



# Full wwPDB X-ray Structure Validation Report ⓘ

Jul 18, 2016 – 11:26 AM EDT

PDB ID : 5HDO  
Title : Crystal structure of a nanobody raised against urokinase-type plasminogen activator  
Authors : Kromann-Hansen, T.  
Deposited on : 2016-01-05  
Resolution : 2.16 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.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7.1 (RC1), CSD as537be (2016)  
Xtrriage (Phenix) : 1.9-1692  
EDS : rb-20027790  
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) : rb-20027790

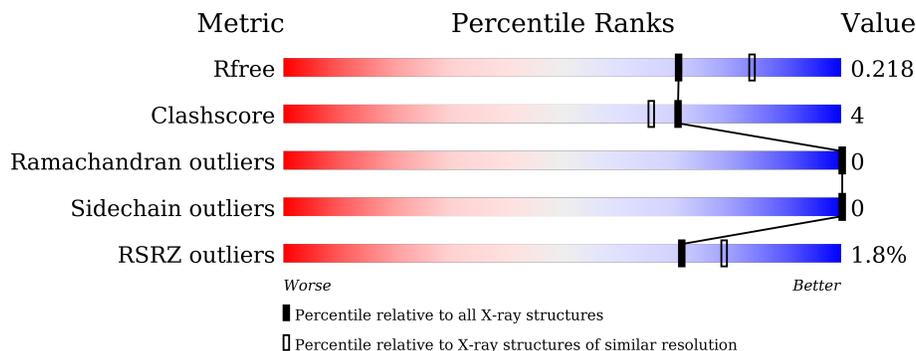
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.16 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	1045 (2.16-2.16)
Clashscore	102246	1152 (2.16-2.16)
Ramachandran outliers	100387	1131 (2.16-2.16)
Sidechain outliers	100360	1131 (2.16-2.16)
RSRZ outliers	91569	1050 (2.16-2.16)

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	128	 3% 88% 10% .
1	B	128	 % 91% 8% .
1	C	128	 2% 91% 7% .
1	D	128	 % 82% 15% .

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	A	201	-	-	-	X
2	SO4	C	201	-	-	X	-
2	SO4	D	201	-	-	X	X

## 2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 4219 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 Anti-HCV NS3/4A serine protease immoglobulin heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	126	941	576	170	190	5	0	0	0
1	B	127	946	579	171	191	5	0	0	0
1	C	125	927	569	166	187	5	0	0	0
1	D	124	921	566	165	185	5	0	0	0

There are 136 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLN	GLU	conflict	UNP A0A0F6YEF6
A	5	GLN	VAL	conflict	UNP A0A0F6YEF6
A	11	LEU	SER	conflict	UNP A0A0F6YEF6
A	27	PHE	TYR	conflict	UNP A0A0F6YEF6
A	29	LEU	TYR	conflict	UNP A0A0F6YEF6
A	30	ASP	CYS	conflict	UNP A0A0F6YEF6
A	33	ALA	GLY	conflict	UNP A0A0F6YEF6
A	34	ILE	MET	conflict	UNP A0A0F6YEF6
A	35	GLY	SER	conflict	UNP A0A0F6YEF6
A	37	PHE	TYR	conflict	UNP A0A0F6YEF6
A	47	GLY	PHE	conflict	UNP A0A0F6YEF6
A	50	CYS	ALA	conflict	UNP A0A0F6YEF6
A	52	SER	-	insertion	UNP A0A0F6YEF6
A	53	ALA	ASP	conflict	UNP A0A0F6YEF6
A	55	GLY	ASP	conflict	UNP A0A0F6YEF6
A	59	ASN	SER	conflict	UNP A0A0F6YEF6
A	72	ARG	GLN	conflict	UNP A0A0F6YEF6
A	87	LYS	ILE	conflict	UNP A0A0F6YEF6
A	88	SER	PRO	conflict	UNP A0A0F6YEF6
A	93	VAL	MET	conflict	UNP A0A0F6YEF6
A	97	ALA	LYS	conflict	UNP A0A0F6YEF6

