Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 03:34 PM GMT

PDB ID	:	4CL1
Title	:	The crystal structure of NS5A domain 1 from genotype 1a reveals new clues to the mechanism of action for dimeric HCV inhibitors
Authors	:	Lambert, S.M.; Langley, D.R.; Garnett, J.A.; Angell, R.; Hedgethorne, K.; Meanwell, N.A.; Matthews, S.J.
Deposited on	:	2014-01-10
Resolution	:	3.50 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
http://wwpdb.org/validation/2016/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:

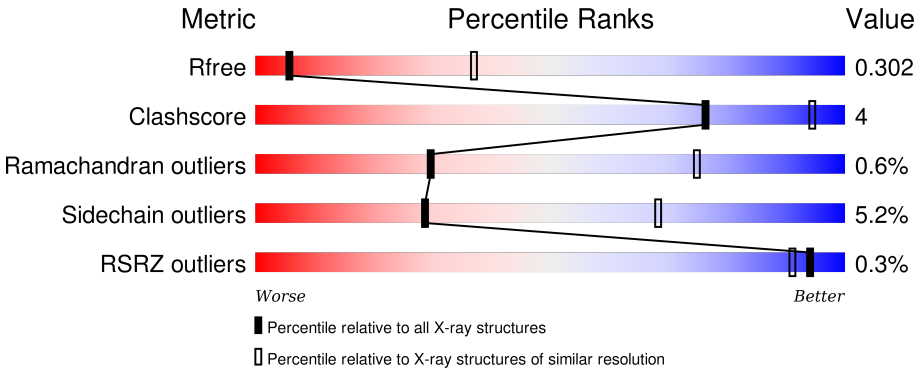
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

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 3.50 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}	91344	1051 (3.60-3.40)
Clashscore	102246	1157 (3.60-3.40)
Ramachandran outliers	100387	1120 (3.60-3.40)
Sidechain outliers	100360	1121 (3.60-3.40)
RSRZ outliers	91569	1058 (3.60-3.40)

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. 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	177	% 77% 6% • • 12%
1	B	177	73% 11% 5% 11%
1	C	177	71% 15% • • 11%
1	D	177	77% 12% • 10%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 4462 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 NON-STRUCTURAL PROTEIN 5A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	155	Total	C	N	O	S	0	0	0
			1101	703	199	187	12			
1	B	157	Total	C	N	O	S	0	0	0
			1128	716	206	193	13			
1	C	157	Total	C	N	O	S	0	0	0
			1091	691	195	192	13			
1	D	160	Total	C	N	O	S	0	0	0
			1133	718	202	200	13			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	GLY	-	EXPRESSION TAG	UNP K4KA16
A	3	SER	-	EXPRESSION TAG	UNP K4KA16
A	174	ASP	-	EXPRESSION TAG	UNP K4KA16
A	175	ASP	-	EXPRESSION TAG	UNP K4KA16
A	176	ASP	-	EXPRESSION TAG	UNP K4KA16
A	177	ASP	-	EXPRESSION TAG	UNP K4KA16
A	178	LYS	-	EXPRESSION TAG	UNP K4KA16
B	2	GLY	-	EXPRESSION TAG	UNP K4KA16
B	3	SER	-	EXPRESSION TAG	UNP K4KA16
B	174	ASP	-	EXPRESSION TAG	UNP K4KA16
B	175	ASP	-	EXPRESSION TAG	UNP K4KA16
B	176	ASP	-	EXPRESSION TAG	UNP K4KA16
B	177	ASP	-	EXPRESSION TAG	UNP K4KA16
B	178	LYS	-	EXPRESSION TAG	UNP K4KA16
C	2	GLY	-	EXPRESSION TAG	UNP K4KA16
C	3	SER	-	EXPRESSION TAG	UNP K4KA16
C	174	ASP	-	EXPRESSION TAG	UNP K4KA16
C	175	ASP	-	EXPRESSION TAG	UNP K4KA16
C	176	ASP	-	EXPRESSION TAG	UNP K4KA16
C	177	ASP	-	EXPRESSION TAG	UNP K4KA16
C	178	LYS	-	EXPRESSION TAG	UNP K4KA16

