377	Total	C	N	O	S	0	6	0
			2970	1905	477	584	4			
1	I	377	Total	C	N	O	S	0	6	0
			2970	1905	477	584	4			
1	J	377	Total	C	N	O	S	0	6	0
			2970	1905	477	584	4			
1	K	377	Total	C	N	O	S	0	6	0
			2970	1905	477	584	4			
1	L	377	Total	C	N	O	S	0	6	0
			2970	1905	477	584	4			
1	M	377	Total	C	N	O	S	0	6	0
			2970	1905	477	584	4			
1	N	377	Total	C	N	O	S	0	6	0
			2970	1905	477	584	4			
1	O	377	Total	C	N	O	S	0	6	0
			2970	1905	477	584	4			
1	P	377	Total	C	N	O	S	0	6	0
			2970	1905	477	584	4			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Q	377	Total	C	N	O	S	0	6	0
			2970	1905	477	584	4			
1	R	377	Total	C	N	O	S	0	6	0
			2970	1905	477	584	4			
1	S	377	Total	C	N	O	S	0	6	0
			2970	1905	477	584	4			
1	T	377	Total	C	N	O	S	0	6	0
			2970	1905	477	584	4			

There are 120 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	382	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
A	383	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
A	384	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
A	385	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
A	386	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
A	387	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
B	382	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
B	383	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
B	384	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
B	385	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
B	386	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
B	387	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
C	382	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
C	383	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
C	384	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
C	385	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
C	386	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
C	387	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
D	382	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
D	383	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
D	384	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
D	385	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
D	386	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
D	387	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
E	382	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
E	383	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
E	384	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
E	385	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
E	386	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
E	387	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
F	382	HIS	-	EXPRESSION TAG	UNP Q6Q0L3

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Chain	Residue	Modelled	Actual	Comment	Reference
F	383	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
F	384	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
F	385	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
F	386	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
F	387	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
G	382	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
G	383	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
G	384	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
G	385	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
G	386	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
G	387	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
H	382	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
H	383	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
H	384	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
H	385	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
H	386	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
H	387	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
I	382	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
I	383	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
I	384	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
I	385	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
I	386	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
I	387	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
J	382	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
J	383	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
J	384	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
J	385	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
J	386	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
J	387	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
K	382	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
K	383	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
K	384	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
K	385	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
K	386	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
K	387	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
L	382	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
L	383	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
L	384	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
L	385	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
L	386	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
L	387	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
M	382	HIS	-	EXPRESSION TAG	UNP Q6Q0L3

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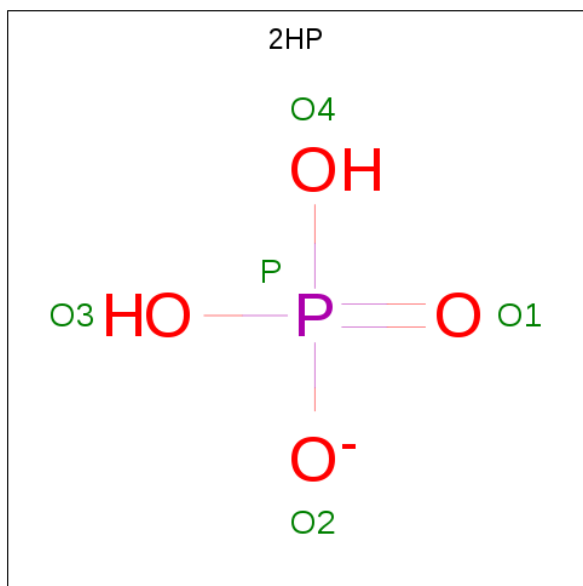
Chain	Residue	Modelled	Actual	Comment	Reference
M	383	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
M	384	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
M	385	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
M	386	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
M	387	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
N	382	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
N	383	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
N	384	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
N	385	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
N	386	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
N	387	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
O	382	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
O	383	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
O	384	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
O	385	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
O	386	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
O	387	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
P	382	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
P	383	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
P	384	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
P	385	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
P	386	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
P	387	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
Q	382	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
Q	383	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
Q	384	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
Q	385	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
Q	386	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
Q	387	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
R	382	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
R	383	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
R	384	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
R	385	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
R	386	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
R	387	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
S	382	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
S	383	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
S	384	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
S	385	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
S	386	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
S	387	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
T	382	HIS	-	EXPRESSION TAG	UNP Q6Q0L3

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Chain	Residue	Modelled	Actual	Comment	Reference
T	383	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
T	384	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
T	385	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
T	386	HIS	-	EXPRESSION TAG	UNP Q6Q0L3
T	387	HIS	-	EXPRESSION TAG	UNP Q6Q0L3

- Molecule 2 is DIHYDROGENPHOSPHATE ION (three-letter code: 2HP) (formula: $\text{H}_2\text{O}_4\text{P}$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O P 5 4 1	0	0
2	A	1	Total O P 5 4 1	0	0
2	A	1	Total O P 5 4 1	0	0
2	B	1	Total O P 5 4 1	0	0
2	B	1	Total O P 5 4 1	0	0
2	B	1	Total O P 5 4 1	0	0
2	B	1	Total O P 5 4 1	0	0
2	C	1	Total O P 5 4 1	0	0
2	C	1	Total O P 5 4 1	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	D	1	Total	O	P	0	0
			5	4	1		
2	D	1	Total	O	P	0	0
			5	4	1		
2	D	1	Total	O	P	0	0
			5	4	1		
2	E	1	Total	O	P	0	0
			5	4	1		
2	E	1	Total	O	P	0	0
			5	4	1		
2	E	1	Total	O	P	0	0
			5	4	1		
2	F	1	Total	O	P	0	0
			5	4	1		
2	F	1	Total	O	P	0	0
			5	4	1		
2	F	1	Total	O	P	0	0
			5	4	1		
2	G	1	Total	O	P	0	0
			5	4	1		
2	G	1	Total	O	P	0	0
			5	4	1		
2	G	1	Total	O	P	0	0
			5	4	1		
2	H	1	Total	O	P	0	0
			5	4	1		
2	H	1	Total	O	P	0	0
			5	4	1		
2	H	1	Total	O	P	0	0
			5	4	1		
2	I	1	Total	O	P	0	0
			5	4	1		
2	I	1	Total	O	P	0	0
			5	4	1		
2	I	1	Total	O	P	0	0
			5	4	1		
2	I	1	Total	O	P	0	0
			5	4	1		
2	J	1	Total	O	P	0	0
			5	4	1		
2	J	1	Total	O	P	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	K	1	Total	O	P	0	0
			5	4	1		
2	K	1	Total	O	P	0	0
			5	4	1		
2	K	1	Total	O	P	0	0
			5	4	1		
2	L	1	Total	O	P	0	0
			5	4	1		
2	L	1	Total	O	P	0	0
			5	4	1		
2	L	1	Total	O	P	0	0
			5	4	1		
2	M	1	Total	O	P	0	0
			5	4	1		
2	M	1	Total	O	P	0	0
			5	4	1		
2	M	1	Total	O	P	0	0
			5	4	1		
2	N	1	Total	O	P	0	0
			5	4	1		
2	N	1	Total	O	P	0	0
			5	4	1		
2	N	1	Total	O	P	0	0
			5	4	1		
2	O	1	Total	O	P	0	0
			5	4	1		
2	O	1	Total	O	P	0	0
			5	4	1		
2	O	1	Total	O	P	0	0
			5	4	1		
2	P	1	Total	O	P	0	0
			5	4	1		
2	P	1	Total	O	P	0	0
			5	4	1		
2	P	1	Total	O	P	0	0
			5	4	1		
2	Q	1	Total	O	P	0	0
			5	4	1		
2	Q	1	Total	O	P	0	0
			5	4	1		
2	Q	1	Total	O	P	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	Q	1	Total	O	P	0	0
			5	4	1		
2	R	1	Total	O	P	0	0
			5	4	1		
2	R	1	Total	O	P	0	0
			5	4	1		
2	S	1	Total	O	P	0	0
			5	4	1		
2	S	1	Total	O	P	0	0
			5	4	1		
2	S	1	Total	O	P	0	0
			5	4	1		
2	T	1	Total	O	P	0	0
			5	4	1		
2	T	1	Total	O	P	0	0
			5	4	1		
2	T	1	Total	O	P	0	0
			5	4	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	213	Total	O	0	0
			213	213		
3	B	207	Total	O	0	0
			207	207		
3	C	214	Total	O	0	0
			214	214		
3	D	244	Total	O	0	0
			244	244		
3	E	233	Total	O	0	0
			233	233		
3	F	230	Total	O	0	0
			230	230		
3	G	251	Total	O	0	0
			251	251		
3	H	259	Total	O	0	0
			259	259		
3	I	213	Total	O	0	0
			213	213		
3	J	229	Total	O	0	0
			229	229		

