wwPDB X-ray Structure Validation Summary Report (i)

Jun 18, 2024 – 08:54 AM EDT

PDB ID	:	4INH
Title	:	Structural Basis of Substrate Specificity and Protease Inhibition in Norwalk Virus
Authors	:	Prasad, B.V.V.; Muhaxhiri, Z.; Deng, L.; Shanker, S.; Sankaran, B.; Estes, M.K.; Palzkill, T.; Song, Y.
Deposited on	:	2013-01-04
Resolution	:	1.70 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 (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

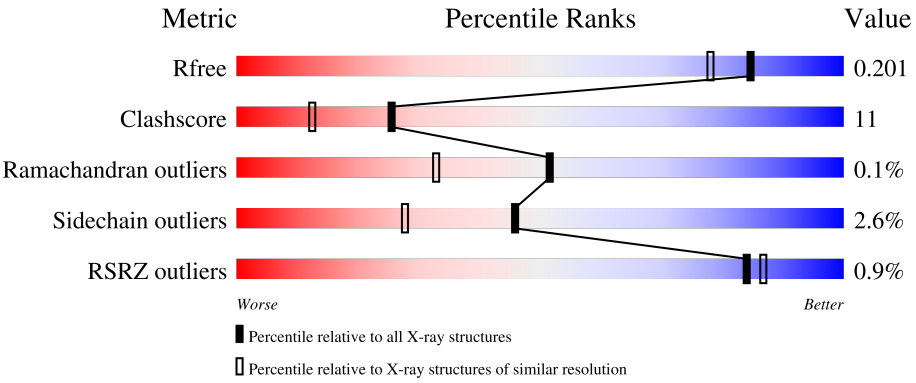
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



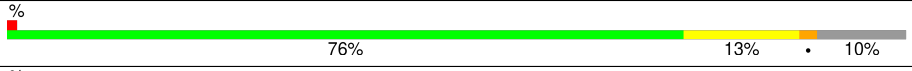
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	185	2% 77% 15% • 7%
1	B	185	% 77% 14% • 8%
1	C	185	% 75% 14% • 10%
1	D	185	% 79% 10% • 10%
1	E	185	80% 10% • 10%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	185	
1	G	185	
1	H	185	
2	J	4	
2	M	4	
2	N	4	
2	O	4	
2	P	4	
2	Q	4	
2	S	4	
2	T	4	

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
3	DMS	A	201	-	X	-	-

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 11854 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 Genome polyprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	172	Total	C	N	O	S	0	0	0
			1278	810	225	233	10			
1	B	170	Total	C	N	O	S	0	0	0
			1268	804	223	231	10			
1	C	166	Total	C	N	O	S	0	0	0
			1241	792	219	220	10			
1	D	167	Total	C	N	O	S	0	0	0
			1248	794	220	224	10			
1	E	167	Total	C	N	O	S	0	0	0
			1242	792	219	221	10			
1	F	167	Total	C	N	O	S	0	0	0
			1249	795	220	224	10			
1	G	167	Total	C	N	O	S	0	0	0
			1245	793	219	223	10			
1	H	168	Total	C	N	O	S	0	0	0
			1254	799	220	224	11			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	ASP	-	EXPRESSION TAG	UNP Q83883
A	-2	ASP	-	EXPRESSION TAG	UNP Q83883
A	-1	ASP	-	EXPRESSION TAG	UNP Q83883
A	0	LYS	-	EXPRESSION TAG	UNP Q83883
B	-3	ASP	-	EXPRESSION TAG	UNP Q83883
B	-2	ASP	-	EXPRESSION TAG	UNP Q83883
B	-1	ASP	-	EXPRESSION TAG	UNP Q83883
B	0	LYS	-	EXPRESSION TAG	UNP Q83883
C	-3	ASP	-	EXPRESSION TAG	UNP Q83883
C	-2	ASP	-	EXPRESSION TAG	UNP Q83883
C	-1	ASP	-	EXPRESSION TAG	UNP Q83883
C	0	LYS	-	EXPRESSION TAG	UNP Q83883
D	-3	ASP	-	EXPRESSION TAG	UNP Q83883

Continued on next page...