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Chain	Residue	Modelled	Actual	Comment	Reference
A	98	ALA	THR	conflict	UNP A0A0F6YEF6
A	100	HIS	GLN	conflict	UNP A0A0F6YEF6
A	101	PRO	THR	conflict	UNP A0A0F6YEF6
A	103	LEU	-	insertion	UNP A0A0F6YEF6
A	104	CYS	-	insertion	UNP A0A0F6YEF6
A	105	THR	GLY	conflict	UNP A0A0F6YEF6
A	107	GLU	TRP	conflict	UNP A0A0F6YEF6
A	108	SER	TRP	conflict	UNP A0A0F6YEF6
A	109	GLY	ALA	conflict	UNP A0A0F6YEF6
A	110	ARG	ASP	conflict	UNP A0A0F6YEF6
A	111	ARG	CYS	conflict	UNP A0A0F6YEF6
A	122	GLN	MET	conflict	UNP A0A0F6YEF6
A	128	ALA	-	expression tag	UNP A0A0F6YEF6
B	1	GLN	GLU	conflict	UNP A0A0F6YEF6
B	5	GLN	VAL	conflict	UNP A0A0F6YEF6
B	11	LEU	SER	conflict	UNP A0A0F6YEF6
B	27	PHE	TYR	conflict	UNP A0A0F6YEF6
B	29	LEU	TYR	conflict	UNP A0A0F6YEF6
B	30	ASP	CYS	conflict	UNP A0A0F6YEF6
B	33	ALA	GLY	conflict	UNP A0A0F6YEF6
B	34	ILE	MET	conflict	UNP A0A0F6YEF6
B	35	GLY	SER	conflict	UNP A0A0F6YEF6
B	37	PHE	TYR	conflict	UNP A0A0F6YEF6
B	47	GLY	PHE	conflict	UNP A0A0F6YEF6
B	50	CYS	ALA	conflict	UNP A0A0F6YEF6
B	52	SER	-	insertion	UNP A0A0F6YEF6
B	53	ALA	ASP	conflict	UNP A0A0F6YEF6
B	55	GLY	ASP	conflict	UNP A0A0F6YEF6
B	59	ASN	SER	conflict	UNP A0A0F6YEF6
B	72	ARG	GLN	conflict	UNP A0A0F6YEF6
B	87	LYS	ILE	conflict	UNP A0A0F6YEF6
B	88	SER	PRO	conflict	UNP A0A0F6YEF6
B	93	VAL	MET	conflict	UNP A0A0F6YEF6
B	97	ALA	LYS	conflict	UNP A0A0F6YEF6
B	98	ALA	THR	conflict	UNP A0A0F6YEF6
B	100	HIS	GLN	conflict	UNP A0A0F6YEF6
B	101	PRO	THR	conflict	UNP A0A0F6YEF6
B	103	LEU	-	insertion	UNP A0A0F6YEF6
B	104	CYS	-	insertion	UNP A0A0F6YEF6
B	105	THR	GLY	conflict	UNP A0A0F6YEF6
B	107	GLU	TRP	conflict	UNP A0A0F6YEF6
B	108	SER	TRP	conflict	UNP A0A0F6YEF6

