

Full wwPDB X-ray Structure Validation Report (i)

Jan 30, 2021 - 02:48 PM EST

PDB ID	:	3EEY
Title	:	CRYSTAL STRUCTURE OF PUTATIVE RRNA-METHYLASE FROM
		Clostridium thermocellum
Authors	:	Patskovsky, Y.; Ramagopal, U.A.; Toro, R.; Rutter, M.; Hu, S.; Bain, K.;
		Sauder, J.M.; Burley, S.K.; Almo, S.C.; New York SGX Research Center for
		Structural Genomics (NYSGXRC)
Deposited on	:	2008-09-06
Resolution	:	2.20 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 following versions of software and data (see references (1)) 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	:	2.16
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)	:	2.16

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 2.20 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R _{free}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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	А	197	7%	1.0%	
		101	7%	1078	•••
1	В	197	90%	7%	••
1	С	197	89%	7%	·
1	р	197	6% 85%	110/	_
		1.51	10%	11%	•
1	Ε	197	82%	14%	•



Mol	Chain	Length	Quality of chain	
1	F	107	9%	
	Г	197	90%	6% • •
1	a	107	10%	
1	G	197	84%	6% • 9%
	**		13%	_
1	H	197	83%	11% • •
			17%	
1	Ι	197	85%	9% • 6%
			22%	
1	J	197	86%	9% • •



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 15399 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.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	Δ	105	Total	С	Ν	0	S	0	2	0
1	Л	195	1536	974	261	293	8	0	5	0
1	В	102	Total	С	Ν	Ο	\mathbf{S}	0	3	0
1	D	152	1504	954	251	291	8	0	5	0
1	C	180	Total	С	Ν	Ο	\mathbf{S}	0	5	0
1	U	105	1487	946	245	288	8	0	5	0
1	П	180	Total	С	Ν	Ο	\mathbf{S}	0	1	0
1	D	105	1462	928	240	286	8	0	T	0
1	E	180	Total	\mathbf{C}	Ν	Ο	\mathbf{S}	0	3	0
-		105	1475	937	243	286	9	0	3	0
1	F	190	Total	\mathbf{C}	Ν	Ο	\mathbf{S}	0	1	0
	L	150	1487	944	245	290	8		т	0
1	G	170	Total	\mathbf{C}	Ν	Ο	\mathbf{S}	0	1	0
	<u> </u>	115	1404	894	231	271	8	0		0
1	н	180	Total	\mathbf{C}	Ν	Ο	\mathbf{S}	0	4	0
	11	105	1482	942	244	288	8	0		0
1	1 I	186	Total	\mathbf{C}	Ν	Ο	\mathbf{S}	0	1	0
		100	1445	919	240	278	8		1	0
1	T	180	Total	\mathbf{C}	N	0	S		1	0
	5	109	1464	929	243	284	8	0		0

• Molecule 1 is a protein called Putative rRNA methylase.

There are 110 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	-1	MET	-	expression tag	UNP A3DDA2
А	0	SER	-	expression tag	UNP A3DDA2
А	1	LEU	-	expression tag	UNP A3DDA2
А	188	GLU	-	expression tag	UNP A3DDA2
А	189	GLY	-	expression tag	UNP A3DDA2
А	190	HIS	-	expression tag	UNP A3DDA2
А	191	HIS	-	expression tag	UNP A3DDA2
А	192	HIS	-	expression tag	UNP A3DDA2
A	193	HIS	-	expression tag	UNP A3DDA2



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Chain	Residue	Modelled	Actual	Comment	Reference
А	194	HIS	-	expression tag	UNP A3DDA2
А	195	HIS	-	expression tag	UNP A3DDA2
В	-1	MET	-	expression tag	UNP A3DDA2
В	0	SER	-	expression tag	UNP A3DDA2
В	1	LEU	-	expression tag	UNP A3DDA2
В	188	GLU	_	expression tag	UNP A3DDA2
В	188A	GLY	_	expression tag	UNP A3DDA2
В	188B	HIS	-	expression tag	UNP A3DDA2
В	188C	HIS	-	expression tag	UNP A3DDA2
В	188D	HIS	-	expression tag	UNP A3DDA2
В	192	HIS	-	expression tag	UNP A3DDA2
В	193	HIS	-	expression tag	UNP A3DDA2
В	194	HIS	-	expression tag	UNP A3DDA2
С	-1	MET	-	expression tag	UNP A3DDA2
С	0	SER	-	expression tag	UNP A3DDA2
С	1	LEU	-	expression tag	UNP A3DDA2
С	188	GLU	-	expression tag	UNP A3DDA2
С	189	GLY	-	expression tag	UNP A3DDA2
С	190	HIS	-	expression tag	UNP A3DDA2
С	191	HIS	-	expression tag	UNP A3DDA2
С	192	HIS	-	expression tag	UNP A3DDA2
С	193	HIS	-	expression tag	UNP A3DDA2
С	194	HIS	-	expression tag	UNP A3DDA2
С	195	HIS	-	expression tag	UNP A3DDA2
D	-1	MET	-	expression tag	UNP A3DDA2
D	0	SER	-	expression tag	UNP A3DDA2
D	1	LEU	_	expression tag	UNP A3DDA2
D	188	GLU	-	expression tag	UNP A3DDA2
D	189	GLY	-	expression tag	UNP A3DDA2
D	190	HIS	-	expression tag	UNP A3DDA2
D	191	HIS	-	expression tag	UNP A3DDA2
D	192	HIS	-	expression tag	UNP A3DDA2
D	193	HIS	-	expression tag	UNP A3DDA2
D	194	HIS	-	expression tag	UNP A3DDA2
D	195	HIS	-	expression tag	UNP A3DDA2
Е	-1	MET	-	expression tag	UNP A3DDA2
Е	0	SER	-	expression tag	UNP A3DDA2
Е	1	LEU	-	expression tag	UNP A3DDA2
Е	188	GLU	-	expression tag	UNP A3DDA2
Е	189	GLY	-	expression tag	UNP A3DDA2
Е	190	HIS	-	expression tag	UNP A3DDA2
Е	191	HIS	-	expression tag	UNP A3DDA2