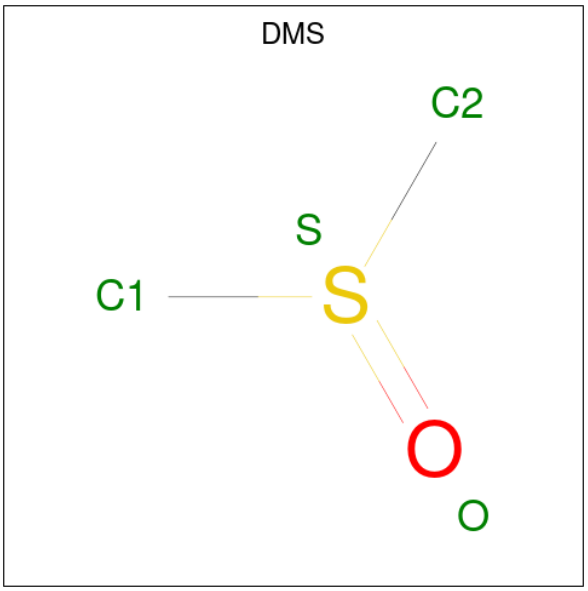
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	-2	ASP	-	EXPRESSION TAG	UNP Q83883
D	-1	ASP	-	EXPRESSION TAG	UNP Q83883
D	0	LYS	-	EXPRESSION TAG	UNP Q83883
E	-3	ASP	-	EXPRESSION TAG	UNP Q83883
E	-2	ASP	-	EXPRESSION TAG	UNP Q83883
E	-1	ASP	-	EXPRESSION TAG	UNP Q83883
E	0	LYS	-	EXPRESSION TAG	UNP Q83883
F	-3	ASP	-	EXPRESSION TAG	UNP Q83883
F	-2	ASP	-	EXPRESSION TAG	UNP Q83883
F	-1	ASP	-	EXPRESSION TAG	UNP Q83883
F	0	LYS	-	EXPRESSION TAG	UNP Q83883
G	-3	ASP	-	EXPRESSION TAG	UNP Q83883
G	-2	ASP	-	EXPRESSION TAG	UNP Q83883
G	-1	ASP	-	EXPRESSION TAG	UNP Q83883
G	0	LYS	-	EXPRESSION TAG	UNP Q83883
H	-3	ASP	-	EXPRESSION TAG	UNP Q83883
H	-2	ASP	-	EXPRESSION TAG	UNP Q83883
H	-1	ASP	-	EXPRESSION TAG	UNP Q83883
H	0	LYS	-	EXPRESSION TAG	UNP Q83883

- Molecule 2 is a protein called peptide inhibitor, syc59.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	J	4	Total	C	N	O	0	0	0
			34	24	4	6			
2	M	4	Total	C	N	O	0	0	0
			34	24	4	6			
2	S	4	Total	C	N	O	0	0	0
			34	24	4	6			
2	T	4	Total	C	N	O	0	0	0
			34	24	4	6			
2	N	4	Total	C	N	O	0	0	0
			34	24	4	6			
2	O	4	Total	C	N	O	0	0	0
			34	24	4	6			
2	P	4	Total	C	N	O	0	0	0
			34	24	4	6			
2	Q	4	Total	C	N	O	0	0	0
			34	24	4	6			

- Molecule 3 is DIMETHYL SULFOXIDE (three-letter code: DMS) (formula: C_2H_6OS).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O S 4 2 1 1	0	0
3	B	1	Total C O S 4 2 1 1	0	0
3	D	1	Total C O S 4 2 1 1	0	0
3	H	1	Total C O S 4 2 1 1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	187	Total O 187 187	0	0
4	B	191	Total O 191 191	0	0
4	C	188	Total O 188 188	0	0
4	D	207	Total O 207 207	0	0
4	E	183	Total O 183 183	0	0
4	F	203	Total O 203 203	0	0
4	G	177	Total O 177 177	0	0
4	H	178	Total O 178 178	0	0

Continued on next page...