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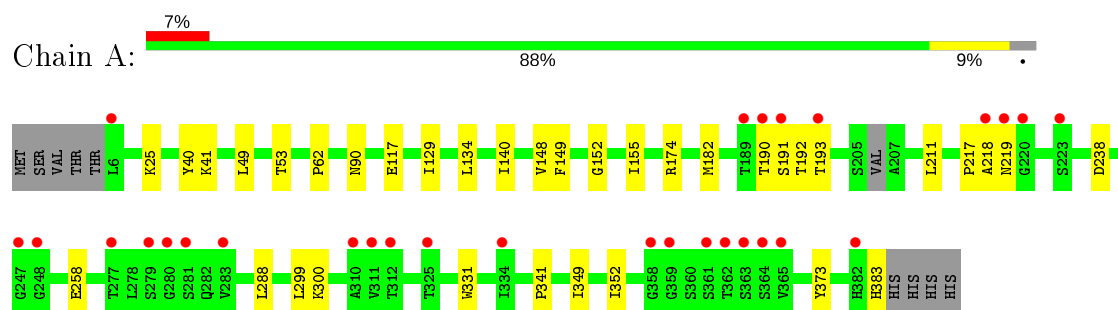
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	K	207	Total 207	O 207	0	0
3	L	197	Total 197	O 197	0	0
3	M	233	Total 233	O 233	0	0
3	N	238	Total 238	O 238	0	0
3	O	240	Total 240	O 240	0	0
3	P	233	Total 233	O 233	0	0
3	Q	216	Total 216	O 216	0	0
3	R	191	Total 191	O 191	0	0
3	S	239	Total 239	O 239	0	0
3	T	233	Total 233	O 233	0	0

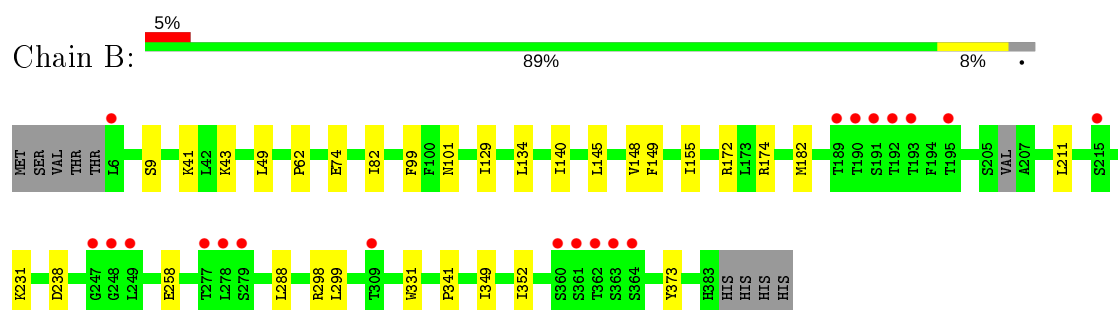
3 Residue-property plots [i](#)

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.