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Chain	Residue	Modelled	Actual	Comment	Reference
Е	192	HIS	-	expression tag	UNP A3DDA2
Е	193	HIS	-	expression tag	UNP A3DDA2
Е	194	HIS	-	expression tag	UNP A3DDA2
Е	195	HIS	-	expression tag	UNP A3DDA2
F	-1	MET	-	expression tag	UNP A3DDA2
F	0	SER	-	expression tag	UNP A3DDA2
F	1	LEU	-	expression tag	UNP A3DDA2
F	188	GLU	-	expression tag	UNP A3DDA2
F	189	GLY	-	expression tag	UNP A3DDA2
F	190	HIS	-	expression tag	UNP A3DDA2
F	191	HIS	-	expression tag	UNP A3DDA2
F	192	HIS	-	expression tag	UNP A3DDA2
F	193	HIS	-	expression tag	UNP A3DDA2
F	194	HIS	-	expression tag	UNP A3DDA2
F	195	HIS	-	expression tag	UNP A3DDA2
G	-1	MET	-	expression tag	UNP A3DDA2
G	0	SER	-	expression tag	UNP A3DDA2
G	1	LEU	-	expression tag	UNP A3DDA2
G	188	GLU	-	expression tag	UNP A3DDA2
G	189	GLY	-	expression tag	UNP A3DDA2
G	190	HIS	-	expression tag	UNP A3DDA2
G	191	HIS	-	expression tag	UNP A3DDA2
G	192	HIS	-	expression tag	UNP A3DDA2
G	193	HIS	-	expression tag	UNP A3DDA2
G	194	HIS	-	expression tag	UNP A3DDA2
G	195	HIS	-	expression tag	UNP A3DDA2
Н	-1	MET	-	expression tag	UNP A3DDA2
Н	0	SER	-	expression tag	UNP A3DDA2
Н	1	LEU	-	expression tag	UNP A3DDA2
Н	188	GLU	-	expression tag	UNP A3DDA2
Н	189	GLY	-	expression tag	UNP A3DDA2
Н	190	HIS	-	expression tag	UNP A3DDA2
Н	191	HIS	-	expression tag	UNP A3DDA2
Н	192	HIS	-	expression tag	UNP A3DDA2
Н	193	HIS	-	expression tag	UNP A3DDA2
Н	194	HIS	-	expression tag	UNP A3DDA2
Н	195	HIS	-	expression tag	UNP A3DDA2
Ι	-1	MET	-	expression tag	UNP A3DDA2
Ι	0	SER	-	expression tag	UNP A3DDA2
Ι	1	LEU	-	expression tag	UNP A3DDA2
Ι	188	GLU	-	expression tag	UNP A3DDA2
Ι	189	GLY	-	expression tag	UNP A3DDA2

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Chain	Residue	Modelled	Actual	Comment	Reference		
Ι	190	HIS	-	expression tag	UNP A3DDA2		
Ι	191	HIS	-	expression tag	UNP A3DDA2		
Ι	192	HIS	-	expression tag	UNP A3DDA2		
Ι	193	HIS	-	expression tag	UNP A3DDA2		
Ι	194	HIS	-	expression tag	UNP A3DDA2		
Ι	195	HIS	-	expression tag	UNP A3DDA2		
J	-1	MET	-	expression tag	UNP A3DDA2		
J	0	SER	-	expression tag	UNP A3DDA2		
J	1	LEU	-	expression tag	UNP A3DDA2		
J	188	GLU	-	expression tag	UNP A3DDA2		
J	189	GLY	-	expression tag	UNP A3DDA2		
J	190	HIS	-	expression tag	UNP A3DDA2		
J	191	HIS	-	expression tag	UNP A3DDA2		
J	192	HIS	-	expression tag	UNP A3DDA2		
J	193	HIS	-	expression tag	UNP A3DDA2		
J	194	HIS	-	expression tag	UNP A3DDA2		
J	195	HIS	-	expression tag	UNP A3DDA2		

• Molecule 2 is S-ADENOSYLMETHIONINE (three-letter code: SAM) (formula: $C_{15}H_{22}N_6O_5S$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
2	2 1	A 1	Total	С	Ν	0	S	0	0
2	Л		27	15	6	5	1	0	
2	В	1	Total	С	Ν	Ο	\mathbf{S}	0	0
2	2 D	L	27	15	6	5	1	0	0
9	С	1	Total	С	Ν	0	S	0	0
	U		27	15	6	5	1	0	0



Mol	Chain	Residues		Ato	\mathbf{ms}			ZeroOcc	AltConf
2	Л	1	Total	С	Ν	0	S	0	0
	D	I	27	15	6	5	1	0	0
9	F	1	Total	С	Ν	0	S	0	0
	Ľ	L	27	15	6	5	1	0	0
2	F	1	Total	С	Ν	0	S	0	0
	T,	I	27	15	6	5	1	0	0
2	Ц	1	Total	С	Ν	0	S	0	0
	11	I	27	15	6	5	1	0	0
2	т	1	Total	С	Ν	0	\mathbf{S}	0	0
	1	I	27	15	6	5	1	0	0
2	т	1	Total	С	Ν	Ο	S	0	0
	1		27	15	6	5	1	0	0

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• Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	В	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	С	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0



• Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 6 & 3 & 3 \end{array}$	0	0
4	В	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 6 3 3 \end{array}$	0	0
4	F	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 6 3 3 \end{array}$	0	0
4	Н	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 6 & 3 & 3 \end{array}$	0	0

• Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	52	$\begin{array}{cc} \text{Total} & \text{O} \\ 52 & 52 \end{array}$	0	0
5	В	64	Total O 64 64	0	0
5	С	51	Total O 51 51	0	0
5	D	45	Total O 45 45	0	0
5	Е	31	TotalO3232	0	1
5	F	28	TotalO2828	0	0
5	G	15	Total O 15 15	0	0



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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	Н	35	$\begin{array}{cc} \text{Total} & \text{O} \\ 35 & 35 \end{array}$	0	0
5	Ι	16	Total O 16 16	0	0
5	J	23	Total O 23 23	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: Putative rRNA methylase



• Molecule 1: Putative rRNA methylase







• Molecule 1: Putative rRNA methylase





• Molecule 1: Putative rRNA methylase







4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	70.16Å 126.91Å 125.61Å	Depositor
a, b, c, α , β , γ	90.00° 99.54° 90.00°	Depositor
Bosolution (Å)	20.00 - 2.20	Depositor
	19.92 - 2.20	EDS
% Data completeness	99.1 (20.00-2.20)	Depositor
(in resolution range)	99.1 (19.92-2.20)	EDS
R_{merge}	0.08	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.43 (at 2.19 Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
B B.	0.244 , 0.278	Depositor
II, II, <i>free</i>	0.237 , 0.266	DCC
R_{free} test set	3257 reflections $(3.00%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	40.9	Xtriage
Anisotropy	0.592	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.31, 58.0	EDS
L-test for $twinning^2$	$ < L >=0.50, < L^2>=0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	15399	wwPDB-VP
Average B, all atoms $(Å^2)$	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.24% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities estimated from amplitudes.

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, SO4, SAM

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).

Mal	Chain	Bond	lengths	Bo	ond angles
	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	0.44	0/1573	0.59	2/2122~(0.1%)
1	В	0.55	0/1537	0.58	0/2074
1	С	0.61	0/1523	0.58	0/2053
1	D	0.47	0/1486	0.57	0/2006
1	Е	0.43	0/1505	0.58	0/2031
1	F	0.42	0/1520	0.55	0/2050
1	G	0.44	0/1433	0.58	1/1929~(0.1%)
1	Н	0.44	0/1515	0.60	0/2043
1	Ι	0.44	0/1469	0.57	0/1983
1	J	0.47	0/1488	0.58	0/2008
All	All	0.48	0/15049	0.58	3/20299~(0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	А	0	1
1	J	0	2
All	All	0	3

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	А	193[A]	HIS	CB-CA-C	5.33	121.06	110.40
1	А	193[B]	HIS	CB-CA-C	5.33	121.06	110.40
1	G	99	LEU	CA-CB-CG	5.10	127.03	115.30



There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	\mathbf{Res}	Type	Group
1	А	194	HIS	Peptide
1	J	140	GLY	Peptide
1	J	141	GLY	Peptide

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	А	1536	0	1543	12	0
1	В	1504	0	1514	6	0
1	С	1487	0	1524	6	0
1	D	1462	0	1481	5	0
1	Е	1475	0	1503	14	0
1	F	1487	0	1516	3	0
1	G	1404	0	1445	2	0
1	Н	1482	0	1513	9	0
1	Ι	1445	0	1474	14	0
1	J	1464	0	1488	9	0
2	А	27	0	22	1	0
2	В	27	0	22	0	0
2	С	27	0	22	0	0
2	D	27	0	22	0	0
2	E	27	0	22	0	0
2	F	27	0	22	1	0
2	Н	27	0	22	0	0
2	Ι	27	0	22	0	0
2	J	27	0	22	1	0
3	А	15	0	0	0	0
3	В	5	0	0	0	0
3	C	5	0	0	1	0
4	А	6	0	8	0	0
4	В	6	0	8	2	0
4	F	6	0	8	0	0
4	Н	6	0	8	0	0
5	A	52	0	0	0	0



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	В	64	0	0	0	0
5	С	51	0	0	0	0
5	D	45	0	0	0	0
5	Е	32	0	0	1	0
5	F	28	0	0	0	0
5	G	15	0	0	0	0
5	Н	35	0	0	0	0
5	Ι	16	0	0	0	0
5	J	23	0	0	0	0
All	All	15399	0	15231	70	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 2.

All (70) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom 1	Atom 2	Interatomic	Clash	
Atom-1	Atom-2	distance (Å)	overlap (Å)	
1:I:73:ARG:HH21	1:I:73:ARG:CG	1.65	1.08	
1:I:73:ARG:HG3	1:I:73:ARG:NH2	1.50	1.05	
1:I:73:ARG:H	1:I:73:ARG:HD2	1.29	0.96	
1:I:73:ARG:HD2	1:I:73:ARG:N	1.91	0.86	
1:B:174:ALA:HB2	1:H:174:ALA:HB2	1.59	0.84	
1:I:70:LEU:O	1:I:73:ARG:HD3	1.80	0.82	
1:I:73:ARG:CD	1:I:73:ARG:H	1.97	0.77	
1:A:193[B]:HIS:CE1	1:D:178:PRO:HD3	2.22	0.74	
1:B:167:ARG:HH22	4:B:302:GOL:H11	1.52	0.74	
1:I:174:ALA:HB2	1:J:174:ALA:HB2	1.77	0.66	
1:I:73:ARG:HH21	1:I:73:ARG:HG3	0.69	0.66	
1:C:174:ALA:HB2	1:D:174:ALA:HB2	1.80	0.62	
1:C:140:GLY:HA3	3:C:301:SO4:O2	2.03	0.58	
1:J:141:GLY:HA2	1:J:144:GLY:H	1.67	0.58	
1:E:160:GLN:HG2	5:E:321:HOH:O	2.03	0.58	
1:E:148:LYS:HD2	1:E:179:ILE:HD12	1.84	0.57	
1:I:43:GLY:O	1:I:73:ARG:NH2	2.41	0.54	
1:E:167:ARG:NH2	1:H:169:ASP:OD2	2.40	0.53	
1:A:175:ASN:HA	1:E:141:GLY:O	2.08	0.53	
1:J:98:ASN:HB3	2:J:300:SAM:HG1	1.91	0.52	
1:A:145:PHE:HZ	1:E:140:GLY:HA2	1.75	0.51	
1:H:25:VAL:HB	1:H:95:VAL:HG13	1.93	0.50	
1:A:195:HIS:N	1:A:195:HIS:CD2	2.80	0.49	
1:J:141:GLY:HA2	1:J:144:GLY:N	2.26	0.49	



