



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 06:26 am GMT

PDB ID : 4QSH  
Title : Crystal Structure of *L. monocytogenes* Pyruvate Carboxylase in complex with Cyclic-di-AMP  
Authors : Choi, P.H.; Tong, L.  
Deposited on : 2014-07-04  
Resolution : 2.51 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 : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
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) : recalc28949

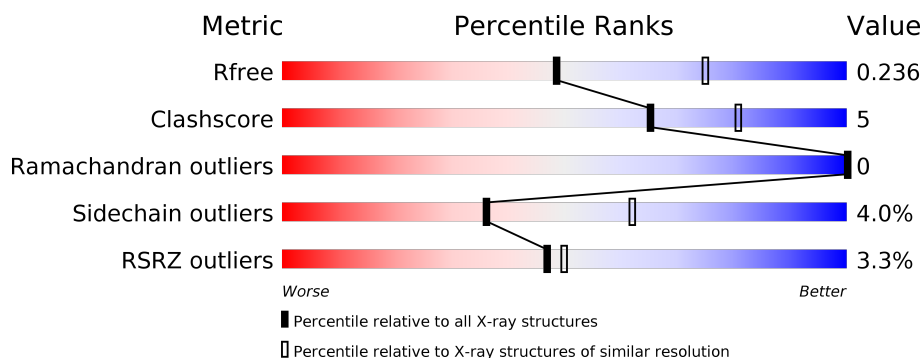
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.51 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	3846 (2.50-2.50)
Clashscore	112137	4554 (2.50-2.50)
Ramachandran outliers	110173	4463 (2.50-2.50)
Sidechain outliers	110143	4465 (2.50-2.50)
RSRZ outliers	101464	3876 (2.50-2.50)

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	1148	<div> <div>3%</div> <div> <div></div> <div>81%</div> <div>11%</div> <div>7%</div> </div> </div>
1	B	1148	<div> <div>4%</div> <div> <div></div> <div>83%</div> <div>9%</div> <div>6%</div> </div> </div>
1	C	1148	<div> <div>4%</div> <div> <div></div> <div>82%</div> <div>11%</div> <div>6%</div> </div> </div>
1	D	1148	<div> <div>2%</div> <div> <div></div> <div>81%</div> <div>11%</div> <div>7%</div> </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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	FLC	A	2001	-	-	X	-
2	FLC	B	2001	-	-	X	-

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 34524 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 Pyruvate carboxylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1072	Total	C	N	O	S	0	0	0
			8447	5361	1435	1612	39			
1	B	1074	Total	C	N	O	S	0	0	0
			8436	5356	1431	1608	41			
1	C	1081	Total	C	N	O	S	0	0	0
			8501	5396	1442	1623	40			
1	D	1072	Total	C	N	O	S	0	0	0
			8446	5363	1431	1611	41			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	HIS	-	EXPRESSION TAG	UNP W6G6F5
A	0	MET	-	EXPRESSION TAG	UNP W6G6F5
B	-1	HIS	-	EXPRESSION TAG	UNP W6G6F5
B	0	MET	-	EXPRESSION TAG	UNP W6G6F5
C	-1	HIS	-	EXPRESSION TAG	UNP W6G6F5
C	0	MET	-	EXPRESSION TAG	UNP W6G6F5
D	-1	HIS	-	EXPRESSION TAG	UNP W6G6F5
D	0	MET	-	EXPRESSION TAG	UNP W6G6F5

- Molecule 2 is CITRATE ANION (three-letter code: FLC) (formula: C<sub>6</sub>H<sub>5</sub>O<sub>7</sub>).

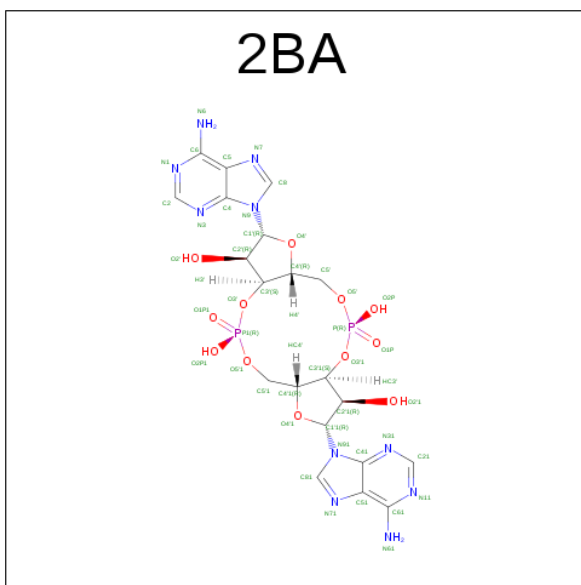


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			13	6	7		
2	B	1	Total	C	O	0	0
			13	6	7		
2	C	1	Total	C	O	0	0
			13	6	7		
2	D	1	Total	C	O	0	0
			13	6	7		

- Molecule 3 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Mn	0	0
			1	1		
3	A	1	Total	Mn	0	0
			1	1		
3	D	1	Total	Mn	0	0
			1	1		
3	C	1	Total	Mn	0	0
			1	1		

- Molecule 4 is (2R,3R,3AS,5R,7AR,9R,10R,10AS,12R,14AR)-2,9-BIS(6-AMINO-9H-PURIN-9-YL)OCTAHYDRO-2H,7H-DIFURO[3,2-D:3',2'-J][1,3,7,9,2,8]TETRAOXADIPHOSPHACYCLODODECINE-3,5,10,12-TETROL 5,12-DIOXIDE (three-letter code: 2BA) (formula: C<sub>20</sub>H<sub>24</sub>N<sub>10</sub>O<sub>12</sub>P<sub>2</sub>).