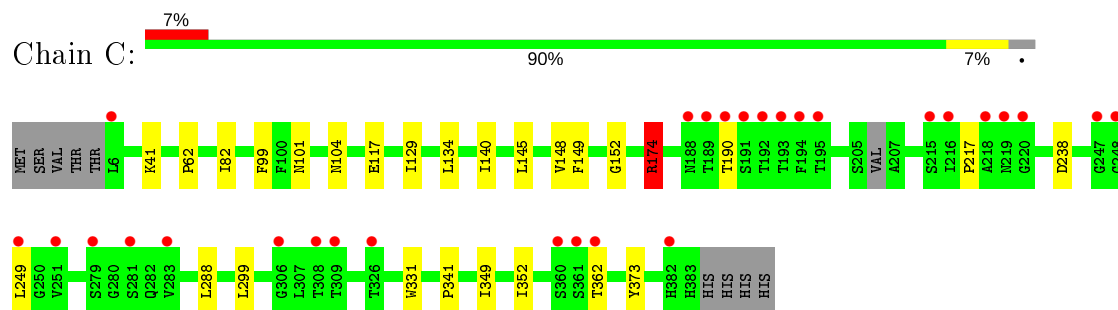
• Molecule 1: C381 turret protein



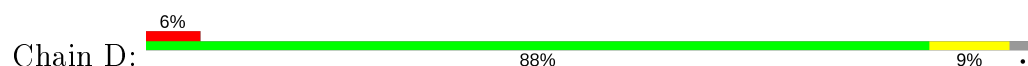
• Molecule 1: C381 turret protein

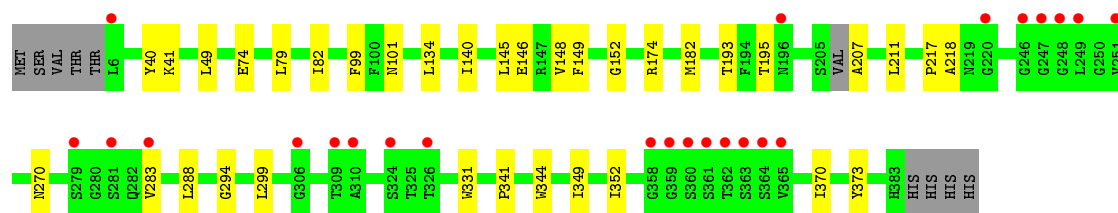


• Molecule 1: C381 turret protein

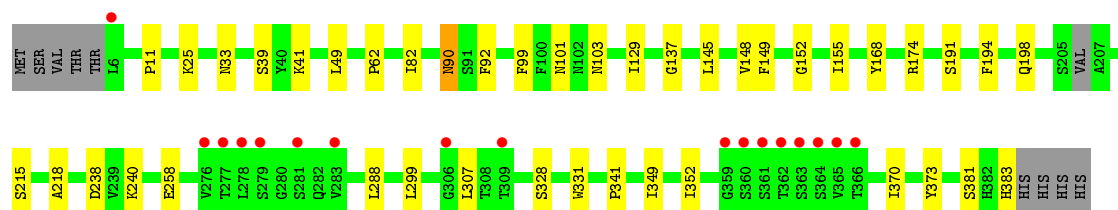
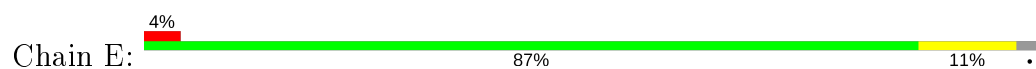


• Molecule 1: C381 turret protein

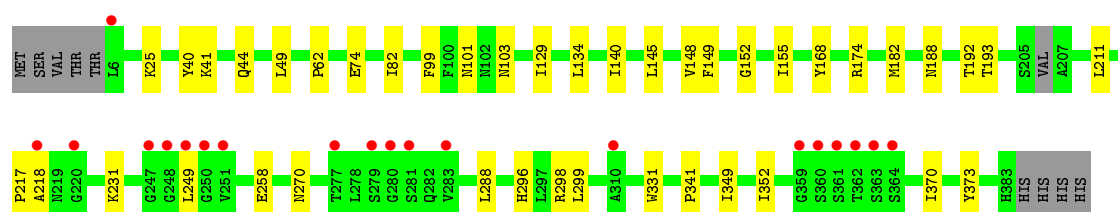
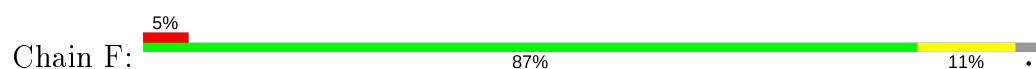




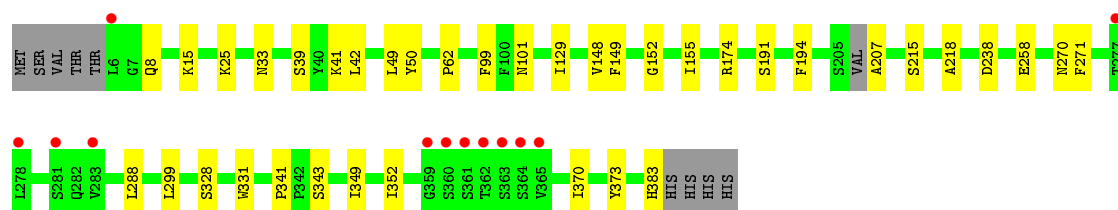
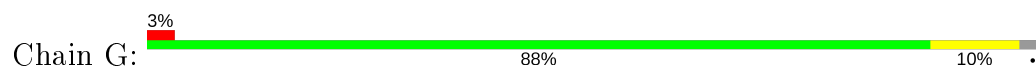
• Molecule 1: C381 turret protein



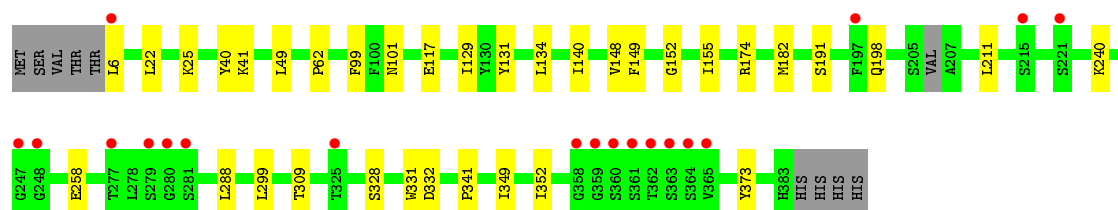
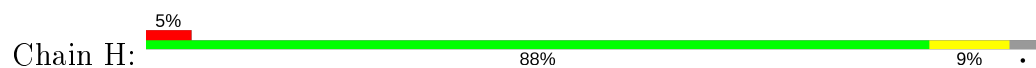
• Molecule 1: C381 turret protein