Atom-1	Atom-2	Interatomic	Clash	
Atom-1	Atom-2	distance (Å)	overlap (Å)	
1:C:155:LEU:HD13	1:C:181:VAL:HG11	1.95	0.48	
1:B:112:ARG:HE	1:B:114:GLU:HG2	1.77	0.48	
1:B:192[B]:HIS:HE1	1:C:175:ASN:O	1.95	0.48	
1:I:155:LEU:HD13	1:I:181:VAL:HG11	1.95	0.48	
1:I:102:LEU:HD23	1:I:105:GLY:HA3	1.95	0.48	
1:I:25:VAL:HB	1:I:95:VAL:HG13	1.96	0.47	
1:I:73:ARG:NH2	1:I:73:ARG:CG	2.37	0.47	
1:A:25:VAL:HB	1:A:95:VAL:HG13	1.97	0.47	
1:H:148[B]:LYS:HE3	1:H:149[B]:GLU:OE2	2.14	0.46	
1:F:29:CYS:HB2	1:F:52:ASP:HB2	1.97	0.46	
1:A:98:ASN:HB3	2:A:300:SAM:HG1	1.99	0.45	
1:E:162:LYS:HE3	1:E:189:GLY:HA3	1.99	0.45	
1:J:148:LYS:HD2	1:J:179:ILE:HD12	1.98	0.45	
1:G:99:LEU:HD12	1:G:137:ILE:HG12	2.00	0.44	
1:C:153[B]:GLU:OE1	1:E:112[B]:ARG:NH1	2.50	0.44	
1:C:29:CYS:HB2	1:C:52:ASP:HB2	1.99	0.44	
1:H:113:PRO:HG3	1:H:147:GLU:HA	2.00	0.44	
1:H:155:LEU:HD13	1:H:181:VAL:HG11	1.99	0.44	
1:D:29:CYS:HB2	1:D:52:ASP:HB2	2.00	0.43	
1:A:145:PHE:CZ	1:E:140:GLY:HA2	2.53	0.43	
1:B:167:ARG:HH22	4:B:302:GOL:C1	2.28	0.43	
1:E:155:LEU:HD13	1:E:181:VAL:HG11	2.01	0.43	
1:E:29:CYS:HB2	1:E:52:ASP:HB2	1.99	0.43	
1:E:47:ARG:NH1	1:E:73:ARG:O	2.52	0.42	
1:G:99:LEU:O	1:G:138:TYR:HD2	2.03	0.42	
1:J:25:VAL:HB	1:J:95:VAL:HG13	2.02	0.42	
1:E:47:ARG:NH1	1:E:73:ARG:C	2.73	0.42	
1:J:167[B]:ARG:NH2	1:J:167[B]:ARG:HG2	2.34	0.42	
1:E:113:PRO:HG3	1:E:147:GLU:HA	2.02	0.41	
1:E:25:VAL:HB	1:E:95:VAL:HG13	2.02	0.41	
1:F:98:ASN:HB3	2:F:300:SAM:HG1	2.02	0.41	
1:H:29:CYS:HB2	1:H:52:ASP:HB2	2.02	0.41	
1:J:53:ILE:HD11	1:J:109:ILE:HD11	2.02	0.41	
1:A:173:GLN:HB2	1:A:177:PRO:HG3	2.02	0.41	
1:D:113:PRO:HG3	1:D:147:GLU:HA	2.02	0.41	
1:A:94:ALA:HA	1:A:132:ILE:O	2.21	0.41	
1:A:29:CYS:HB2	1:A:52:ASP:HB2	2.02	0.41	
1:H:139:TYR:N	1:H:139:TYR:CD1	2.89	0.41	
1:H:94:ALA:HA	1:H:132:ILE:O	2.21	0.40	
1:I:29:CYS:HB2	1:I:52:ASP:HB2	2.02	0.40	
1:B:94:ALA:HA	1:B:132:ILE:O	2.22	0.40	



Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)	
1:A:113:PRO:HG3	1:A:147:GLU:HA	2.01	0.40	
1:A:73:ARG:HA	1:A:73:ARG:HD2	1.46	0.40	
1:D:102:LEU:HA	1:D:103:PRO:HD3	1.98	0.40	
1:F:43:GLY:O	1:F:73:ARG:HD3	2.21	0.40	

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	entiles
1	А	196/197~(100%)	193 (98%)	1 (0%)	2(1%)	15	14
1	В	190/197~(96%)	189 (100%)	1 (0%)	0	100	100
1	С	192/197~(98%)	190 (99%)	2(1%)	0	100	100
1	D	188/197~(95%)	185 (98%)	3 (2%)	0	100	100
1	Е	190/197~(96%)	187 (98%)	3 (2%)	0	100	100
1	F	192/197~(98%)	190 (99%)	2(1%)	0	100	100
1	G	179/197~(91%)	177~(99%)	2(1%)	0	100	100
1	Н	191/197~(97%)	185 (97%)	5 (3%)	1 (0%)	29	31
1	Ι	185/197~(94%)	182 (98%)	3 (2%)	0	100	100
1	J	188/197~(95%)	181 (96%)	6 (3%)	1 (0%)	29	31
All	All	1891/1970~(96%)	1859 (98%)	28 (2%)	4 (0%)	47	55

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	193[A]	HIS
1	А	193[B]	HIS
1	J	142	ASP



Continued from previous page...

