



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 31, 2017 – 02:31 PM EDT

PDB ID : 3M5N  
Title : Crystal structure of HCV NS3/4A protease in complex with N-terminal product 4B5A  
Authors : Schiffer, C.A.; Romano, K.P.  
Deposited on : unknown  
Resolution : 1.90 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/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 : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20030345  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20030345

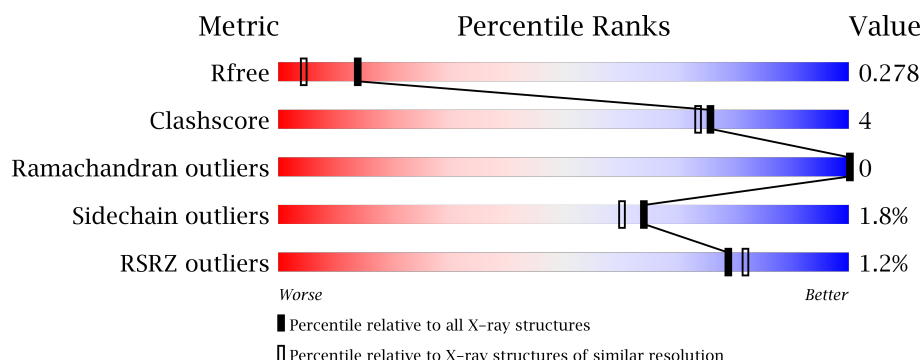
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	100719	5047 (1.90-1.90)
Clashscore	112137	5731 (1.90-1.90)
Ramachandran outliers	110173	5669 (1.90-1.90)
Sidechain outliers	110143	5670 (1.90-1.90)
RSRZ outliers	101464	5100 (1.90-1.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	203	
1	B	203	
1	C	203	
1	D	203	
2	F	7	

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
2	G	7	<div> <div>43%</div> <div>86%</div> <div>14%</div> </div>
2	H	7	<div> <div>29%</div> <div>100%</div> </div>

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	SO4	B	2	-	-	-	X
3	SO4	C	3	-	-	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6372 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 NS3/4A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	200	Total	C	N	O	S	0	0	0
			1445	894	266	277	8			
1	B	199	Total	C	N	O	S	0	0	0
			1420	880	257	275	8			
1	C	197	Total	C	N	O	S	0	0	0
			1418	881	260	269	8			
1	D	198	Total	C	N	O	S	0	0	0
			1421	881	257	275	8			

There are 108 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	981	SER	-	EXPRESSION TAG	UNP A8DG50
A	982	HIS	-	EXPRESSION TAG	UNP A8DG50
A	983	MET	-	EXPRESSION TAG	UNP A8DG50
A	984	ALA	-	EXPRESSION TAG	UNP A8DG50
A	985	SER	-	EXPRESSION TAG	UNP A8DG50
A	986	MET	-	ENGINEERED MUTATION	UNP A8DG50
A	987	LYS	-	ENGINEERED MUTATION	UNP A8DG50
A	988	LYS	-	ENGINEERED MUTATION	UNP A8DG50
A	989	LYS	-	ENGINEERED MUTATION	UNP A8DG50
A	991	SER	CYS	SEE REMARK 999	UNP A8DG50
A	998	ILE	VAL	SEE REMARK 999	UNP A8DG50
A	999	ASN	ILE	SEE REMARK 999	UNP A8DG50
A	1001	SER	ALA	ENGINEERED MUTATION	UNP A8DG50
A	1002	GLY	PRO	ENGINEERED MUTATION	UNP A8DG50
A	1003	ASP	ILE	ENGINEERED MUTATION	UNP A8DG50
A	1013	GLU	LEU	ENGINEERED MUTATION	UNP A8DG50
A	1014	GLU	LEU	ENGINEERED MUTATION	UNP A8DG50
A	1017	GLN	ILE	ENGINEERED MUTATION	UNP A8DG50
A	1018	GLU	ILE	ENGINEERED MUTATION	UNP A8DG50
A	1021	GLN	LEU	ENGINEERED MUTATION	UNP A8DG50
A	1040	THR	ALA	ENGINEERED MUTATION	UNP A8DG50