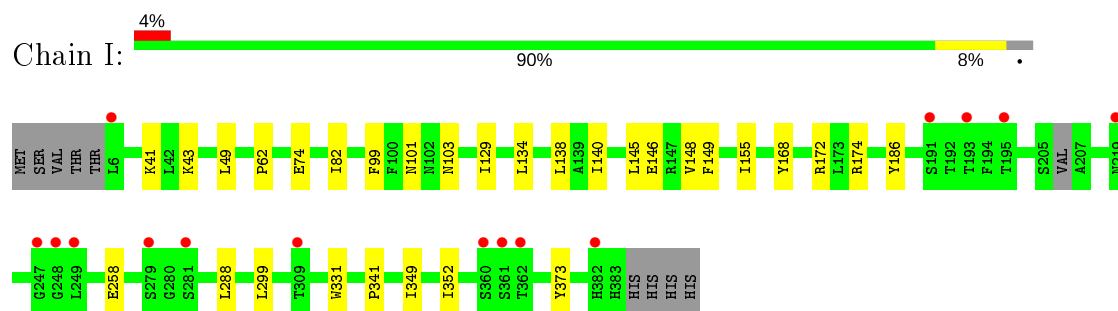
• Molecule 1: C381 turret protein



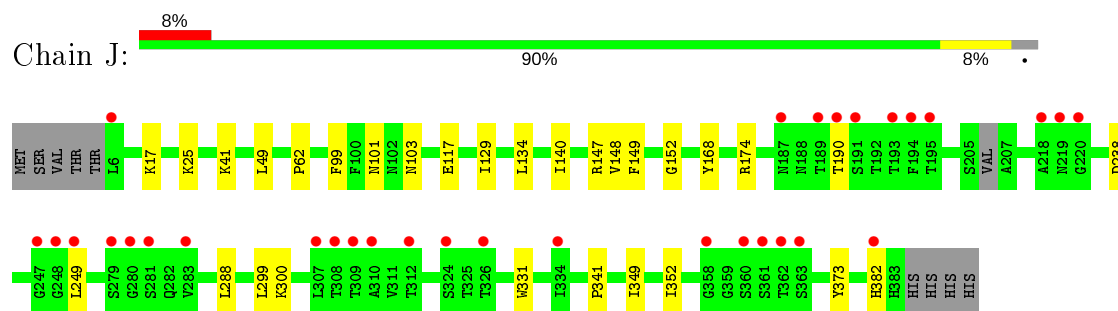
• Molecule 1: C381 turret protein



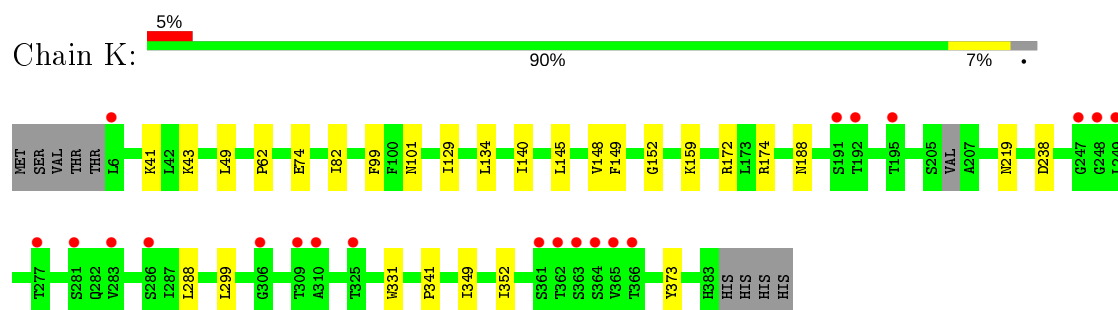
- Molecule 1: C381 turret protein



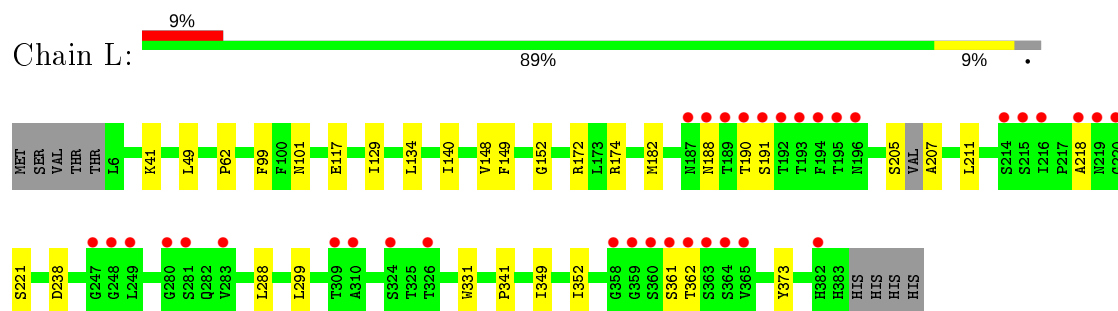
- Molecule 1: C381 turret protein



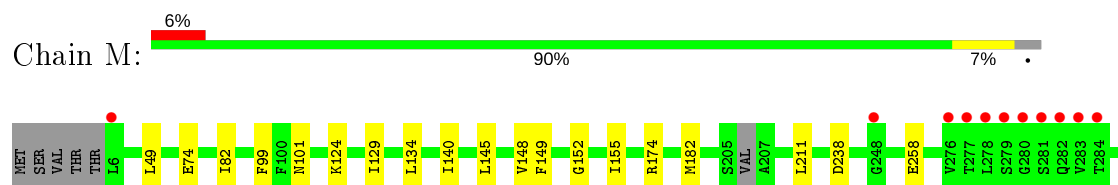
- Molecule 1: C381 turret protein

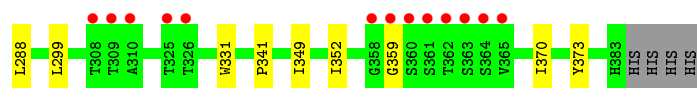


- Molecule 1: C381 turret protein

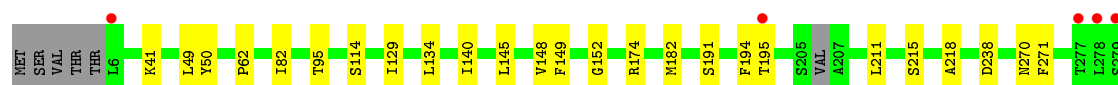
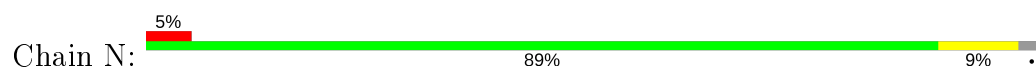


- Molecule 1: C381 turret protein

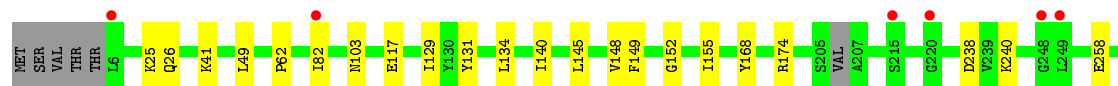
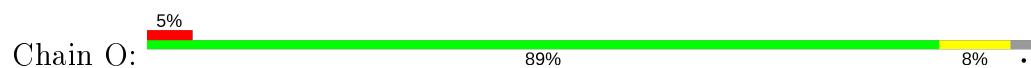




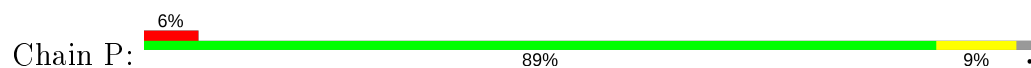
- Molecule 1: C381 turret protein



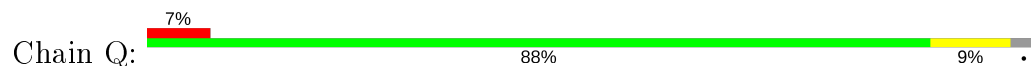
- Molecule 1: C381 turret protein



- Molecule 1: C381 turret protein

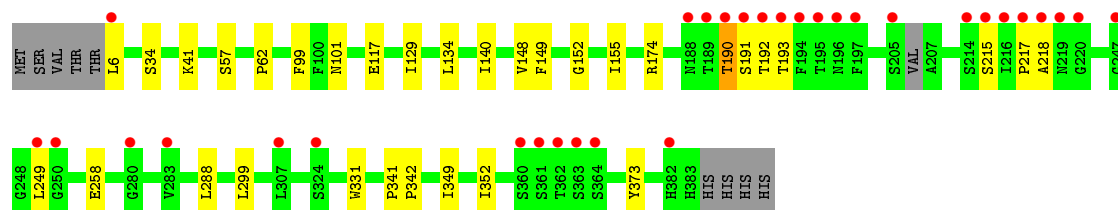
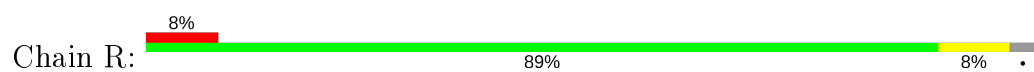