Continued from previous page...

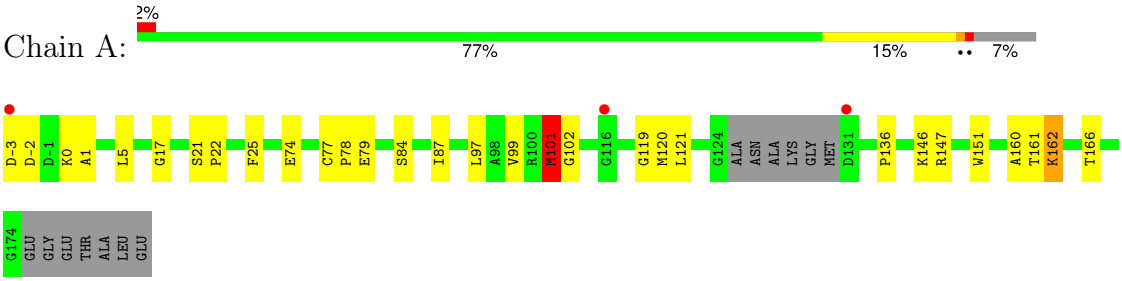
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	J	3	Total O 3 3	0	0
4	M	1	Total O 1 1	0	0
4	S	5	Total O 5 5	0	0
4	T	2	Total O 2 2	0	0
4	N	4	Total O 4 4	0	0
4	O	2	Total O 2 2	0	0
4	P	5	Total O 5 5	0	0
4	Q	5	Total O 5 5	0	0

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.

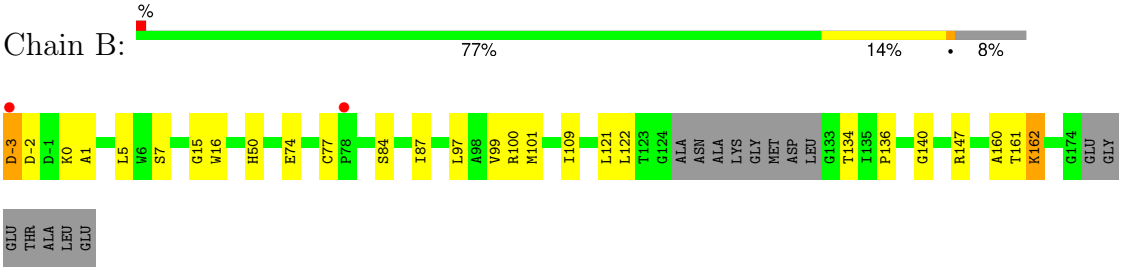
• Molecule 1: Genome polyprotein

Chain A:



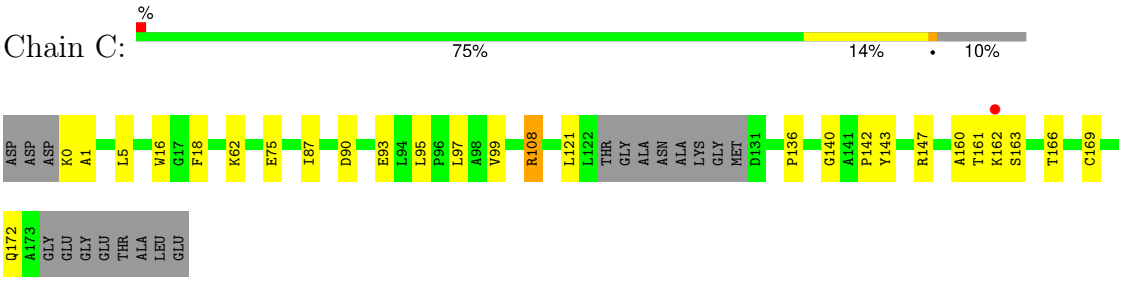
• Molecule 1: Genome polyprotein

Chain B:



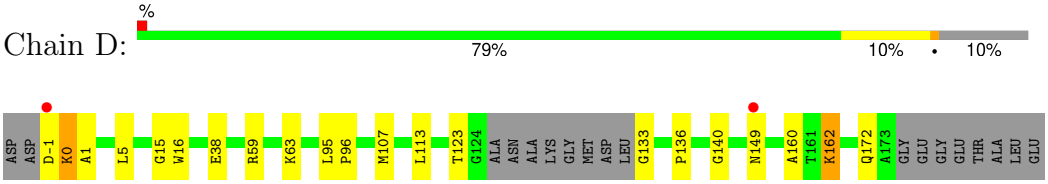
• Molecule 1: Genome polyprotein

Chain C:



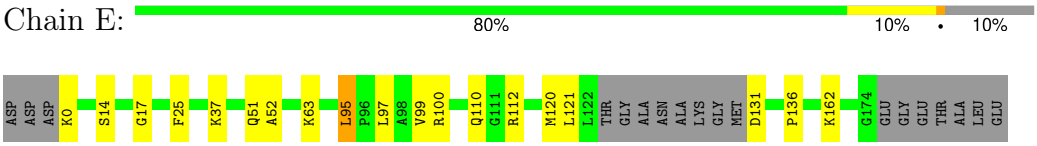
• Molecule 1: Genome polyprotein

Chain D:



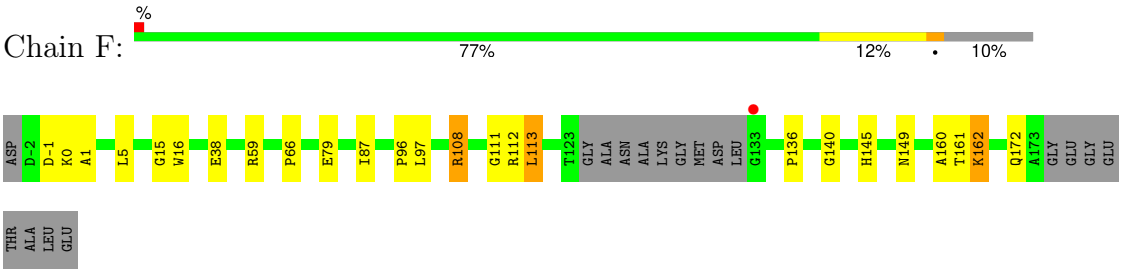
• Molecule 1: Genome polyprotein

Chain E:



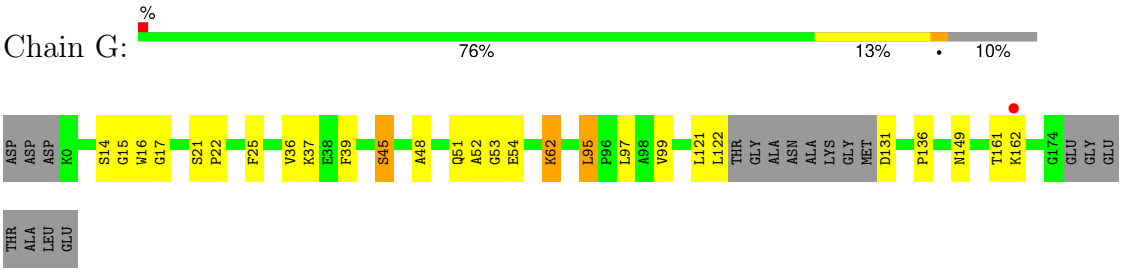
• Molecule 1: Genome polyprotein

Chain F:



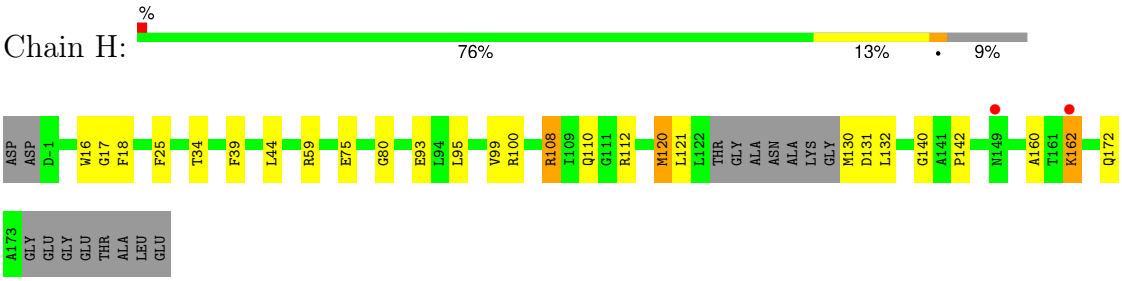
• Molecule 1: Genome polyprotein

Chain G:



• Molecule 1: Genome polyprotein

Chain H:

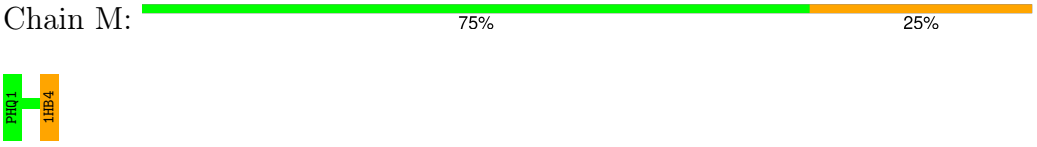


• Molecule 2: peptide inhibitor, syc59

Chain J:

• Molecule 2: peptide inhibitor, syc59

Chain M:



• Molecule 2: peptide inhibitor, syc59

Chain S:

• Molecule 2: peptide inhibitor, syc59

Chain T:

• Molecule 2: peptide inhibitor, syc59

Chain N:

• Molecule 2: peptide inhibitor, syc59

Chain O:

• Molecule 2: peptide inhibitor, syc59

Chain P:

• Molecule 2: peptide inhibitor, syc59

Chain Q:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	56.34Å 66.92Å 100.46Å 89.99° 90.09° 75.93°	Depositor
Resolution (Å)	32.45 – 1.70 32.45 – 1.64	Depositor EDS
% Data completeness (in resolution range)	96.1 (32.45-1.70) 96.1 (32.45-1.64)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.36 (at 1.64Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7_650)	Depositor
R, R_{free}	0.176 , 0.208 0.171 , 0.201	Depositor DCC
R_{free} test set	8369 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	19.0	Xtriage
Anisotropy	0.158	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 32.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	0.447 for -h,-k,l	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	11854	wwPDB-VP
Average B, all atoms (Å^2)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 60.79 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.4429e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 1HB, PHQ, DMS

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	0.49	0/1308	0.77	1/1774 (0.1%)
1	B	0.52	0/1298	0.76	0/1760
1	C	0.49	0/1271	0.68	0/1723
1	D	0.47	0/1278	0.68	0/1733
1	E	0.51	0/1272	0.69	0/1726
1	F	0.51	0/1279	0.71	0/1735
1	G	0.47	0/1275	0.69	0/1730
1	H	0.48	0/1284	0.70	0/1742
2	J	0.78	0/12	2.28	1/15 (6.7%)
2	M	0.96	0/12	2.18	0/15
2	N	1.10	0/12	2.28	1/15 (6.7%)
2	O	1.06	0/12	1.80	1/15 (6.7%)
2	P	0.55	0/12	1.50	0/15
2	Q	1.60	1/12 (8.3%)	1.61	0/15
2	S	0.73	0/12	1.90	0/15
2	T	0.85	0/12	1.97	0/15
All	All	0.50	1/10361 (0.0%)	0.73	4/14043 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	Q	2	ALA	C-N	-5.33	1.21	1.34