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
A	1047	SER	CYS	ENGINEERED MUTATION	UNP A8DG50
A	1052	LEU	CYS	ENGINEERED MUTATION	UNP A8DG50
A	1072	THR	ILE	ENGINEERED MUTATION	UNP A8DG50
A	1086	GLN	PRO	ENGINEERED MUTATION	UNP A8DG50
A	1139	ALA	SER	ENGINEERED MUTATION	UNP A8DG50
A	1159	SER	CYS	ENGINEERED MUTATION	UNP A8DG50
B	981	SER	-	EXPRESSION TAG	UNP A8DG50
B	982	HIS	-	EXPRESSION TAG	UNP A8DG50
B	983	MET	-	EXPRESSION TAG	UNP A8DG50
B	984	ALA	-	EXPRESSION TAG	UNP A8DG50
B	985	SER	-	EXPRESSION TAG	UNP A8DG50
B	986	MET	-	ENGINEERED MUTATION	UNP A8DG50
B	987	LYS	-	ENGINEERED MUTATION	UNP A8DG50
B	988	LYS	-	ENGINEERED MUTATION	UNP A8DG50
B	989	LYS	-	ENGINEERED MUTATION	UNP A8DG50
B	991	SER	CYS	SEE REMARK 999	UNP A8DG50
B	998	ILE	VAL	SEE REMARK 999	UNP A8DG50
B	999	ASN	ILE	SEE REMARK 999	UNP A8DG50
B	1001	SER	ALA	ENGINEERED MUTATION	UNP A8DG50
B	1002	GLY	PRO	ENGINEERED MUTATION	UNP A8DG50
B	1003	ASP	ILE	ENGINEERED MUTATION	UNP A8DG50
B	1013	GLU	LEU	ENGINEERED MUTATION	UNP A8DG50
B	1014	GLU	LEU	ENGINEERED MUTATION	UNP A8DG50
B	1017	GLN	ILE	ENGINEERED MUTATION	UNP A8DG50
B	1018	GLU	ILE	ENGINEERED MUTATION	UNP A8DG50
B	1021	GLN	LEU	ENGINEERED MUTATION	UNP A8DG50
B	1040	THR	ALA	ENGINEERED MUTATION	UNP A8DG50
B	1047	SER	CYS	ENGINEERED MUTATION	UNP A8DG50
B	1052	LEU	CYS	ENGINEERED MUTATION	UNP A8DG50
B	1072	THR	ILE	ENGINEERED MUTATION	UNP A8DG50
B	1086	GLN	PRO	ENGINEERED MUTATION	UNP A8DG50
B	1139	ALA	SER	ENGINEERED MUTATION	UNP A8DG50
B	1159	SER	CYS	ENGINEERED MUTATION	UNP A8DG50
C	981	SER	-	EXPRESSION TAG	UNP A8DG50
C	982	HIS	-	EXPRESSION TAG	UNP A8DG50
C	983	MET	-	EXPRESSION TAG	UNP A8DG50
C	984	ALA	-	EXPRESSION TAG	UNP A8DG50
C	985	SER	-	EXPRESSION TAG	UNP A8DG50
C	986	MET	-	ENGINEERED MUTATION	UNP A8DG50
C	987	LYS	-	ENGINEERED MUTATION	UNP A8DG50
C	988	LYS	-	ENGINEERED MUTATION	UNP A8DG50
C	989	LYS	-	ENGINEERED MUTATION	UNP A8DG50