- Molecule 1: C381 turret protein

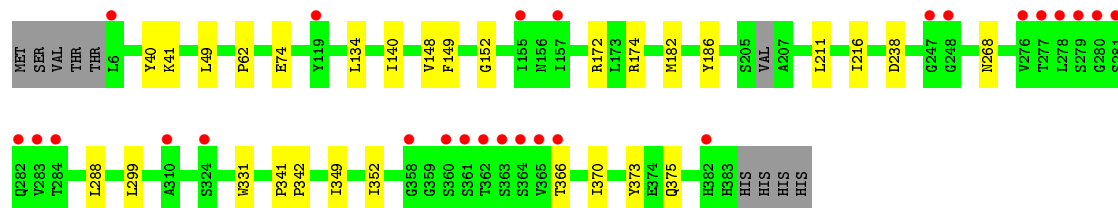
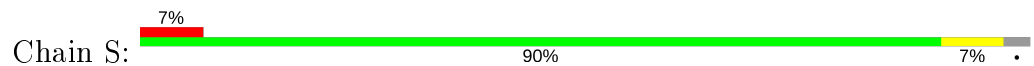


- Molecule 1: C381 turret protein

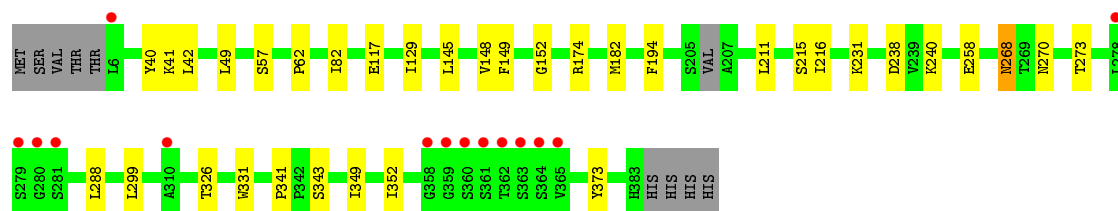
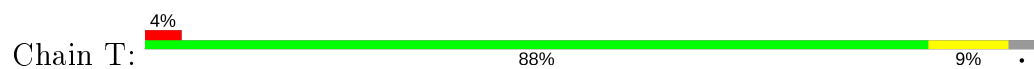




- Molecule 1: C381 turret protein



- Molecule 1: C381 turret protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	81.77Å 167.00Å 186.97Å 81.84° 82.17° 81.44°	Depositor
Resolution (Å)	39.19 – 1.80 39.18 – 1.76	Depositor EDS
% Data completeness (in resolution range)	86.9 (39.19-1.80) 81.9 (39.18-1.76)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	0.04	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.14 (at 1.76Å)	Xtriage
Refinement program	PHENIX 1.8.1_1168	Depositor
R, R_{free}	0.188 , 0.217 0.190 , 0.216	Depositor DCC
R_{free} test set	39151 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	29.6	Xtriage
Anisotropy	0.141	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 44.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	64220	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.05% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 2HP

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	0.48	2/3032 (0.1%)	0.59	0/4127
1	B	0.43	0/3032	0.58	0/4127
1	C	0.43	0/3032	0.80	3/4127 (0.1%)
1	D	0.44	0/3032	0.59	0/4127
1	E	0.52	4/3032 (0.1%)	0.60	0/4127
1	F	0.46	0/3032	0.59	0/4127
1	G	0.46	0/3032	0.60	0/4127
1	H	0.46	0/3032	0.60	0/4127
1	I	0.42	0/3032	0.58	0/4127
1	J	0.44	0/3032	0.59	0/4127
1	K	0.42	0/3032	0.58	0/4127
1	L	0.42	0/3032	0.58	0/4127
1	M	0.44	0/3032	0.58	0/4127
1	N	0.45	0/3032	0.59	0/4127
1	O	0.43	0/3032	0.58	0/4127
1	P	0.43	0/3032	0.58	0/4127
1	Q	0.48	2/3032 (0.1%)	0.58	0/4127
1	R	0.44	0/3032	0.59	0/4127
1	S	0.46	0/3032	0.59	0/4127
1	T	0.49	2/3032 (0.1%)	0.59	0/4127
All	All	0.45	10/60640 (0.0%)	0.60	3/82540 (0.0%)

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	90	ASN	CG-ND2	-8.86	1.10	1.32
1	Q	90	ASN	CG-ND2	-8.79	1.10	1.32
1	T	268	ASN	CG-ND2	-8.63	1.11	1.32
1	E	198	GLN	CD-NE2	-8.58	1.11	1.32
1	Q	90	ASN	CG-OD1	-8.44	1.05	1.24

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	174	ARG	NE-CZ-NH1	-24.25	108.17	120.30
1	C	174	ARG	NE-CZ-NH2	23.42	132.01	120.30
1	C	174	ARG	CD-NE-CZ	10.42	138.19	123.60

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	2970	0	2938	54	0
1	B	2970	0	2938	30	0
1	C	2970	0	2938	26	1
1	D	2970	0	2938	44	1
1	E	2970	0	2938	49	0
1	F	2970	0	2938	72	0
1	G	2970	0	2938	52	0
1	H	2970	0	2938	45	1
1	I	2970	0	2938	31	0
1	J	2970	0	2938	30	0
1	K	2970	0	2938	28	0
1	L	2970	0	2938	40	2
1	M	2970	0	2938	27	0
1	N	2970	0	2938	34	1
1	O	2970	0	2938	30	3
1	P	2970	0	2938	37	0
1	Q	2970	0	2938	40	0
1	R	2970	0	2938	54	0
1	S	2970	0	2938	28	1
1	T	2970	0	2938	34	1
2	A	15	0	0	3	0
2	B	20	0	0	5	0
2	C	10	0	0	2	0
2	D	15	0	0	2	0
2	E	15	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	15	0	0	5	0
2	G	15	0	0	3	0
2	H	15	0	0	1	0
2	I	20	0	0	2	0
2	J	10	0	0	1	0
2	K	15	0	0	2	0
2	L	15	0	0	2	0
2	M	15	0	0	2	0
2	N	15	0	0	2	0
2	O	15	0	0	1	0
2	P	15	0	0	4	0
2	Q	20	0	0	3	0
2	R	10	0	0	2	0
2	S	15	0	0	3	0
2	T	15	0	0	3	0
3	A	213	0	0	2	0
3	B	207	0	0	5	0
3	C	214	0	0	4	0
3	D	244	0	0	9	0
3	E	233	0	0	5	0
3	F	230	0	0	11	0
3	G	251	0	0	6	0
3	H	259	0	0	5	0
3	I	213	0	0	5	0
3	J	229	0	0	6	0
3	K	207	0	0	4	0
3	L	197	0	0	2	0
3	M	233	0	0	3	0
3	N	238	0	0	4	1
3	O	240	0	0	4	0
3	P	233	0	0	4	0
3	Q	216	0	0	5	0
3	R	191	0	0	3	0
3	S	239	0	0	5	2
3	T	233	0	0	5	0
All	All	64220	0	58760	654	7

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 6.