Mol	Chain	Res	Type
1	Н	105	GLY

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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 side chain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	А	172/171~(101%)	162 (94%)	10 (6%)	20 23
1	В	170/171~(99%)	161~(95%)	9~(5%)	22 27
1	С	168/171~(98%)	162~(96%)	6 (4%)	35 45
1	D	164/171~(96%)	151 (92%)	13 (8%)	12 12
1	Ε	166/171~(97%)	158~(95%)	8 (5%)	25 32
1	F	168/171~(98%)	159~(95%)	9~(5%)	22 26
1	G	158/171~(92%)	148 (94%)	10 (6%)	18 20
1	Н	167/171~(98%)	154 (92%)	13 (8%)	12 13
1	Ι	162/171~(95%)	155~(96%)	7 (4%)	29 36
1	J	164/171~(96%)	155 (94%)	9~(6%)	21 26
All	All	1659/1710~(97%)	1565 (94%)	94 (6%)	21 24

All (94) residues with a non-rotameric sidechain are listed below:

Mol	Chain	\mathbf{Res}	Type
1	А	35	THR
1	А	42	VAL
1	А	64	LYS
1	А	72	ASP
1	А	73	ARG
1	А	81	HIS
1	А	129	THR
1	А	132	ILE
1	А	190	HIS
1	А	195	HIS
1	В	15	LYS
1	В	35	THR



Mol	Chain	Res	Type
1	В	42	VAL
1	B	44	GLU
1	B	64	LYS
1	B	73	ARG
1	B	81	HIS
1	В	112	ARG
1	В	193	HIS
1	С	19	LYS
1	С	42	VAL
1	С	81	HIS
1	С	101	TYR
1	С	129	THR
1	С	132	ILE
1	D	15	LYS
1	D	19	LYS
1	D	35	THR
1	D	42	VAL
1	D	44	GLU
1	D	72	ASP
1	D	73	ARG
1	D	81	HIS
1	D	121	SER
1	D	129	THR
1	D	132	ILE
1	D	143	THR
1	D	187	SER
1	Е	19	LYS
1	Е	35	THR
1	Е	42	VAL
1	Е	81	HIS
1	Е	129	THR
1	Е	132	ILE
1	Е	143	THR
1	Е	187	SER
1	F	35	THR
1	F	42	VAL
1	F	73	ARG
1	F	81	HIS
1	F	112	ARG
1	F	129	THR
1	F	132	ILE
1	F	167[A]	ARG



Mol	Chain	Res	Type
1	F	167[B]	ARG
1	G	15	LYS
1	G	35	THR
1	G	42	VAL
1	G	67	ASP
1	G	73	ARG
1	G	81	HIS
1	G	93	LYS
1	G	112	ARG
1	G	129	THR
1	G	132	ILE
1	Н	19	LYS
1	Н	35	THR
1	Н	42	VAL
1	Н	64	LYS
1	Н	73	ARG
1	Н	81	HIS
1	Н	112	ARG
1	Н	129	THR
1	Н	132	ILE
1	Н	139	TYR
1	Н	149[A]	GLU
1	Н	149[B]	GLU
1	Н	161	LYS
1	Ι	35	THR
1	Ι	42	VAL
1	I	72	ASP
1	Ι	73	ARG
1	I	81	HIS
1	Ι	129	THR
1	Ι	132	ILE
1	J	35	THR
1	J	42	VAL
1	J	81	HIS
1	J	109	ILE
1	J	129	THR
1	J	132	ILE
1	J	139	TYR
1	J	142	ASP
1	J	143	THR

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



Mol	Chain	Res	Type
1	А	191	HIS

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)

18 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).

Mal	Turne	Chain	Dec	Tink	Bo	ond leng	ths	B	ond ang	les
WIOI	туре	Ullalli	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SO4	А	301	-	4,4,4	0.78	0	6,6,6	0.73	0
2	SAM	Ι	300	-	21,29,29	1.14	2 (9%)	18,42,42	1.70	1 (5%)
3	SO4	В	301	-	4,4,4	0.58	0	6,6,6	0.66	0
3	SO4	А	302	-	4,4,4	0.14	0	6,6,6	0.05	0
4	GOL	А	304	-	$5,\!5,\!5$	0.35	0	$5,\!5,\!5$	0.37	0
4	GOL	В	302	-	$5,\!5,\!5$	0.55	0	$5,\!5,\!5$	0.87	0
3	SO4	С	301	-	4,4,4	0.15	0	6,6,6	0.09	0
4	GOL	Н	301	-	$5,\!5,\!5$	0.36	0	$5,\!5,\!5$	0.32	0
2	SAM	Е	300	-	21,29,29	1.20	2 (9%)	18,42,42	1.67	1 (5%)
2	SAM	В	300	-	21,29,29	1.10	2 (9%)	18,42,42	1.85	3 (16%)
2	SAM	D	300	-	21,29,29	1.15	2 (9%)	18,42,42	1.74	2 (11%)
2	SAM	С	300	-	21,29,29	1.20	2 (9%)	18,42,42	1.69	1 (5%)