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
C	991	SER	CYS	SEE REMARK 999	UNP A8DG50
C	998	ILE	VAL	SEE REMARK 999	UNP A8DG50
C	999	ASN	ILE	SEE REMARK 999	UNP A8DG50
C	1001	SER	ALA	ENGINEERED MUTATION	UNP A8DG50
C	1002	GLY	PRO	ENGINEERED MUTATION	UNP A8DG50
C	1003	ASP	ILE	ENGINEERED MUTATION	UNP A8DG50
C	1013	GLU	LEU	ENGINEERED MUTATION	UNP A8DG50
C	1014	GLU	LEU	ENGINEERED MUTATION	UNP A8DG50
C	1017	GLN	ILE	ENGINEERED MUTATION	UNP A8DG50
C	1018	GLU	ILE	ENGINEERED MUTATION	UNP A8DG50
C	1021	GLN	LEU	ENGINEERED MUTATION	UNP A8DG50
C	1040	THR	ALA	ENGINEERED MUTATION	UNP A8DG50
C	1047	SER	CYS	ENGINEERED MUTATION	UNP A8DG50
C	1052	LEU	CYS	ENGINEERED MUTATION	UNP A8DG50
C	1072	THR	ILE	ENGINEERED MUTATION	UNP A8DG50
C	1086	GLN	PRO	ENGINEERED MUTATION	UNP A8DG50
C	1139	ALA	SER	ENGINEERED MUTATION	UNP A8DG50
C	1159	SER	CYS	ENGINEERED MUTATION	UNP A8DG50
D	981	SER	-	EXPRESSION TAG	UNP A8DG50
D	982	HIS	-	EXPRESSION TAG	UNP A8DG50
D	983	MET	-	EXPRESSION TAG	UNP A8DG50
D	984	ALA	-	EXPRESSION TAG	UNP A8DG50
D	985	SER	-	EXPRESSION TAG	UNP A8DG50
D	986	MET	-	ENGINEERED MUTATION	UNP A8DG50
D	987	LYS	-	ENGINEERED MUTATION	UNP A8DG50
D	988	LYS	-	ENGINEERED MUTATION	UNP A8DG50
D	989	LYS	-	ENGINEERED MUTATION	UNP A8DG50
D	991	SER	CYS	SEE REMARK 999	UNP A8DG50
D	998	ILE	VAL	SEE REMARK 999	UNP A8DG50
D	999	ASN	ILE	SEE REMARK 999	UNP A8DG50
D	1001	SER	ALA	ENGINEERED MUTATION	UNP A8DG50
D	1002	GLY	PRO	ENGINEERED MUTATION	UNP A8DG50
D	1003	ASP	ILE	ENGINEERED MUTATION	UNP A8DG50
D	1013	GLU	LEU	ENGINEERED MUTATION	UNP A8DG50
D	1014	GLU	LEU	ENGINEERED MUTATION	UNP A8DG50
D	1017	GLN	ILE	ENGINEERED MUTATION	UNP A8DG50
D	1018	GLU	ILE	ENGINEERED MUTATION	UNP A8DG50
D	1021	GLN	LEU	ENGINEERED MUTATION	UNP A8DG50
D	1040	THR	ALA	ENGINEERED MUTATION	UNP A8DG50
D	1047	SER	CYS	ENGINEERED MUTATION	UNP A8DG50
D	1052	LEU	CYS	ENGINEERED MUTATION	UNP A8DG50
D	1072	THR	ILE	ENGINEERED MUTATION	UNP A8DG50

*Continued on next page...*

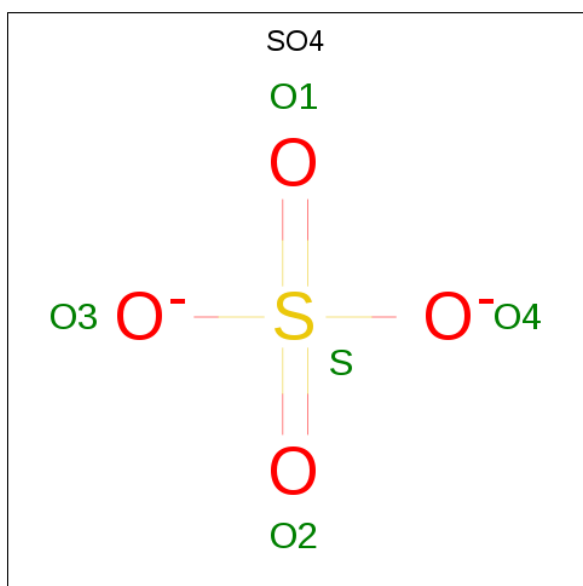
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	1086	GLN	PRO	ENGINEERED MUTATION	UNP A8DG50
D	1139	ALA	SER	ENGINEERED MUTATION	UNP A8DG50
D	1159	SER	CYS	ENGINEERED MUTATION	UNP A8DG50