The worst 5 of 654 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:40:TYR:CZ	1:H:25:LYS:HE3	1.35	1.57
1:A:25:LYS:HE3	1:F:40:TYR:CZ	1.41	1.55
1:A:25:LYS:HE3	1:F:40:TYR:CE1	1.62	1.33
1:F:249:LEU:HD12	1:R:215:SER:OG	1.31	1.29
1:L:361:SER:OG	1:Q:360:SER:HB3	1.08	1.25

The worst 5 of 7 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:25:LYS:NZ	3:S:706:HOH:O[1_554]	1.75	0.45
1:D:195:THR:OG1	1:L:221:SER:OG[1_565]	1.92	0.28
1:C:362:THR:CG2	1:H:309:THR:OG1[1_654]	1.96	0.24
1:T:40:TYR:OH	3:N:695:HOH:O[1_556]	2.02	0.18
1:O:25:LYS:CE	1:S:40:TYR:CZ[1_554]	2.15	0.05

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	379/387 (98%)	364 (96%)	15 (4%)	0	100	100
1	B	379/387 (98%)	366 (97%)	13 (3%)	0	100	100
1	C	379/387 (98%)	368 (97%)	11 (3%)	0	100	100
1	D	379/387 (98%)	367 (97%)	12 (3%)	0	100	100
1	E	379/387 (98%)	367 (97%)	12 (3%)	0	100	100
1	F	379/387 (98%)	364 (96%)	15 (4%)	0	100	100
1	G	379/387 (98%)	367 (97%)	12 (3%)	0	100	100
1	H	379/387 (98%)	366 (97%)	13 (3%)	0	100	100
1	I	379/387 (98%)	365 (96%)	14 (4%)	0	100	100
1	J	379/387 (98%)	367 (97%)	12 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	K	379/387 (98%)	366 (97%)	13 (3%)	0	100	100
1	L	379/387 (98%)	365 (96%)	14 (4%)	0	100	100
1	M	379/387 (98%)	363 (96%)	16 (4%)	0	100	100
1	N	379/387 (98%)	368 (97%)	11 (3%)	0	100	100
1	O	379/387 (98%)	367 (97%)	12 (3%)	0	100	100
1	P	379/387 (98%)	367 (97%)	12 (3%)	0	100	100
1	Q	379/387 (98%)	368 (97%)	11 (3%)	0	100	100
1	R	379/387 (98%)	365 (96%)	13 (3%)	1 (0%)	41	27
1	S	379/387 (98%)	366 (97%)	13 (3%)	0	100	100
1	T	379/387 (98%)	367 (97%)	12 (3%)	0	100	100
All	All	7580/7740 (98%)	7323 (97%)	256 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	R	34	SER

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	336/340 (99%)	336 (100%)	0	100	100
1	B	336/340 (99%)	336 (100%)	0	100	100
1	C	336/340 (99%)	335 (100%)	1 (0%)	92	91
1	D	336/340 (99%)	336 (100%)	0	100	100
1	E	336/340 (99%)	336 (100%)	0	100	100
1	F	336/340 (99%)	336 (100%)	0	100	100
1	G	336/340 (99%)	336 (100%)	0	100	100
1	H	336/340 (99%)	335 (100%)	1 (0%)	92	91

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	I	336/340 (99%)	336 (100%)	0	100	100
1	J	336/340 (99%)	336 (100%)	0	100	100
1	K	336/340 (99%)	336 (100%)	0	100	100
1	L	336/340 (99%)	336 (100%)	0	100	100
1	M	336/340 (99%)	336 (100%)	0	100	100
1	N	336/340 (99%)	336 (100%)	0	100	100
1	O	336/340 (99%)	336 (100%)	0	100	100
1	P	336/340 (99%)	336 (100%)	0	100	100
1	Q	336/340 (99%)	336 (100%)	0	100	100
1	R	336/340 (99%)	335 (100%)	1 (0%)	92	91
1	S	336/340 (99%)	336 (100%)	0	100	100
1	T	336/340 (99%)	336 (100%)	0	100	100
All	All	6720/6800 (99%)	6717 (100%)	3 (0%)	100	100

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	174	ARG
1	H	191	SER
1	R	190	THR