Mal	l Type Chain Bes Lin		Tink	Bo	ond leng	$_{\rm ths}$	Bond angles			
MIOI	туре	Unam	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	SAM	Н	300	-	21,29,29	1.21	2 (9%)	18,42,42	1.65	1 (5%)
2	SAM	J	300	-	21,29,29	1.14	2 (9%)	18,42,42	1.69	1 (5%)
4	GOL	F	301	-	5,5,5	0.42	0	$5,\!5,\!5$	0.33	0
2	SAM	А	300	-	21,29,29	1.12	2(9%)	18,42,42	1.76	1 (5%)
3	SO4	А	303	-	4,4,4	0.17	0	6,6,6	0.08	0
2	SAM	F	300	-	21,29,29	1.19	2 (9%)	18,42,42	1.77	2 (11%)

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
4	GOL	F	301	-	-	2/4/4/4	-
2	SAM	Ι	300	-	-	0/8/33/33	0/3/3/3
4	GOL	А	304	-	-	2/4/4/4	-
4	GOL	В	302	-	-	4/4/4/4	-
2	SAM	С	300	-	-	2/8/33/33	0/3/3/3
4	GOL	Н	301	-	-	0/4/4/4	-
2	SAM	Е	300	-	-	4/8/33/33	0/3/3/3
2	SAM	В	300	-	-	0/8/33/33	0/3/3/3
2	SAM	D	300	-	-	1/8/33/33	0/3/3/3
2	SAM	F	300	-	-	<mark>3/8/33/33</mark>	0/3/3/3
2	SAM	Н	300	-	-	2/8/33/33	0/3/3/3
2	SAM	J	300	-	-	2/8/33/33	0/3/3/3
2	SAM	А	300	-	-	2/8/33/33	0/3/3/3

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	$\operatorname{Ideal}(\operatorname{\AA})$
2	Е	300	SAM	C2-N3	4.06	1.38	1.32
2	Н	300	SAM	C2-N3	4.04	1.38	1.32
2	С	300	SAM	C2-N3	3.89	1.38	1.32
2	F	300	SAM	C2-N3	3.87	1.38	1.32
2	Ι	300	SAM	C2-N3	3.84	1.38	1.32
2	J	300	SAM	C2-N3	3.82	1.38	1.32
2	D	300	SAM	C2-N3	3.68	1.38	1.32
2	В	300	SAM	C2-N3	3.47	1.37	1.32
2	А	300	SAM	C2-N3	3.42	1.37	1.32



Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	$\mathrm{Ideal}(\mathrm{\AA})$
2	С	300	SAM	C2-N1	2.70	1.38	1.33
2	Н	300	SAM	C2-N1	2.60	1.38	1.33
2	F	300	SAM	C2-N1	2.55	1.38	1.33
2	Ε	300	SAM	C2-N1	2.55	1.38	1.33
2	Ι	300	SAM	C2-N1	2.44	1.38	1.33
2	D	300	SAM	C2-N1	2.37	1.38	1.33
2	А	300	SAM	C2-N1	2.33	1.38	1.33
2	J	300	SAM	C2-N1	2.32	1.38	1.33
2	В	300	SAM	C2-N1	2.32	1.38	1.33

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	В	300	SAM	N3-C2-N1	-6.38	118.71	128.68
2	D	300	SAM	N3-C2-N1	-6.32	118.79	128.68
2	F	300	SAM	N3-C2-N1	-6.24	118.93	128.68
2	А	300	SAM	N3-C2-N1	-6.22	118.95	128.68
2	J	300	SAM	N3-C2-N1	-6.13	119.09	128.68
2	Ι	300	SAM	N3-C2-N1	-6.12	119.11	128.68
2	Ε	300	SAM	N3-C2-N1	-6.07	119.20	128.68
2	С	300	SAM	N3-C2-N1	-6.05	119.22	128.68
2	Н	300	SAM	N3-C2-N1	-5.94	119.39	128.68
2	В	300	SAM	C1'-N9-C4	-2.27	122.65	126.64
2	В	300	SAM	C2-N1-C6	2.19	122.50	118.75
2	F	300	SAM	C3'-C2'-C1'	2.05	104.06	100.98
2	D	300	SAM	C1'-N9-C4	-2.00	123.12	126.64

There are no chirality outliers.

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	В	302	GOL	O1-C1-C2-C3
4	В	302	GOL	C1-C2-C3-O3
2	С	300	SAM	C-CA-CB-CG
2	С	300	SAM	CA-CB-CG-SD
2	Е	300	SAM	C-CA-CB-CG
2	D	300	SAM	CA-CB-CG-SD
2	F	300	SAM	CA-CB-CG-SD
2	F	300	SAM	O4'-C4'-C5'-SD
2	F	300	SAM	C3'-C4'-C5'-SD
2	J	300	SAM	CA-CB-CG-SD
4	F	301	GOL	O1-C1-C2-O2



Mol	Chain	Res	Type	Atoms
4	F	301	GOL	O1-C1-C2-C3
2	А	300	SAM	CA-CB-CG-SD
4	В	302	GOL	O1-C1-C2-O2
4	В	302	GOL	O2-C2-C3-O3
2	Н	300	SAM	C-CA-CB-CG
2	Ε	300	SAM	O4'-C4'-C5'-SD
2	Н	300	SAM	O4'-C4'-C5'-SD
2	Е	300	SAM	CA-CB-CG-SD
2	Ε	300	SAM	C3'-C4'-C5'-SD
4	А	304	GOL	O1-C1-C2-C3
4	А	304	GOL	O1-C1-C2-O2
2	J	300	SAM	C-CA-CB-CG
2	А	300	SAM	C-CA-CB-CG

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There are no ring outliers.