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	101	MET	CG-SD-CE	7.32	111.92	100.20
2	N	2	ALA	O-C-N	-5.54	113.84	122.70
2	J	2	ALA	O-C-N	-5.31	114.20	122.70
2	O	2	ALA	N-CA-CB	-5.11	102.94	110.10

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1278	0	1269	45	0
1	B	1268	0	1265	30	0
1	C	1241	0	1252	23	0
1	D	1248	0	1254	33	0
1	E	1242	0	1245	23	0
1	F	1249	0	1253	34	1
1	G	1245	0	1247	20	2
1	H	1254	0	1255	27	0
2	J	34	0	34	3	0
2	M	34	0	34	3	0
2	N	34	0	34	1	0
2	O	34	0	34	2	0
2	P	34	0	34	2	0
2	Q	34	0	34	1	0
2	S	34	0	34	3	0
2	T	34	0	34	2	0
3	A	4	0	6	0	0
3	B	4	0	6	1	0
3	D	4	0	6	0	0
3	H	4	0	6	0	0
4	A	187	0	0	4	0
4	B	191	0	0	4	0
4	C	188	0	0	4	0
4	D	207	0	0	6	0
4	E	183	0	0	5	0
4	F	203	0	0	7	1
4	G	177	0	0	1	0
4	H	178	0	0	7	0
4	J	3	0	0	0	0
4	M	1	0	0	0	0
4	N	4	0	0	0	0
4	O	2	0	0	0	0
4	P	5	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	Q	5	0	0	0	0
4	S	5	0	0	0	0
4	T	2	0	0	0	0
All	All	11854	0	10336	219	2

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 11.

The worst 5 of 219 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:80:GLY:O	1:H:100:ARG:NH1	1.79	1.14
1:D:162:LYS:H	1:D:162:LYS:CD	1.62	1.12
1:B:162:LYS:H	1:B:162:LYS:CD	1.57	1.11
1:B:162:LYS:N	1:B:162:LYS:HD2	1.55	1.08
1:A:101:MET:CE	1:A:119:GLY:HA3	1.87	1.04

All (2) 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:G:14:SER:CB	4:F:385:HOH:O[1_545]	2.14	0.06
1:F:149:ASN:ND2	1:G:162:LYS:NZ[1_565]	2.19	0.01

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	168/185 (91%)	160 (95%)	8 (5%)	0	100	100
1	B	166/185 (90%)	159 (96%)	7 (4%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	162/185 (88%)	160 (99%)	2 (1%)	0	100	100
1	D	163/185 (88%)	158 (97%)	4 (2%)	1 (1%)	25	11
1	E	163/185 (88%)	158 (97%)	5 (3%)	0	100	100
1	F	163/185 (88%)	159 (98%)	4 (2%)	0	100	100
1	G	163/185 (88%)	158 (97%)	5 (3%)	0	100	100
1	H	164/185 (89%)	162 (99%)	2 (1%)	0	100	100
2	J	1/4 (25%)	1 (100%)	0	0	100	100
2	M	1/4 (25%)	1 (100%)	0	0	100	100
2	N	1/4 (25%)	1 (100%)	0	0	100	100
2	O	1/4 (25%)	1 (100%)	0	0	100	100
2	P	1/4 (25%)	1 (100%)	0	0	100	100
2	Q	1/4 (25%)	1 (100%)	0	0	100	100
2	S	1/4 (25%)	1 (100%)	0	0	100	100
2	T	1/4 (25%)	1 (100%)	0	0	100	100
All	All	1320/1512 (87%)	1282 (97%)	37 (3%)	1 (0%)	51	33

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	0	LYS

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	136/146 (93%)	134 (98%)	2 (2%)	65	51
1	B	136/146 (93%)	134 (98%)	2 (2%)	65	51
1	C	133/146 (91%)	129 (97%)	4 (3%)	41	22
1	D	134/146 (92%)	132 (98%)	2 (2%)	65	51