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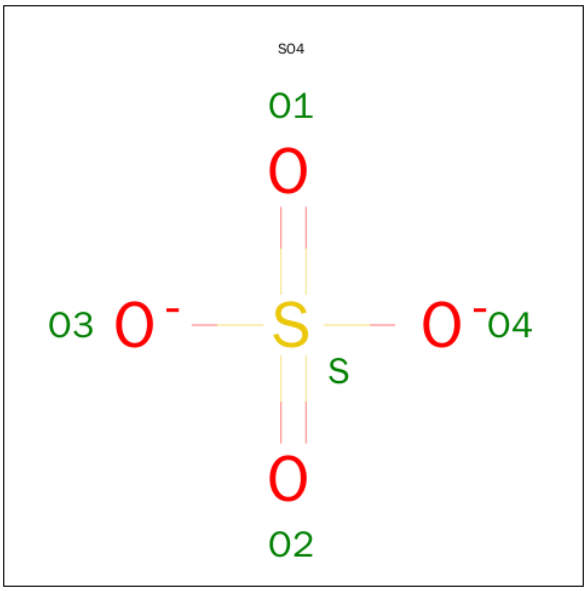
Chain	Residue	Modelled	Actual	Comment	Reference
D	2	GLY	-	EXPRESSION TAG	UNP K4KA16
D	3	SER	-	EXPRESSION TAG	UNP K4KA16
D	174	ASP	-	EXPRESSION TAG	UNP K4KA16
D	175	ASP	-	EXPRESSION TAG	UNP K4KA16
D	176	ASP	-	EXPRESSION TAG	UNP K4KA16
D	177	ASP	-	EXPRESSION TAG	UNP K4KA16
D	178	LYS	-	EXPRESSION TAG	UNP K4KA16

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

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



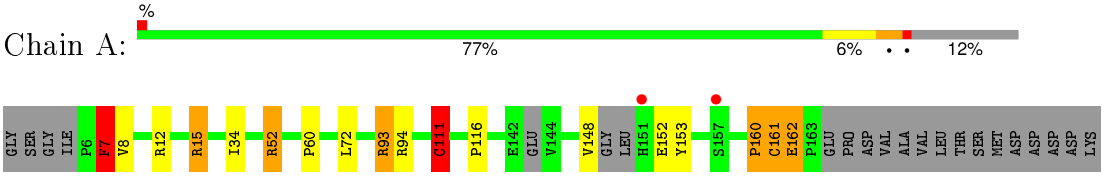
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O S 5 4 1	0	0

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 errors 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.

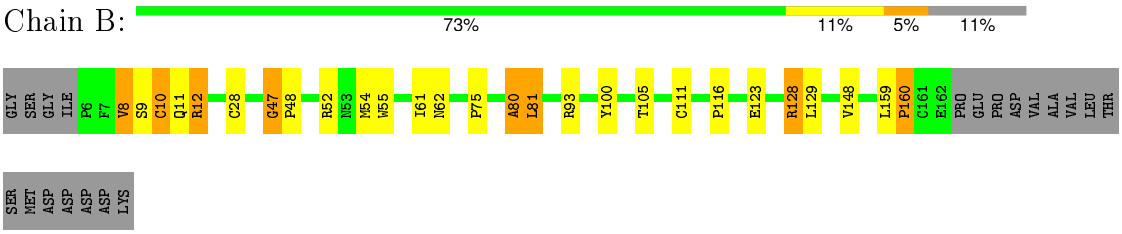
- Molecule 1: NON-STRUCTURAL PROTEIN 5A

Chain A:



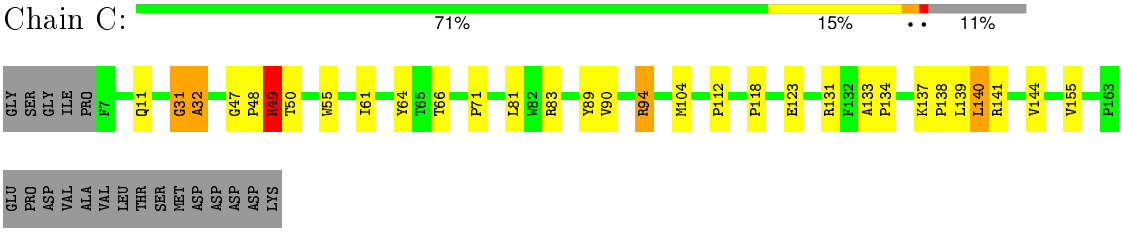
- Molecule 1: NON-STRUCTURAL PROTEIN 5A

Chain B:



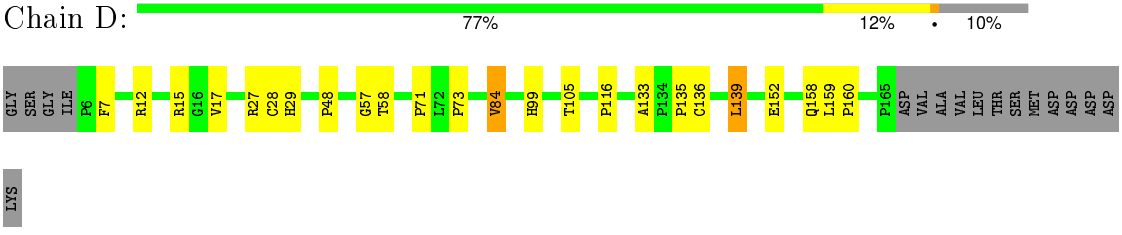
- Molecule 1: NON-STRUCTURAL PROTEIN 5A

Chain C:



- Molecule 1: NON-STRUCTURAL PROTEIN 5A

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	100.23Å 101.76Å 149.79Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.12 – 3.50 50.11 – 3.50	Depositor EDS
% Data completeness (in resolution range)	86.0 (50.12-3.50) 86.1 (50.11-3.50)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.51 (at 3.48Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.225 , 0.266 0.267 , 0.302	Depositor DCC
R_{free} test set	865 reflections (5.05%)	DCC
Wilson B-factor (Å^2)	103.9	Xtriage
Anisotropy	0.130	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 108.9	EDS
Estimated twinning fraction	0.015 for k,h,-l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Outliers	0 of 17137 reflections	Xtriage
F_o,F_c correlation	0.86	EDS
Total number of atoms	4462	wwPDB-VP
Average B, all atoms (Å^2)	90.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.56% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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	0.68	3/1137 (0.3%)	1.06	10/1561 (0.6%)
1	B	0.71	4/1166 (0.3%)	1.17	12/1599 (0.8%)
1	C	0.60	3/1128 (0.3%)	1.20	14/1553 (0.9%)
1	D	0.66	2/1171 (0.2%)	1.05	10/1607 (0.6%)
All	All	0.67	12/4602 (0.3%)	1.12	46/6320 (0.7%)

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	A	0	8
1	B	0	6
1	C	0	4
1	D	1	2
All	All	1	20

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	116	PRO	N-CD	10.43	1.62	1.47
1	B	116	PRO	N-CD	10.25	1.62	1.47
1	B	80	ALA	C-N	8.26	1.53	1.34
1	A	161	CYS	C-N	-7.97	1.15	1.34
1	C	112	PRO	N-CD	7.78	1.58	1.47
1	C	71	PRO	N-CD	7.05	1.57	1.47
1	B	81	LEU	C-N	6.39	1.48	1.34
1	D	135	PRO	N-CD	6.21	1.56	1.47
1	A	116	PRO	N-CD	5.80	1.55	1.47
1	A	60	PRO	N-CD	-5.53	1.40	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	49	ARG	C-N	-5.27	1.22	1.34
1	B	160	PRO	N-CD	5.02	1.54	1.47