- Molecule 2 is a protein called SECTTPC peptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	F	7	Total	C	N	O	S	0	0	0
			49	27	7	13	2			
2	G	7	Total	C	N	O	S	0	0	0
			49	27	7	13	2			
2	H	7	Total	C	N	O	S	0	0	0
			49	27	7	13	2			

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total 1	Zn 1	0	0
4	A	1	Total 1	Zn 1	0	0
4	D	1	Total 1	Zn 1	0	0
4	C	1	Total 1	Zn 1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	131	Total 135	O 135	0	4
5	B	141	Total 142	O 142	0	1
5	C	103	Total 107	O 107	0	4
5	D	105	Total 107	O 107	0	2
5	F	3	Total 3	O 3	0	0
5	G	2	Total 2	O 2	0	0
5	H	1	Total 1	O 1	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: NS3/4A

Chain A:  92% 6% .




- Molecule 1: NS3/4A

Chain B:  93% 5% .




- Molecule 1: NS3/4A

Chain C:  86% 10% .




- Molecule 1: NS3/4A

Chain D:  89% 8% .




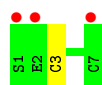
- Molecule 2: SECTTPC peptide

Chain F:  43% 86% 14% .



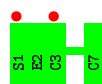
- Molecule 2: SECTTPC peptide

Chain G: 



- Molecule 2: SECTTPC peptide

Chain H: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	67.31Å 58.89Å 98.27Å 90.00° 101.01° 90.00°	Depositor
Resolution (Å)	50.00 – 1.90 43.07 – 1.90	Depositor EDS
% Data completeness (in resolution range)	98.9 (50.00-1.90) 98.9 (43.07-1.90)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.05	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.02 (at 1.89Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.188 , 0.240 0.234 , 0.278	Depositor DCC
$R_{free}$ test set	2995 reflections (5.31%)	DCC
Wilson B-factor (Å <sup>2</sup> )	20.5	Xtriage
Anisotropy	0.166	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 44.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	6372	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	29.0	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 36.41 % 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 5.0213e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup> Intensities estimated from amplitudes.

<sup>2</sup> Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, SO4

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.46	0/1470	0.80	2/2001 (0.1%)
1	B	0.48	0/1445	0.82	2/1971 (0.1%)
1	C	0.41	0/1442	0.76	1/1962 (0.1%)
1	D	0.42	0/1446	0.76	0/1971
2	F	0.50	0/49	0.78	0/65
2	G	0.54	0/49	0.77	0/65
2	H	0.41	0/49	0.70	0/65
All	All	0.44	0/5950	0.78	5/8100 (0.1%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1123	ARG	NE-CZ-NH1	6.19	123.40	120.30
1	B	1011	ARG	NE-CZ-NH2	-5.76	117.42	120.30
1	B	1011	ARG	NE-CZ-NH1	5.74	123.17	120.30
1	C	1143	LEU	CA-CB-CG	5.11	127.05	115.30
1	A	1123	ARG	NE-CZ-NH2	-5.04	117.78	120.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1445	0	1423	5	0
1	B	1420	0	1382	7	0
1	C	1418	0	1412	16	0
1	D	1421	0	1390	14	0
2	F	49	0	44	1	0
2	G	49	0	44	0	0
2	H	49	0	44	0	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
3	C	5	0	0	0	0
3	D	5	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	A	135	0	0	1	0
5	B	142	0	0	0	0
5	C	107	0	0	1	0
5	D	107	0	0	1	0
5	F	3	0	0	0	0
5	G	2	0	0	0	0
5	H	1	0	0	0	0
All	All	6372	0	5739	42	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (42) 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:B:1132:ILE:HD11	2:F:5:THR:HB	1.61	0.82
1:C:1042:THR:HG21	1:C:1109:ARG:HH22	1.44	0.82
1:B:1042:THR:HG21	1:B:1109:ARG:HH22	1.45	0.81
1:D:1114:ILE:HD11	1:D:1134:TYR:HE2	1.52	0.75
1:C:1042:THR:CG2	1:C:1109:ARG:HH22	2.01	0.72
1:C:1160:THR:HG22	1:C:1161:ARG:HG3	1.71	0.71
1:B:1042:THR:HG22	1:B:1109:ARG:HH12	1.57	0.70
1:D:1042:THR:HG21	1:D:1109:ARG:HH22	1.59	0.67
1:C:1174:SER:HA	1:C:1177:THR:HG22	1.78	0.65
1:C:1132:ILE:HD11	1:C:1159:SER:OG	1.97	0.65
1:D:1042:THR:HG22	1:D:1109:ARG:HH12	1.64	0.62
1:C:1042:THR:HG22	1:C:1109:ARG:HH12	1.65	0.61