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	E	132/146 (90%)	128 (97%)	4 (3%)	41 22
1	F	134/146 (92%)	131 (98%)	3 (2%)	52 34
1	G	133/146 (91%)	128 (96%)	5 (4%)	33 14
1	H	134/146 (92%)	128 (96%)	6 (4%)	27 10
2	J	1/1 (100%)	1 (100%)	0	100 100
2	M	1/1 (100%)	1 (100%)	0	100 100
2	N	1/1 (100%)	1 (100%)	0	100 100
2	O	1/1 (100%)	1 (100%)	0	100 100
2	P	1/1 (100%)	1 (100%)	0	100 100
2	Q	1/1 (100%)	1 (100%)	0	100 100
2	S	1/1 (100%)	1 (100%)	0	100 100
2	T	1/1 (100%)	1 (100%)	0	100 100
All	All	1080/1176 (92%)	1052 (97%)	28 (3%)	46 28

5 of 28 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	108	ARG
1	H	162	LYS
1	G	37	LYS
1	H	112	ARG
1	F	162	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	149	ASN
1	E	149	ASN
1	F	51	GLN
1	F	145	HIS
1	H	51	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

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

8 non-standard protein/DNA/RNA residues 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	1HB	O	4	2,1	10,10,10	1.56	1 (10%)	11,12,12	1.52	2 (18%)
2	1HB	Q	4	2,1	10,10,10	1.61	2 (20%)	11,12,12	1.65	2 (18%)
2	1HB	N	4	2,1	10,10,10	1.74	1 (10%)	11,12,12	1.64	2 (18%)
2	1HB	M	4	2,1	10,10,10	1.66	2 (20%)	11,12,12	1.75	3 (27%)
2	1HB	S	4	2,1	10,10,10	1.72	2 (20%)	11,12,12	1.46	1 (9%)
2	1HB	J	4	2,1	10,10,10	1.61	1 (10%)	11,12,12	1.73	5 (45%)
2	1HB	P	4	2,1	10,10,10	1.89	2 (20%)	11,12,12	1.71	2 (18%)
2	1HB	T	4	2,1	10,10,10	1.85	3 (30%)	11,12,12	1.67	2 (18%)

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	1HB	O	4	2,1	-	0/11/11/11	-
2	1HB	Q	4	2,1	-	0/11/11/11	-
2	1HB	N	4	2,1	-	0/11/11/11	-
2	1HB	M	4	2,1	-	0/11/11/11	-
2	1HB	S	4	2,1	-	0/11/11/11	-
2	1HB	J	4	2,1	-	1/11/11/11	-
2	1HB	P	4	2,1	-	0/11/11/11	-
2	1HB	T	4	2,1	-	0/11/11/11	-

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	N	4	1HB	O-C	-4.64	1.22	1.42
2	Q	4	1HB	O-C	-4.44	1.23	1.42

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	S	4	1HB	O-C	-4.38	1.24	1.42
2	P	4	1HB	O-C	-4.32	1.24	1.42
2	M	4	1HB	O-C	-4.29	1.24	1.42

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	M	4	1HB	CG-CD-NE2	-3.21	113.39	118.03
2	T	4	1HB	O-C-CA	3.14	123.59	111.52
2	O	4	1HB	O-C-CA	2.96	122.89	111.52
2	Q	4	1HB	O-C-CA	2.88	122.61	111.52
2	S	4	1HB	O-C-CA	2.84	122.46	111.52

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	J	4	1HB	O-C-CA-N

There are no ring outliers.