All (46) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	137	LYS	C-N-CD	-27.06	61.06	120.60
1	D	84	VAL	C-N-CA	18.53	168.03	121.70
1	B	81	LEU	O-C-N	-18.07	93.80	122.70
1	D	158	GLN	CB-CA-C	13.95	138.29	110.40
1	B	80	ALA	O-C-N	-12.57	102.59	122.70
1	B	81	LEU	CA-C-N	12.12	143.86	117.20
1	B	81	LEU	C-N-CA	11.73	151.03	121.70
1	B	123	GLU	CB-CA-C	-11.21	87.97	110.40
1	B	8	VAL	N-CA-C	11.21	141.27	111.00
1	A	161	CYS	C-N-CA	10.49	147.92	121.70
1	D	84	VAL	N-CA-C	9.65	137.07	111.00
1	A	161	CYS	O-C-N	-9.54	107.43	122.70
1	B	128	ARG	CB-CA-C	9.51	129.42	110.40
1	A	153	TYR	CB-CA-C	-8.73	92.94	110.40
1	C	104	MET	CB-CA-C	8.35	127.10	110.40
1	A	162	GLU	N-CA-C	8.25	133.29	111.00
1	C	31	GLY	N-CA-C	8.24	133.71	113.10
1	C	11	GLN	CB-CA-C	-8.11	94.19	110.40
1	B	75	PRO	CB-CA-C	-8.08	91.80	112.00
1	C	140	LEU	N-CA-C	8.01	132.63	111.00
1	A	152	GLU	CB-CA-C	-7.57	95.25	110.40
1	B	8	VAL	C-N-CA	7.32	139.99	121.70
1	C	140	LEU	CB-CA-C	-7.03	96.85	110.20
1	C	50	THR	N-CA-C	6.95	129.76	111.00
1	B	47	GLY	C-N-CD	-6.83	105.56	120.60
1	B	8	VAL	CB-CA-C	-6.73	98.60	111.40
1	D	99	HIS	CB-CA-C	-6.57	97.26	110.40
1	C	131	ARG	CB-CA-C	6.50	123.41	110.40
1	C	31	GLY	C-N-CA	6.47	137.89	121.70
1	C	32	ALA	CB-CA-C	6.23	119.44	110.10
1	C	64	TYR	N-CA-C	5.96	127.08	111.00
1	D	158	GLN	N-CA-C	-5.92	95.02	111.00
1	A	34	ILE	CG1-CB-CG2	-5.74	98.78	111.40
1	A	161	CYS	CA-C-N	5.74	129.82	117.20
1	D	17	VAL	CB-CA-C	-5.72	100.54	111.40
1	A	111	CYS	C-N-CD	-5.65	108.18	120.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	80	ALA	CA-C-N	5.64	129.61	117.20
1	A	7	PHE	C-N-CA	5.62	135.75	121.70
1	C	49	ARG	O-C-N	-5.50	113.90	122.70
1	D	133	ALA	CB-CA-C	5.38	118.17	110.10
1	C	61	ILE	CB-CA-C	-5.34	100.92	111.60
1	D	136	CYS	CB-CA-C	5.33	121.06	110.40
1	C	141	ARG	N-CA-C	5.20	125.03	111.00
1	D	48	PRO	CB-CA-C	-5.13	99.18	112.00
1	A	160	PRO	CB-CA-C	-5.01	99.47	112.00
1	D	57	GLY	N-CA-C	5.00	125.61	113.10

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	D	84	VAL	CA

All (20) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	12	ARG	Sidechain
1	A	15	ARG	Sidechain
1	A	161	CYS	Mainchain,Peptide
1	A	52	ARG	Sidechain
1	A	7	PHE	Peptide
1	A	93	ARG	Sidechain
1	A	94	ARG	Sidechain
1	B	12	ARG	Sidechain
1	B	52	ARG	Sidechain
1	B	8	VAL	Peptide
1	B	80	ALA	Mainchain
1	B	81	LEU	Mainchain
1	B	93	ARG	Sidechain
1	C	139	LEU	Peptide
1	C	140	LEU	Peptide
1	C	31	GLY	Peptide
1	C	94	ARG	Sidechain
1	D	12	ARG	Sidechain
1	D	27	ARG	Sidechain

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	1101	0	940	5	0
1	B	1128	0	970	8	2
1	C	1091	0	898	13	0
1	D	1133	0	963	5	2
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	5	0	0	0	0
All	All	4462	0	3771	30	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 4.