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1115:PRO:HB2	1:C:1127:LEU:HD22	1.86	0.57
1:C:1132:ILE:HD11	1:C:1159:SER:CB	2.35	0.56
1:C:1155:ARG:HG3	1:C:1170:ILE:HG13	1.89	0.55
1:D:1042:THR:CG2	1:D:1109:ARG:HH22	2.20	0.54
1:B:1042:THR:CG2	1:B:1109:ARG:HH22	2.18	0.52
1:A:1096:PRO:HB3	1:A:1172:VAL:HG21	1.92	0.51
1:A:1106:LEU:HD11	5:A:127:HOH:O	2.12	0.49
1:D:1132:ILE:HD12	1:D:1162:GLY:HA2	1.94	0.49
1:D:1132:ILE:HD11	1:D:1159:SER:OG	2.13	0.48
1:D:1115:PRO:HB2	1:D:1127:LEU:HD22	1.95	0.48
1:C:1114:ILE:HD11	1:C:1134:TYR:HE2	1.77	0.48
1:D:1116:VAL:HG22	1:D:1126:LEU:HD23	1.96	0.48
1:A:1115:PRO:HB2	1:A:1127:LEU:HD22	1.95	0.47
1:C:1149:HIS:ND1	5:C:486:HOH:O	2.22	0.47
1:D:1104:LEU:HD11	1:D:1118:ARG:HG3	1.97	0.47
1:B:1116:VAL:HG22	1:B:1126:LEU:HD23	1.96	0.47
1:D:1127:LEU:N	1:D:1127:LEU:CD1	2.78	0.47
1:C:1042:THR:HG21	1:C:1109:ARG:NH2	2.24	0.46
1:C:1042:THR:CG2	1:C:1109:ARG:NH2	2.76	0.46
1:D:1114:ILE:HD11	1:D:1134:TYR:CE2	2.42	0.45
1:D:1106:LEU:HD11	5:D:90:HOH:O	2.16	0.45
1:C:1116:VAL:HG22	1:C:1126:LEU:HD23	1.99	0.45
1:A:1114:ILE:HG23	1:A:1130:ARG:NH1	2.33	0.44
1:B:1123:ARG:NE	1:B:1168:ASP:OD2	2.51	0.44
1:C:1114:ILE:HD11	1:C:1134:TYR:CE2	2.53	0.43
1:D:1123:ARG:HG2	1:D:1168:ASP:OD2	2.19	0.43
1:A:1132:ILE:HD11	1:A:1157:ALA:HB3	2.01	0.42
1:D:1036:VAL:O	1:D:1042:THR:HG23	2.21	0.41
1:C:1106:LEU:HD13	1:C:1143:LEU:HD22	2.03	0.40
1:B:1042:THR:CG2	1:B:1109:ARG:HH12	2.32	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	198/203 (98%)	197 (100%)	1 (0%)	0	100	100
1	B	197/203 (97%)	194 (98%)	3 (2%)	0	100	100
1	C	195/203 (96%)	194 (100%)	1 (0%)	0	100	100
1	D	196/203 (97%)	195 (100%)	1 (0%)	0	100	100
2	F	5/7 (71%)	5 (100%)	0	0	100	100
2	G	5/7 (71%)	5 (100%)	0	0	100	100
2	H	5/7 (71%)	5 (100%)	0	0	100	100
All	All	801/833 (96%)	795 (99%)	6 (1%)	0	100	100

There are no Ramachandran outliers to report.