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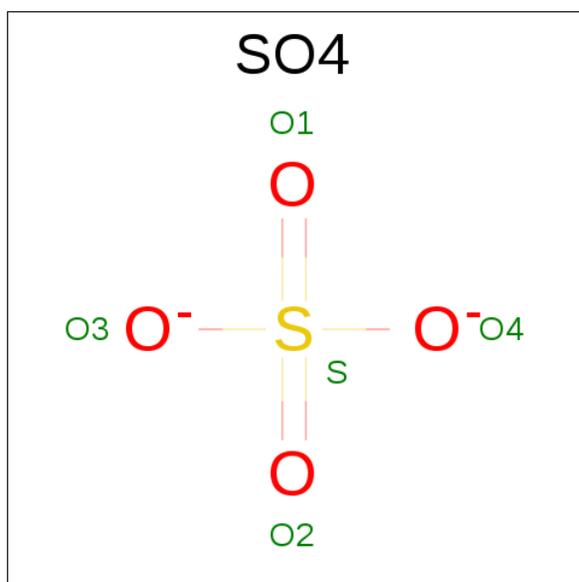
Chain	Residue	Modelled	Actual	Comment	Reference
B	109	GLY	ALA	conflict	UNP A0A0F6YEF6
B	110	ARG	ASP	conflict	UNP A0A0F6YEF6
B	111	ARG	CYS	conflict	UNP A0A0F6YEF6
B	122	GLN	MET	conflict	UNP A0A0F6YEF6
B	128	ALA	-	expression tag	UNP A0A0F6YEF6
C	1	GLN	GLU	conflict	UNP A0A0F6YEF6
C	5	GLN	VAL	conflict	UNP A0A0F6YEF6
C	11	LEU	SER	conflict	UNP A0A0F6YEF6
C	27	PHE	TYR	conflict	UNP A0A0F6YEF6
C	29	LEU	TYR	conflict	UNP A0A0F6YEF6
C	30	ASP	CYS	conflict	UNP A0A0F6YEF6
C	33	ALA	GLY	conflict	UNP A0A0F6YEF6
C	34	ILE	MET	conflict	UNP A0A0F6YEF6
C	35	GLY	SER	conflict	UNP A0A0F6YEF6
C	37	PHE	TYR	conflict	UNP A0A0F6YEF6
C	47	GLY	PHE	conflict	UNP A0A0F6YEF6
C	50	CYS	ALA	conflict	UNP A0A0F6YEF6
C	52	SER	-	insertion	UNP A0A0F6YEF6
C	53	ALA	ASP	conflict	UNP A0A0F6YEF6
C	55	GLY	ASP	conflict	UNP A0A0F6YEF6
C	59	ASN	SER	conflict	UNP A0A0F6YEF6
C	72	ARG	GLN	conflict	UNP A0A0F6YEF6
C	87	LYS	ILE	conflict	UNP A0A0F6YEF6
C	88	SER	PRO	conflict	UNP A0A0F6YEF6
C	93	VAL	MET	conflict	UNP A0A0F6YEF6
C	97	ALA	LYS	conflict	UNP A0A0F6YEF6
C	98	ALA	THR	conflict	UNP A0A0F6YEF6
C	100	HIS	GLN	conflict	UNP A0A0F6YEF6
C	101	PRO	THR	conflict	UNP A0A0F6YEF6
C	103	LEU	-	insertion	UNP A0A0F6YEF6
C	104	CYS	-	insertion	UNP A0A0F6YEF6
C	105	THR	GLY	conflict	UNP A0A0F6YEF6
C	107	GLU	TRP	conflict	UNP A0A0F6YEF6
C	108	SER	TRP	conflict	UNP A0A0F6YEF6
C	109	GLY	ALA	conflict	UNP A0A0F6YEF6
C	110	ARG	ASP	conflict	UNP A0A0F6YEF6
C	111	ARG	CYS	conflict	UNP A0A0F6YEF6
C	122	GLN	MET	conflict	UNP A0A0F6YEF6
C	128	ALA	-	expression tag	UNP A0A0F6YEF6
D	1	GLN	GLU	conflict	UNP A0A0F6YEF6
D	5	GLN	VAL	conflict	UNP A0A0F6YEF6
D	11	LEU	SER	conflict	UNP A0A0F6YEF6

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Chain	Residue	Modelled	Actual	Comment	Reference
D	27	PHE	TYR	conflict	UNP A0A0F6YEF6
D	29	LEU	TYR	conflict	UNP A0A0F6YEF6
D	30	ASP	CYS	conflict	UNP A0A0F6YEF6
D	33	ALA	GLY	conflict	UNP A0A0F6YEF6
D	34	ILE	MET	conflict	UNP A0A0F6YEF6
D	35	GLY	SER	conflict	UNP A0A0F6YEF6
D	37	PHE	TYR	conflict	UNP A0A0F6YEF6
D	47	GLY	PHE	conflict	UNP A0A0F6YEF6
D	50	CYS	ALA	conflict	UNP A0A0F6YEF6
D	52	SER	-	insertion	UNP A0A0F6YEF6
D	53	ALA	ASP	conflict	UNP A0A0F6YEF6
D	55	GLY	ASP	conflict	UNP A0A0F6YEF6
D	59	ASN	SER	conflict	UNP A0A0F6YEF6
D	72	ARG	GLN	conflict	UNP A0A0F6YEF6
D	87	LYS	ILE	conflict	UNP A0A0F6YEF6
D	88	SER	PRO	conflict	UNP A0A0F6YEF6
D	93	VAL	MET	conflict	UNP A0A0F6YEF6
D	97	ALA	LYS	conflict	UNP A0A0F6YEF6
D	98	ALA	THR	conflict	UNP A0A0F6YEF6
D	100	HIS	GLN	conflict	UNP A0A0F6YEF6
D	101	PRO	THR	conflict	UNP A0A0F6YEF6
D	103	LEU	-	insertion	UNP A0A0F6YEF6
D	104	CYS	-	insertion	UNP A0A0F6YEF6
D	105	THR	GLY	conflict	UNP A0A0F6YEF6
D	107	GLU	TRP	conflict	UNP A0A0F6YEF6
D	108	SER	TRP	conflict	UNP A0A0F6YEF6
D	109	GLY	ALA	conflict	UNP A0A0F6YEF6
D	110	ARG	ASP	conflict	UNP A0A0F6YEF6
D	111	ARG	CYS	conflict	UNP A0A0F6YEF6
D	122	GLN	MET	conflict	UNP A0A0F6YEF6
D	128	ALA	-	expression tag	UNP A0A0F6YEF6