5 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	В	302	GOL	2	0
3	С	301	SO4	1	0
2	J	300	SAM	1	0
2	А	300	SAM	1	0
2	F	300	SAM	1	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 then 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 (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, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	$\langle RSRZ \rangle$	#RSRZ>2	2	$\mathbf{OWAB}(\mathbf{\AA}^2)$	Q < 0.9
1	А	195/197~(98%)	0.31	14 (7%) 15	14	26, 48, 85, 109	0
1	В	192/197~(97%)	0.31	14 (7%) 15	14	26, 45, 86, 107	0
1	С	189/197~(95%)	0.30	13 (6%) 16	15	26, 47, 92, 121	0
1	D	189/197~(95%)	0.28	12 (6%) 20	19	26, 47, 89, 110	0
1	Ε	189/197~(95%)	0.45	19 (10%) 7	6	28,50,95,143	0
1	\mathbf{F}	190/197~(96%)	0.52	18 (9%) 8	7	28, 52, 87, 117	0
1	G	179/197~(90%)	0.55	19 (10%) 6	5	29, 48, 83, 95	0
1	Η	189/197~(95%)	0.66	25~(13%) 3	3	30, 51, 108, 159	0
1	Ι	186/197~(94%)	0.91	34~(18%) 1	1	27, 53, 96, 146	0
1	J	189/197~(95%)	1.17	44 (23%) 0	0	33, 53, 108, 160	0
All	All	1887/1970~(95%)	0.54	212 (11%) 5	4	26, 50, 93, 160	0

All (212) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	J	105	GLY	10.2
1	Ι	102	LEU	8.5
1	Н	105	GLY	7.9
1	J	102	LEU	7.6
1	Ι	105	GLY	7.5
1	G	53	ILE	7.3
1	Ι	101	TYR	6.6
1	Н	102	LEU	6.5
1	Н	103	PRO	6.3
1	Ι	108	SER	5.9
1	J	188	GLU	5.8
1	J	104	SER	5.8
1	Н	104	SER	5.8



Mol	Chain	Res	Type	RSRZ
1	Н	107	HIS	5.7
1	Н	189	GLY	5.7
1	Ε	103	PRO	5.6
1	Н	188	GLU	5.4
1	Е	107	HIS	5.3
1	F	189	GLY	5.3
1	J	103	PRO	5.2
1	В	107	HIS	5.2
1	Ι	103	PRO	5.2
1	Ι	44	GLU	5.1
1	А	193[A]	HIS	5.1
1	J	107	HIS	5.1
1	Н	101	TYR	5.1
1	Ι	104	SER	5.0
1	Е	102	LEU	5.0
1	G	175	ASN	4.9
1	D	107	HIS	4.9
1	J	189	GLY	4.8
1	Ι	106	ASP	4.8
1	Ι	43	GLY	4.7
1	С	189	GLY	4.6
1	Е	104	SER	4.6
1	J	187	SER	4.6
1	Ι	59	ALA	4.6
1	J	90	CYS	4.5
1	С	107	HIS	4.4
1	F	45	ASN	4.4
1	С	103	PRO	4.4
1	В	0	SER	4.4
1	F	0	SER	4.4
1	Н	106	ASP	4.4
1	Е	141	GLY	4.2
1	Ι	89	ASP	4.2
1	G	2	THR	4.1
1	J	101	TYR	4.0
1	G	31	ASN	4.0
1	Ι	100	GLY	4.0
1	J	18	VAL	3.9
1	С	187	SER	3.9
1	J	55	ASP	3.9
1	Е	109	ILE	3.8
1	F	104	SER	3.8



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Mol	Chain	Res	Type	RSRZ				
1	J	67	ASP	3.8				
1	Ι	109	ILE	3.8				
1	F	63	LYS	3.8				
1	D	29	CYS	3.8				
1	F	66	THR	3.7				
1	Ι	46	GLY	3.7				
1	Н	45	ASN	3.6				
1	А	191	HIS	3.6				
1	J	108	SER	3.6				
1	А	194	HIS	3.6				
1	G	57	ALA	3.5				
1	G	138	TYR	3.5				
1	F	175	ASN	3.5				
1	С	188	GLU	3.5				
1	Н	187	SER	3.5				
1	J	66	THR	3.5				
1	Ι	45	ASN	3.4				
1	F	46	GLY	3.4				
1	J	106	ASP	3.4				
1	J	21	GLY	3.3				
1	J	46	GLY	3.3				
1	G	56	LYS	3.3				
1	А	190	HIS	3.3				
1	С	63	LYS	3.3				
1	Ε	1	LEU	3.2				
1	Ε	189	GLY	3.2				
1	F	103	PRO	3.2				
1	J	128	VAL	3.2				
1	Н	89	ASP	3.2				
1	J	40	SER	3.2				
1	Ι	21	GLY	3.2				
1	F	55	ASP	3.2				
1	Ι	66	THR	3.1				
1	G	189	GLY	3.1				
1	J	59	ALA	3.1				
1	Н	62	THR	3.1				
1	В	193	HIS	3.1				
1	J	22	ASP	3.1				
1	D	45	ASN	3.1				
1	G	54	GLN	3.1				
1	Н	46	GLY	3.1				
1	А	29	CYS	3.0				