### 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	152/164 (93%)	149 (98%)	3 (2%)	60	55
1	B	148/164 (90%)	146 (99%)	2 (1%)	71	69
1	C	149/164 (91%)	146 (98%)	3 (2%)	60	55
1	D	149/164 (91%)	147 (99%)	2 (1%)	73	72
2	F	7/7 (100%)	7 (100%)	0	100	100
2	G	7/7 (100%)	6 (86%)	1 (14%)	4	1
2	H	7/7 (100%)	7 (100%)	0	100	100
All	All	619/677 (91%)	608 (98%)	11 (2%)	64	60

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	985	SER
1	A	1021	GLN

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	1121	ASP
1	B	1095	THR
1	B	1117	ARG
1	C	1066	SER
1	C	1095	THR
1	C	1165	LYS
1	D	1127	LEU
1	D	1165	LYS
2	G	3	CYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1027	ASN
1	B	1034	GLN
1	C	1027	ASN
1	C	1034	GLN
1	D	1027	ASN
1	D	1034	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 for Mogul analysis.

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	SO4	A	1	-	4,4,4	0.26	0	6,6,6	0.30	0
3	SO4	B	2	-	4,4,4	0.17	0	6,6,6	0.17	0
3	SO4	C	3	-	4,4,4	0.27	0	6,6,6	0.26	0
3	SO4	D	4	-	4,4,4	0.21	0	6,6,6	0.43	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	SO4	A	1	-	-	0/0/0/0	0/0/0/0
3	SO4	B	2	-	-	0/0/0/0	0/0/0/0
3	SO4	C	3	-	-	0/0/0/0	0/0/0/0
3	SO4	D	4	-	-	0/0/0/0	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data [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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	200/203 (98%)	0.06	1 (0%) 90 92	14, 28, 47, 64	0
1	B	199/203 (98%)	0.05	0 100 100	13, 26, 43, 62	0
1	C	197/203 (97%)	0.01	0 100 100	18, 30, 51, 62	0
1	D	198/203 (97%)	0.15	1 (0%) 90 92	16, 29, 49, 63	0
2	F	7/7 (100%)	2.10	3 (42%) 0 0	45, 47, 55, 55	0
2	G	7/7 (100%)	2.16	3 (42%) 0 0	48, 49, 61, 61	0
2	H	7/7 (100%)	1.65	2 (28%) 1 0	44, 45, 56, 58	0
All	All	815/833 (97%)	0.12	10 (1%) 79 82	13, 29, 50, 64	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	G	7	CYS	4.9
2	F	3	CYS	4.2
2	F	7	CYS	4.1
2	H	1	SER	3.5
2	G	2	GLU	3.4
2	G	1	SER	2.9
2	H	3	CYS	2.5
1	D	985	SER	2.5
1	A	985	SER	2.1
2	F	4	THR	2.1

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

### 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	SO4	C	3	5/5	0.95	0.18	9.74	38,40,42,45	0
3	SO4	B	2	5/5	0.97	0.13	3.24	37,40,42,42	0
3	SO4	D	4	5/5	0.94	0.12	0.88	40,41,44,44	0
3	SO4	A	1	5/5	0.96	0.12	0.66	36,36,39,39	0
4	ZN	D	1181	1/1	0.97	0.07	-1.59	33,33,33,33	0
4	ZN	C	1181	1/1	0.98	0.07	-1.73	41,41,41,41	0
4	ZN	A	1181	1/1	0.98	0.04	-2.86	34,34,34,34	0
4	ZN	B	1181	1/1	0.98	0.05	-3.00	28,28,28,28	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.