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

Mol	Chain	Res	Type
1	T	268	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

60 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	2HP	C	401	-	4,4,4	0.86	0	6,6,6	0.93	0
2	2HP	Q	403	-	4,4,4	1.73	1 (25%)	6,6,6	1.28	1 (16%)
2	2HP	M	402	-	4,4,4	0.87	0	6,6,6	1.03	1 (16%)
2	2HP	I	403	-	4,4,4	1.81	1 (25%)	6,6,6	0.98	1 (16%)
2	2HP	T	402	-	4,4,4	1.66	1 (25%)	6,6,6	1.12	1 (16%)
2	2HP	E	402	-	4,4,4	1.66	1 (25%)	6,6,6	0.76	0
2	2HP	A	403	-	4,4,4	0.83	0	6,6,6	1.19	1 (16%)
2	2HP	M	401	-	4,4,4	0.88	0	6,6,6	1.47	1 (16%)
2	2HP	D	402	-	4,4,4	1.55	1 (25%)	6,6,6	1.12	1 (16%)
2	2HP	S	403	-	4,4,4	1.95	1 (25%)	6,6,6	0.99	1 (16%)
2	2HP	B	403	-	4,4,4	1.73	1 (25%)	6,6,6	1.14	1 (16%)
2	2HP	R	401	-	4,4,4	0.85	0	6,6,6	1.41	1 (16%)
2	2HP	J	401	-	4,4,4	0.85	0	6,6,6	1.21	1 (16%)
2	2HP	M	403	-	4,4,4	1.49	1 (25%)	6,6,6	1.03	0
2	2HP	J	402	-	4,4,4	1.50	1 (25%)	6,6,6	0.96	0
2	2HP	S	401	-	4,4,4	0.94	0	6,6,6	1.07	1 (16%)
2	2HP	K	402	-	4,4,4	0.87	0	6,6,6	1.03	0
2	2HP	G	403	-	4,4,4	1.52	1 (25%)	6,6,6	1.32	1 (16%)
2	2HP	B	401	-	4,4,4	0.76	0	6,6,6	1.24	0
2	2HP	E	403	-	4,4,4	1.77	1 (25%)	6,6,6	0.86	0
2	2HP	D	401	-	4,4,4	0.92	0	6,6,6	1.18	1 (16%)
2	2HP	D	403	-	4,4,4	1.83	1 (25%)	6,6,6	1.04	1 (16%)
2	2HP	A	402	-	4,4,4	1.62	1 (25%)	6,6,6	1.11	1 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	2HP	N	403	-	4,4,4	1.68	1 (25%)	6,6,6	0.81	0
2	2HP	E	401	-	4,4,4	0.84	0	6,6,6	0.99	0
2	2HP	R	402	-	4,4,4	1.74	1 (25%)	6,6,6	1.13	1 (16%)
2	2HP	P	401	-	4,4,4	0.81	0	6,6,6	1.14	1 (16%)
2	2HP	S	402	-	4,4,4	1.60	1 (25%)	6,6,6	0.66	0
2	2HP	O	403	-	4,4,4	1.59	1 (25%)	6,6,6	1.12	1 (16%)
2	2HP	P	403	-	4,4,4	1.62	1 (25%)	6,6,6	1.11	1 (16%)
2	2HP	L	401	-	4,4,4	0.74	0	6,6,6	1.32	1 (16%)
2	2HP	L	403	-	4,4,4	1.74	1 (25%)	6,6,6	1.07	1 (16%)
2	2HP	H	402	-	4,4,4	0.84	0	6,6,6	0.92	0
2	2HP	T	401	-	4,4,4	0.85	0	6,6,6	1.33	1 (16%)
2	2HP	I	402	-	4,4,4	0.85	0	6,6,6	1.17	1 (16%)
2	2HP	F	401	-	4,4,4	0.85	0	6,6,6	1.36	1 (16%)
2	2HP	B	402	-	4,4,4	1.64	1 (25%)	6,6,6	1.02	0
2	2HP	C	402	-	4,4,4	1.84	1 (25%)	6,6,6	1.02	1 (16%)
2	2HP	O	401	-	4,4,4	0.50	0	6,6,6	1.37	1 (16%)
2	2HP	Q	404	-	4,4,4	1.52	1 (25%)	6,6,6	0.81	0
2	2HP	I	404	-	4,4,4	0.81	0	6,6,6	1.12	1 (16%)
2	2HP	G	401	-	4,4,4	0.59	0	6,6,6	1.23	0
2	2HP	F	403	-	4,4,4	1.77	1 (25%)	6,6,6	1.44	1 (16%)
2	2HP	K	403	-	4,4,4	1.57	1 (25%)	6,6,6	0.98	0
2	2HP	T	403	-	4,4,4	1.61	1 (25%)	6,6,6	1.24	1 (16%)
2	2HP	P	402	-	4,4,4	1.55	0	6,6,6	0.63	0
2	2HP	H	401	-	4,4,4	0.72	0	6,6,6	1.35	1 (16%)
2	2HP	Q	402	-	4,4,4	1.61	1 (25%)	6,6,6	1.01	0
2	2HP	B	404	-	4,4,4	1.52	1 (25%)	6,6,6	0.45	0
2	2HP	Q	401	-	4,4,4	0.67	0	6,6,6	1.30	1 (16%)
2	2HP	N	402	-	4,4,4	0.94	0	6,6,6	0.98	0
2	2HP	L	402	-	4,4,4	0.95	0	6,6,6	0.92	0
2	2HP	O	402	-	4,4,4	0.88	0	6,6,6	0.97	0
2	2HP	I	401	-	4,4,4	0.65	0	6,6,6	1.14	0
2	2HP	K	401	-	4,4,4	0.67	0	6,6,6	1.04	0
2	2HP	F	402	-	4,4,4	0.58	0	6,6,6	1.38	1 (16%)
2	2HP	H	403	-	4,4,4	1.80	1 (25%)	6,6,6	0.88	0
2	2HP	G	402	-	4,4,4	0.80	0	6,6,6	1.19	0
2	2HP	A	401	-	4,4,4	0.88	0	6,6,6	1.42	1 (16%)
2	2HP	N	401	-	4,4,4	0.69	0	6,6,6	1.32	1 (16%)

The worst 5 of 28 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	S	403	2HP	P-O1	3.19	1.58	1.50
2	H	403	2HP	P-O1	3.03	1.58	1.50
2	C	402	2HP	P-O1	3.01	1.57	1.50
2	D	403	2HP	P-O1	2.90	1.57	1.50
2	E	403	2HP	P-O1	2.89	1.57	1.50

The worst 5 of 35 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	R	401	2HP	O2-P-O1	-3.00	99.92	110.89
2	F	402	2HP	O2-P-O1	-2.80	100.64	110.89
2	A	401	2HP	O2-P-O1	-2.77	100.75	110.89
2	F	403	2HP	O3-P-O2	-2.72	99.24	107.97
2	M	401	2HP	O2-P-O1	-2.71	100.96	110.89

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

40 monomers are involved in 50 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	401	2HP	2	0
2	Q	403	2HP	1	0
2	M	402	2HP	1	0
2	T	402	2HP	1	0
2	E	402	2HP	1	0
2	M	401	2HP	1	0
2	B	403	2HP	2	0
2	R	401	2HP	2	0
2	J	401	2HP	1	0
2	S	401	2HP	2	0
2	K	402	2HP	1	0
2	B	401	2HP	1	0
2	D	401	2HP	1	0
2	D	403	2HP	1	0
2	A	402	2HP	1	0
2	E	401	2HP	1	0
2	P	401	2HP	1	0
2	S	402	2HP	1	0
2	P	403	2HP	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	L	401	2HP	1	0
2	T	401	2HP	1	0
2	F	401	2HP	2	0
2	B	402	2HP	1	0
2	I	404	2HP	1	0
2	G	401	2HP	2	0
2	F	403	2HP	3	0
2	T	403	2HP	1	0
2	P	402	2HP	2	0
2	H	401	2HP	1	0
2	Q	402	2HP	1	0
2	B	404	2HP	1	0
2	Q	401	2HP	1	0
2	N	402	2HP	1	0
2	L	402	2HP	1	0
2	O	402	2HP	1	0
2	I	401	2HP	1	0
2	K	401	2HP	1	0
2	G	402	2HP	1	0
2	A	401	2HP	2	0
2	N	401	2HP	1	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 ⓘ