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Cl 1 1	0	0
3	D	2	Total Cl 2 2	0	0
3	C	1	Total Cl 1 1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	140	Total O 140 140	0	0
4	B	118	Total O 118 118	0	0

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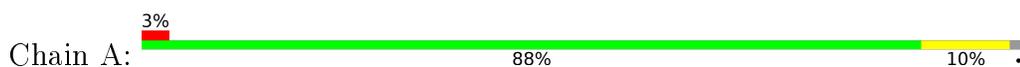
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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
4	C	105	Total 105	O 105	0	0
4	D	97	Total 97	O 97	0	0

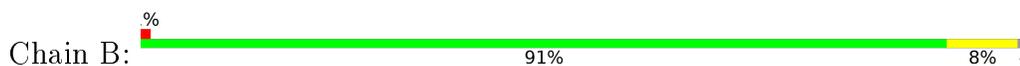
### 3 Residue-property plots [i](#)

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: Anti-HCV NS3/4A serine protease immoglobulin heavy chain



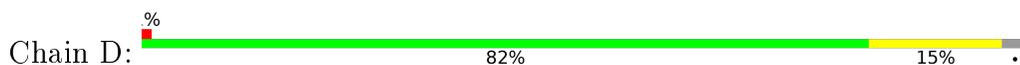
- Molecule 1: Anti-HCV NS3/4A serine protease immoglobulin heavy chain



- Molecule 1: Anti-HCV NS3/4A serine protease immoglobulin heavy chain



- Molecule 1: Anti-HCV NS3/4A serine protease immoglobulin heavy chain



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	99.83Å 99.83Å 127.33Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.28 – 2.16 47.28 – 2.16	Depositor EDS
% Data completeness (in resolution range)	99.9 (47.28-2.16) 99.9 (47.28-2.16)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.86 (at 2.16Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, $R_{free}$	0.177 , 0.218 0.177 , 0.218	Depositor DCC
$R_{free}$ test set	1767 reflections (5.03%)	DCC
Wilson B-factor (Å <sup>2</sup> )	34.6	Xtrriage
Anisotropy	0.162	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 41.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	4219	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	38.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 31.16 % 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 1.1601e-03. 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 [i](#)

### 5.1 Standard geometry [i](#)

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

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	0.36	0/956	0.57	0/1290
1	B	0.33	0/961	0.55	0/1297
1	C	0.38	0/941	0.54	0/1270
1	D	0.36	0/935	0.52	0/1262
All	All	0.36	0/3793	0.55	0/5119

There are no bond length outliers.

There are no bond angle outliers.