8 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	O	4	1HB	2	0
2	Q	4	1HB	1	0
2	N	4	1HB	1	0
2	M	4	1HB	3	0
2	S	4	1HB	2	0
2	J	4	1HB	3	0
2	P	4	1HB	1	0
2	T	4	1HB	2	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

4 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	$\#\|Z\| > 2$
3	DMS	B	201	-	3,3,3	2.42	1 (33%)	3,3,3	0.84	0
3	DMS	H	201	-	3,3,3	2.76	1 (33%)	3,3,3	1.81	1 (33%)
3	DMS	A	201	-	3,3,3	2.75	1 (33%)	3,3,3	1.87	2 (66%)
3	DMS	D	201	-	3,3,3	2.77	1 (33%)	3,3,3	1.81	1 (33%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	201	DMS	O-S	4.54	1.80	1.50
3	H	201	DMS	O-S	4.53	1.80	1.50
3	A	201	DMS	O-S	4.52	1.80	1.50
3	B	201	DMS	O-S	4.12	1.77	1.50

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	H	201	DMS	O-S-C1	2.42	118.59	106.49
3	A	201	DMS	O-S-C1	2.37	118.37	106.49
3	D	201	DMS	O-S-C1	2.11	117.06	106.49
3	A	201	DMS	C2-S-C1	-2.03	88.02	98.42

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	201	DMS	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, 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	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	172/185 (92%)	-0.13	3 (1%) 70 74	13, 23, 46, 64	0
1	B	170/185 (91%)	-0.14	2 (1%) 79 82	12, 23, 45, 63	0
1	C	166/185 (89%)	-0.33	1 (0%) 89 91	12, 21, 40, 71	0
1	D	167/185 (90%)	-0.27	2 (1%) 79 82	12, 19, 39, 55	0
1	E	167/185 (90%)	-0.30	0 100 100	11, 22, 44, 53	0
1	F	167/185 (90%)	-0.24	1 (0%) 89 91	12, 20, 39, 59	0
1	G	167/185 (90%)	-0.26	1 (0%) 89 91	11, 22, 44, 55	0
1	H	168/185 (90%)	-0.20	2 (1%) 79 82	12, 22, 44, 70	0
2	J	2/4 (50%)	-0.29	0 100 100	26, 26, 26, 27	0
2	M	2/4 (50%)	-0.41	0 100 100	26, 26, 26, 27	0
2	N	2/4 (50%)	0.86	0 100 100	18, 18, 18, 26	0
2	O	2/4 (50%)	-0.28	0 100 100	24, 24, 24, 26	0
2	P	2/4 (50%)	0.44	0 100 100	19, 19, 19, 26	0
2	Q	2/4 (50%)	-0.42	0 100 100	21, 21, 21, 26	0
2	S	2/4 (50%)	0.40	0 100 100	23, 23, 23, 26	0
2	T	2/4 (50%)	-0.12	0 100 100	22, 22, 22, 26	0
All	All	1360/1512 (89%)	-0.23	12 (0%) 84 87	11, 22, 44, 71	0

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	-3	ASP	4.2
1	H	162	LYS	3.2
1	B	-3	ASP	3.1
1	B	78	PRO	2.9
1	C	162	LYS	2.6

6.2 Non-standard residues in protein, DNA, RNA chains (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	B-factors(Å^2)	Q<0.9
2	1HB	J	4	11/11	0.89	0.09	16,21,25,28	0
2	1HB	T	4	11/11	0.91	0.09	15,16,24,26	0
2	1HB	Q	4	11/11	0.92	0.10	16,18,24,25	0
2	1HB	O	4	11/11	0.93	0.09	17,19,23,24	0
2	1HB	M	4	11/11	0.93	0.10	15,21,24,27	0
2	1HB	P	4	11/11	0.94	0.09	12,14,18,19	0
2	1HB	S	4	11/11	0.95	0.08	15,17,23,23	0
2	1HB	N	4	11/11	0.96	0.06	13,15,17,17	0

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	B-factors(Å^2)	Q<0.9
3	DMS	D	201	4/4	0.78	0.22	13,13,36,94	0
3	DMS	B	201	4/4	0.86	0.21	11,13,19,101	0
3	DMS	A	201	4/4	0.87	0.20	11,11,35,88	0
3	DMS	H	201	4/4	0.87	0.20	11,12,35,90	0

6.5 Other polymers (i)

There are no such residues in this entry.