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	377/387 (97%)	0.09	29 (7%)	13	10	23, 36, 68, 95	0
1	B	377/387 (97%)	-0.03	20 (5%)	26	21	25, 36, 62, 86	0
1	C	377/387 (97%)	0.01	29 (7%)	13	10	23, 38, 68, 105	0
1	D	377/387 (97%)	0.09	24 (6%)	19	15	23, 36, 67, 103	0
1	E	377/387 (97%)	-0.16	17 (4%)	33	27	22, 35, 67, 101	0
1	F	377/387 (97%)	-0.04	20 (5%)	26	21	22, 34, 62, 117	0
1	G	377/387 (97%)	-0.26	12 (3%)	47	41	22, 32, 63, 98	0
1	H	377/387 (97%)	-0.01	19 (5%)	28	23	23, 33, 62, 92	0
1	I	377/387 (97%)	-0.12	15 (3%)	38	32	24, 35, 66, 103	0
1	J	377/387 (97%)	0.06	32 (8%)	10	8	23, 36, 64, 107	0
1	K	377/387 (97%)	-0.06	21 (5%)	24	19	24, 38, 65, 107	0
1	L	377/387 (97%)	0.16	35 (9%)	8	6	24, 39, 76, 114	0
1	M	377/387 (97%)	0.06	24 (6%)	19	15	23, 35, 64, 91	0
1	N	377/387 (97%)	-0.21	19 (5%)	28	23	21, 34, 60, 92	0
1	O	377/387 (97%)	0.00	19 (5%)	28	23	24, 35, 65, 121	0
1	P	377/387 (97%)	0.13	25 (6%)	18	14	24, 36, 67, 94	0
1	Q	377/387 (97%)	0.12	29 (7%)	13	10	24, 36, 64, 103	0
1	R	377/387 (97%)	0.07	32 (8%)	10	8	22, 37, 71, 99	0
1	S	377/387 (97%)	0.13	26 (6%)	16	13	22, 35, 64, 88	0
1	T	377/387 (97%)	-0.22	14 (3%)	41	36	22, 34, 60, 91	0
All	All	7540/7740 (97%)	-0.01	461 (6%)	21	16	21, 36, 66, 121	0

The worst 5 of 461 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	249	LEU	12.0
1	F	249	LEU	8.7
1	F	220	GLY	8.3
1	D	362	THR	7.8
1	R	219	ASN	7.6

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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
2	2HP	E	403	5/5	0.42	0.30	73,116,122,124	0
2	2HP	L	403	5/5	0.57	0.22	82,97,121,122	0
2	2HP	I	403	5/5	0.58	0.22	67,95,110,111	0
2	2HP	H	403	5/5	0.62	0.18	63,85,96,103	0
2	2HP	A	403	5/5	0.63	0.23	89,92,120,120	0
2	2HP	G	403	5/5	0.65	0.20	91,96,117,117	0
2	2HP	F	403	5/5	0.74	0.19	54,111,114,114	0
2	2HP	M	403	5/5	0.77	0.21	102,104,109,121	0
2	2HP	N	403	5/5	0.80	0.15	53,91,95,98	0
2	2HP	T	403	5/5	0.80	0.17	70,100,107,135	0
2	2HP	C	402	5/5	0.83	0.19	59,91,113,117	0
2	2HP	P	403	5/5	0.83	0.17	64,94,107,108	0
2	2HP	J	402	5/5	0.83	0.22	68,92,97,117	0
2	2HP	B	403	5/5	0.84	0.23	67,102,106,108	0
2	2HP	Q	403	5/5	0.86	0.15	67,92,102,103	0
2	2HP	S	403	5/5	0.87	0.13	57,82,105,107	0
2	2HP	D	403	5/5	0.87	0.13	64,66,100,101	0
2	2HP	O	403	5/5	0.88	0.12	63,84,99,100	0
2	2HP	R	402	5/5	0.90	0.15	80,84,98,101	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	2HP	K	403	5/5	0.91	0.10	87,93,98,99	0
2	2HP	K	401	5/5	0.95	0.16	51,55,62,102	0
2	2HP	I	401	5/5	0.96	0.14	38,57,59,81	0
2	2HP	D	402	5/5	0.96	0.09	37,49,57,73	0
2	2HP	Q	401	5/5	0.96	0.13	47,47,51,76	0
2	2HP	N	401	5/5	0.96	0.12	43,51,61,140	0
2	2HP	L	401	5/5	0.97	0.13	50,52,55,115	0
2	2HP	F	401	5/5	0.97	0.11	46,46,54,65	0
2	2HP	P	402	5/5	0.97	0.10	39,47,50,79	0
2	2HP	Q	402	5/5	0.97	0.08	43,44,55,83	0
2	2HP	P	401	5/5	0.97	0.10	43,49,54,66	0
2	2HP	D	401	5/5	0.97	0.08	43,45,62,69	0
2	2HP	O	401	5/5	0.97	0.10	42,45,53,78	0
2	2HP	G	401	5/5	0.97	0.08	37,48,71,74	0
2	2HP	A	401	5/5	0.97	0.12	35,46,54,55	0
2	2HP	J	401	5/5	0.97	0.11	47,48,51,64	0
2	2HP	C	401	5/5	0.98	0.11	44,46,68,74	0
2	2HP	B	401	5/5	0.98	0.12	34,41,53,82	0
2	2HP	E	402	5/5	0.98	0.08	45,45,54,63	0
2	2HP	R	401	5/5	0.98	0.11	40,46,52,60	0
2	2HP	S	401	5/5	0.98	0.07	34,40,44,64	0
2	2HP	A	402	5/5	0.98	0.09	44,48,52,77	0
2	2HP	H	402	5/5	0.98	0.09	39,40,44,65	0
2	2HP	L	402	5/5	0.98	0.09	45,46,61,68	0
2	2HP	O	402	5/5	0.98	0.09	40,43,49,93	0
2	2HP	T	401	5/5	0.98	0.11	42,52,68,160	0
2	2HP	I	402	5/5	0.98	0.08	43,45,57,58	0
2	2HP	F	402	5/5	0.98	0.07	39,46,58,79	0
2	2HP	B	402	5/5	0.98	0.08	41,47,54,74	0
2	2HP	G	402	5/5	0.98	0.09	39,45,58,59	0
2	2HP	K	402	5/5	0.98	0.06	42,45,51,53	0
2	2HP	E	401	5/5	0.98	0.09	49,49,70,135	0
2	2HP	M	401	5/5	0.99	0.09	38,44,52,77	0
2	2HP	M	402	5/5	0.99	0.12	50,51,58,62	0
2	2HP	T	402	5/5	0.99	0.10	39,39,52,81	0
2	2HP	Q	404	5/5	0.99	0.08	41,43,49,95	0
2	2HP	H	401	5/5	0.99	0.06	34,38,43,55	0
2	2HP	I	404	5/5	0.99	0.06	38,39,50,55	0
2	2HP	B	404	5/5	0.99	0.11	43,44,55,86	0
2	2HP	S	402	5/5	0.99	0.12	41,47,53,83	0
2	2HP	N	402	5/5	0.99	0.09	40,41,56,58	0

6.5 Other polymers [i](#)

There are no such residues in this entry.