All (30) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:32:ALA:HB1	1:C:48:PRO:HG2	1.58	0.85
1:B:9:SER:CB	1:B:11:GLN:HA	2.16	0.75
1:C:49:ARG:HG3	1:C:49:ARG:O	1.85	0.75
1:C:32:ALA:HB1	1:C:48:PRO:CG	2.21	0.70
1:B:10:CYS:HA	1:B:28:CYS:SG	2.32	0.69
1:B:128:ARG:O	1:B:129:LEU:HD23	1.96	0.65
1:B:9:SER:HA	1:B:10:CYS:C	2.16	0.64
1:A:148:VAL:HG11	1:A:160:PRO:HG2	1.85	0.59
1:C:89:TYR:OH	1:C:134:PRO:HD2	2.04	0.57
1:B:148:VAL:O	1:B:148:VAL:HG12	2.04	0.57
1:C:49:ARG:CG	1:C:49:ARG:O	2.54	0.55
1:D:15:ARG:HB2	1:D:58:THR:HG22	1.89	0.54
1:A:111:CYS:HB3	1:A:148:VAL:HG23	1.90	0.53
1:C:83:ARG:HB2	1:C:89:TYR:CE2	2.47	0.49
1:D:28:CYS:SG	1:D:29:HIS:N	2.88	0.47
1:B:61:ILE:HD12	1:B:128:ARG:O	2.17	0.45
1:B:47:GLY:HA2	1:B:48:PRO:HD3	1.67	0.44
1:B:159:LEU:HA	1:B:160:PRO:HD3	1.86	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:81:LEU:HB2	1:C:123:GLU:HB2	2.00	0.44
1:C:47:GLY:HA2	1:C:48:PRO:HD3	1.79	0.43
1:D:159:LEU:HA	1:D:160:PRO:HD3	1.77	0.43
1:C:89:TYR:OH	1:C:133:ALA:HB1	2.18	0.43
1:C:32:ALA:HB1	1:C:48:PRO:CB	2.49	0.43
1:D:139:LEU:HA	1:D:139:LEU:HD22	1.76	0.43
1:A:72:LEU:HA	1:A:72:LEU:HD23	1.80	0.42
1:A:93:ARG:HH11	1:A:93:ARG:HG2	1.83	0.42
1:C:32:ALA:HB1	1:C:48:PRO:HB2	2.02	0.42
1:C:81:LEU:CG	1:C:123:GLU:HB2	2.51	0.40
1:A:7:PHE:HB3	1:C:55:TRP:CD2	2.55	0.40
1:D:71:PRO:C	1:D:73:PRO:HD3	2.42	0.40

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:B:55:TRP:C	1:D:7:PHE:CZ[3_555]	1.92	0.28
1:B:55:TRP:O	1:D:7:PHE:CE2[3_555]	2.09	0.11

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	149/177 (84%)	141 (95%)	7 (5%)	1 (1%)	26 72
1	B	155/177 (88%)	138 (89%)	17 (11%)	0	100 100
1	C	155/177 (88%)	140 (90%)	13 (8%)	2 (1%)	15 60
1	D	158/177 (89%)	143 (90%)	14 (9%)	1 (1%)	30 75
All	All	617/708 (87%)	562 (91%)	51 (8%)	4 (1%)	30 75

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	162	GLU
1	C	138	PRO
1	C	118	PRO
1	D	84	VAL

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	95/153 (62%)	91 (96%)	4 (4%)	36	74
1	B	99/153 (65%)	92 (93%)	7 (7%)	18	58
1	C	92/153 (60%)	86 (94%)	6 (6%)	21	62
1	D	101/153 (66%)	98 (97%)	3 (3%)	48	81
All	All	387/612 (63%)	367 (95%)	20 (5%)	29	68

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	VAL
1	A	15	ARG
1	A	52	ARG
1	A	111	CYS
1	B	10	CYS
1	B	12	ARG
1	B	54	MET
1	B	62	ASN
1	B	100	TYR
1	B	105	THR
1	B	111	CYS
1	C	49	ARG
1	C	66	THR
1	C	90	VAL
1	C	94	ARG
1	C	144	VAL
1	C	155	VAL
1	D	105	THR

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Mol	Chain	Res	Type
1	D	139	LEU
1	D	152	GLU

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

Mol	Chain	Res	Type
1	C	25	HIS

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

Of 5 ligands modelled in this entry, 4 are monoatomic - leaving 1 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	200	-	4,4,4	0.14	0	6,6,6	0.37	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	200	-	-	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

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	155/177 (87%)	0.12	2 (1%) 79 70	26, 85, 118, 133	0
1	B	157/177 (88%)	0.02	0 100 100	26, 86, 122, 130	0
1	C	157/177 (88%)	0.03	0 100 100	28, 91, 128, 154	0
1	D	160/177 (90%)	-0.08	0 100 100	68, 88, 125, 150	0
All	All	629/708 (88%)	0.02	2 (0%) 94 91	26, 88, 125, 154	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	151	HIS	3.3
1	A	157	SER	2.5

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. 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^{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	LLDF	B-factors(Å^2)	Q<0.9
2	ZN	A	199	1/1	0.99	0.19	-0.82	76,76,76,76	0
2	ZN	C	199	1/1	0.99	0.15	-1.05	78,78,78,78	0
2	ZN	B	199	1/1	0.99	0.18	-1.18	70,70,70,70	0
2	ZN	D	199	1/1	0.94	0.16	-1.22	79,79,79,79	0
3	SO4	A	200	5/5	0.92	0.28	-1.39	75,79,87,89	0

6.5 Other polymers (i)

There are no such residues in this entry.