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	941	0	901	8	1
1	B	946	0	903	6	1
1	C	927	0	885	6	0
1	D	921	0	877	13	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
2	C	5	0	0	2	0
2	D	5	0	0	2	0
3	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	1	0	0	0	0
3	D	2	0	0	1	0
4	A	140	0	0	2	0
4	B	118	0	0	1	0
4	C	105	0	0	0	1
4	D	97	0	0	1	1
All	All	4219	0	3566	32	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 (32) 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:32:TYR:O	1:B:72:ARG:NH2	2.15	0.79
1:A:5:GLN:OE1	4:A:301:HOH:O	2.10	0.70
1:B:72:ARG:NH1	1:B:74:ASN:OD1	2.29	0.64
1:C:57:SER:OG	2:C:201:SO4:O4	2.15	0.62
1:C:54:SER:OG	2:C:201:SO4:O2	2.19	0.60
1:D:2:VAL:HG12	1:D:27:PHE:HB3	1.86	0.57
1:D:110:ARG:N	4:D:303:HOH:O	2.38	0.56
1:D:22:CYS:HB3	1:D:79:VAL:HG22	1.90	0.54
1:D:97:ALA:HB1	1:D:100:HIS:CD2	2.44	0.53
1:D:34:ILE:HG13	1:D:79:VAL:HG11	1.92	0.51
1:D:99:ASP:HB3	1:D:114:LEU:HB2	1.93	0.50
1:B:111:ARG:O	4:B:301:HOH:O	2.19	0.48
1:D:60:TYR:HB2	1:D:65:LYS:HG3	1.94	0.48
1:C:99:ASP:O	1:C:113:TYR:HB3	2.14	0.47
1:D:99:ASP:O	1:D:113:TYR:HB3	2.14	0.47
1:A:119:GLN:HG3	1:C:10:GLY:HA2	1.97	0.47
1:D:29:LEU:HD22	1:D:34:ILE:HD11	1.97	0.47
2:D:201:SO4:O1	3:D:203:CL:CL	2.72	0.45
1:C:2:VAL:HG12	1:C:27:PHE:HB3	1.99	0.45
1:D:35:GLY:HA3	1:D:103:LEU:HD21	2.00	0.44
1:A:34:ILE:HG13	1:A:79:VAL:HG21	2.00	0.44
1:B:119:GLN:HG3	1:D:10:GLY:HA2	1.98	0.43
1:A:2:VAL:HG12	1:A:27:PHE:HB3	2.01	0.43
1:A:12:VAL:HG21	1:A:18:LEU:HD21	2.01	0.42
1:A:99:ASP:HB3	1:A:114:LEU:HB2	2.01	0.42
1:C:100:HIS:HA	1:C:101:PRO:HD3	1.95	0.41
1:D:57:SER:OG	2:D:201:SO4:O2	2.32	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:110:ARG:CZ	4:A:311:HOH:O	2.68	0.41
1:B:99:ASP:HB3	1:B:114:LEU:HB2	2.03	0.41
1:A:6:GLU:HA	1:A:21:SER:O	2.21	0.40
1:B:12:VAL:HG21	1:B:18:LEU:HD21	2.03	0.40
1:D:100:HIS:CE1	1:D:117:TRP:NE1	2.90	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:A:110:ARG:NH2	1:B:91:THR:CB[3_444]	2.13	0.07
4:C:373:HOH:O	4:D:318:HOH:O[6_445]	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	124/128 (97%)	122 (98%)	2 (2%)	0	100	100
1	B	125/128 (98%)	123 (98%)	2 (2%)	0	100	100
1	C	121/128 (94%)	118 (98%)	3 (2%)	0	100	100
1	D	120/128 (94%)	118 (98%)	2 (2%)	0	100	100
All	All	490/512 (96%)	481 (98%)	9 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	99/100 (99%)	99 (100%)	0	100	100
1	B	99/100 (99%)	99 (100%)	0	100	100
1	C	97/100 (97%)	97 (100%)	0	100	100
1	D	96/100 (96%)	96 (100%)	0	100	100
All	All	391/400 (98%)	391 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	100	HIS
1	D	100	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 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
2	SO4	A	201	-	4,4,4	0.23	0	6,6,6	0.19	0
2	SO4	B	201	-	4,4,4	0.20	0	6,6,6	0.18	0
2	SO4	C	201	-	4,4,4	0.29	0	6,6,6	0.18	0
2	SO4	D	201	-	4,4,4	0.32	0	6,6,6	0.51	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
2	SO4	A	201	-	-	0/0/0/0	0/0/0/0
2	SO4	B	201	-	-	0/0/0/0	0/0/0/0
2	SO4	C	201	-	-	0/0/0/0	0/0/0/0
2	SO4	D	201	-	-	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.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	201	SO4	2	0
2	D	201	SO4	2	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 [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	126/128 (98%)	0.00	4 (3%) 51 61	24, 32, 54, 84	0
1	B	127/128 (99%)	0.04	1 (0%) 87 90	24, 34, 65, 81	0
1	C	125/128 (97%)	-0.01	3 (2%) 62 71	24, 33, 60, 84	0
1	D	124/128 (96%)	0.01	1 (0%) 87 90	25, 35, 59, 91	0
All	All	502/512 (98%)	0.01	9 (1%) 71 79	24, 34, 61, 91	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	110	ARG	6.7
1	C	106	SER	4.8
1	C	127	SER	4.7
1	A	107	GLU	4.2
1	C	128	ALA	4.1
1	A	108	SER	3.0
1	D	127	SER	2.7
1	A	111	ARG	2.4
1	B	110	ARG	2.0

### 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(Å <sup>2</sup> )	Q<0.9
2	SO4	D	201	5/5	0.91	0.30	12.95	54,55,74,98	0
2	SO4	A	201	5/5	0.74	0.20	7.27	48,59,83,95	0
2	SO4	C	201	5/5	0.98	0.14	1.91	52,57,65,70	0
3	CL	C	202	1/1	0.85	0.14	0.56	66,66,66,66	0
3	CL	B	202	1/1	0.79	0.12	0.42	68,68,68,68	0
3	CL	D	202	1/1	0.94	0.14	0.23	73,73,73,73	0
2	SO4	B	201	5/5	0.90	0.13	-0.00	65,66,86,100	0
3	CL	D	203	1/1	0.87	0.07	-	55,55,55,55	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.