 29
 CYS
 3.0

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Mol	Chain	Res	Type	RSRZ	
1	Е	145	PHE	3.0	
1	Н	55	ASP	3.0	
1	Ι	56	LYS	3.0	
1	D	109	ILE	3.0	
1	D	104	SER	3.0	
1	Ι	57	ALA	3.0	
1	Ι	42	VAL	3.0	
1	Ι	90	CYS	3.0	
1	С	105	105 GLY		
1	Н	91	PRO	3.0	
1	В	106	ASP	2.9	
1	В	192[A]	HIS	2.9	
1	В	104	SER	2.9	
1	В	29	CYS	2.9	
1	J	109	ILE	2.9	
1	J	91	PRO	2.9	
1	J	89	ASP	2.9	
1	Ε	110	SER	2.9	
1	Н	63	LYS	2.9	
1	Е	101	TYR	2.9	
1	Ι	161	LYS	2.8	
1	F	139	TYR	2.8	
1	С	56	LYS	2.8	
1	Н	20	GLU	2.8	
1	Ι	91	PRO	2.8	
1	Е	108	SER	2.8	
1	J	30	GLY	2.8	
1	Ι	76	LEU	2.8	
1	A	189	GLY	2.8	
1	D	108	SER	2.8	
1	Ι	55	ASP	2.8	
1	I	162	LYS	2.8	
1	G	174	ALA	2.7	
1	G	183	ILE	2.7	
1	J	86	LYS	2.7	
1	Ι	63	LYS	2.7	
1	J	73	ARG	2.7	
1	G	89	ASP	2.7	
1	F	44	GLU	2.7	
1	D	28	THR	2.7	
1	J	54	GLN	2.7	
1	Н	90	CYS	2.6	



Mol	Chain	Res	Type	RSRZ	
1	А	95	VAL	2.6	
1	G	25	VAL	2.6	
1	Ι	110	SER	2.6	
1	Н	109	ILE	2.6	
1	J	162	LYS	2.6	
1	С	1	LEU	2.6	
1	А	103	PRO	2.6	
1	J	45	ASN	2.6	
1	D	56	LYS	2.6	
1	А	68	LEU	2.5	
1	J	49	PHE	2.5	
1	Ι	73	ARG	2.5	
1	F	43	GLY	2.5	
1	Е	105	GLY	2.5	
1	Е	27	ALA	2.4	
1	А	141	GLY	2.4	
1	Н	68	LEU	2.4	
1	J	48	VAL	2.4	
1	F	105	GLY	2.4	
1	В	28	THR	2.4	
1	F	188	GLU	2.4	
1	F	68	LEU	2.4	
1	D	106	ASP	2.4	
1	Е	56	LYS	2.4	
1	J	63	LYS	2.3	
1	G	142	ASP	2.3	
1	В	95	VAL	2.3	
1	С	104	SER	2.3	
1	C	106	ASP	2.3	
1	D	101	TYR	2.3	
1	J	126	LEU	2.3	
1	D	105	GLY	2.3	
1	А	70	LEU	2.3	
1	F	83	ASN	2.3	
1	F	89	ASP	2.3	
1	В	109	ILE	2.3	
1	Ι	58	ILE	2.3	
1	Ι	64	LYS	2.3	
1	В	27	ALA	2.3	
1	В	102	LEU	2.3	
1	E	45	ASN	2.3	
1	G	60	ASN	2.3	



Mol	Chain	Res	Type	RSRZ	
1	G	24	VAL	2.2	
1	Е	46	GLY	2.2	
1	J	74	VAL	2.2	
1	C 53		ILE	2.2	
1	Ι	1	LEU	2.2	
1	Е	174	ALA	2.2	
1	G	45	ASN	2.2	
1	G	176	CYS	2.2	
1	J	71	ILE	2.2	
1	С	101	TYR	2.2	
1	J	50	GLY	2.2	
1	D	51	PHE	2.2	
1	Ι	70	LEU	2.2	
1	Н	28	THR	2.1	
1	Н	40	SER	2.1	
1	J	7	LEU	2.1	
1	В	108	SER	2.1	
1	J	38	LEU	2.1	
1	Н	66	THR	2.1	
1	Ι	18	VAL	2.1	
1	А	104	SER	2.1	
1	J	141	GLY	2.1	
1	E	89	ASP	2.0	
1	G	52	ASP	2.0	
1	J	51	PHE	2.0	
1	A	1	LEU	2.0	
1	А	175	ASN	2.0	
1	В	24	VAL	2.0	
1	Н	162	LYS	2.0	
1	J	29	CYS	2.0	
1	J	43	GLY	2.0	

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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, 95^{th} 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	$\operatorname{B-factors}(\operatorname{\AA}^2)$	Q < 0.9
4	GOL	F	301	6/6	0.76	0.14	89,95,97,100	0
2	SAM	J	300	27/27	0.77	0.27	$63,\!81,\!117,\!118$	0
4	GOL	В	302	6/6	0.82	0.12	69,73,79,81	0
2	SAM	Е	300	27/27	0.86	0.21	$76,\!88,\!107,\!107$	0
2	SAM	Ι	300	27/27	0.87	0.21	58,81,87,97	0
2	SAM	Н	300	27/27	0.87	0.17	58,79,93,97	0
2	SAM	С	300	27/27	0.89	0.17	$53,\!68,\!81,\!87$	0
2	SAM	F	300	27/27	0.90	0.18	$25,\!67,\!93,\!97$	0
3	SO4	В	301	5/5	0.90	0.26	68,79,85,88	0
3	SO4	А	303	5/5	0.90	0.14	87,89,92,96	0
2	SAM	D	300	27/27	0.91	0.16	43,61,71,73	0
4	GOL	Н	301	6/6	0.91	0.09	69,82,88,90	0
3	SO4	А	302	5/5	0.93	0.18	69,70,71,71	5
2	SAM	В	300	27/27	0.93	0.14	31,48,68,76	0
4	GOL	А	304	6/6	0.95	0.09	56,71,75,75	0
3	SO4	С	301	5/5	0.95	0.17	76, 76, 80, 85	0
2	SAM	A	300	27/27	0.96	0.10	30,46,62,68	0
3	SO4	A	301	5/5	0.96	0.11	79,82,87,89	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.





















6.5 Other polymers (i)

There are no such residues in this entry.