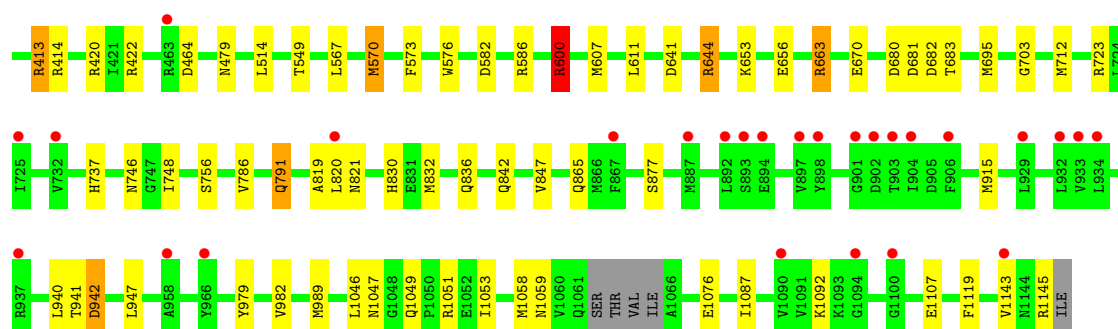


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total 44	C 20	N 10	O 12	P 2	0	0
4	A	1	Total 44	C 20	N 10	O 12	P 2	0	0
4	C	1	Total 44	C 20	N 10	O 12	P 2	0	0

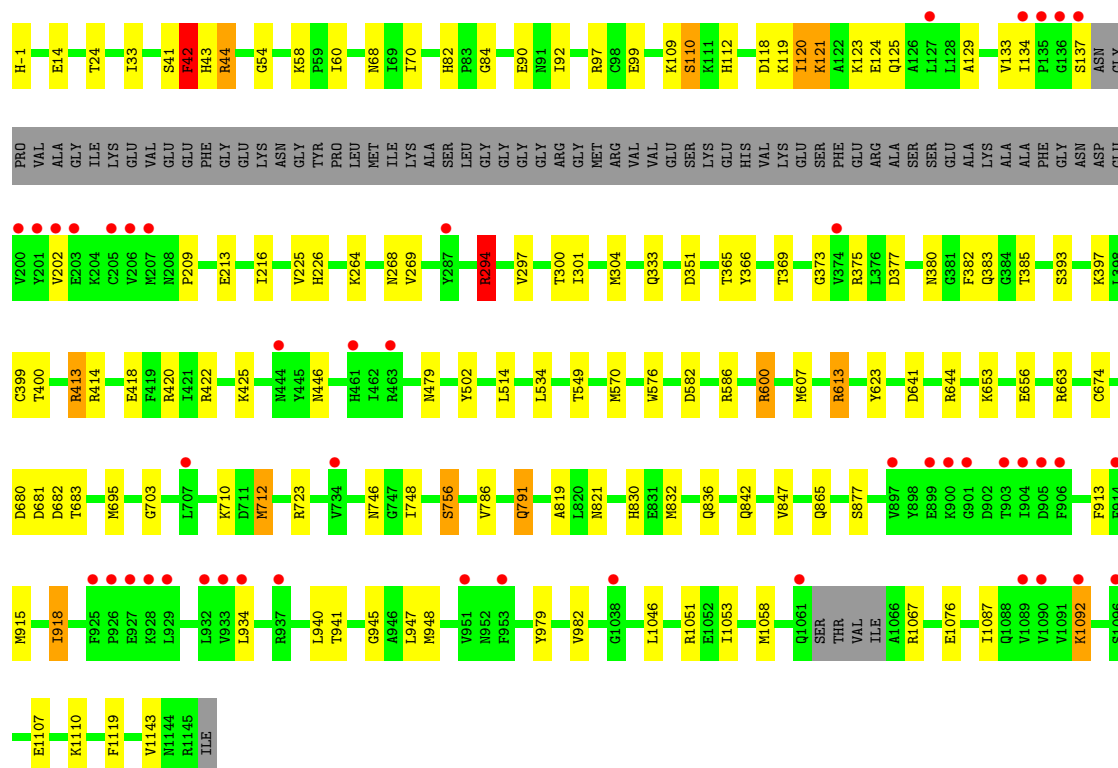
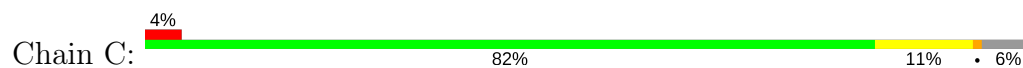
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	163	Total O 163 163	0	0
5	B	79	Total O 79 79	0	0
5	C	82	Total O 82 82	0	0
5	D	182	Total O 182 182	0	0

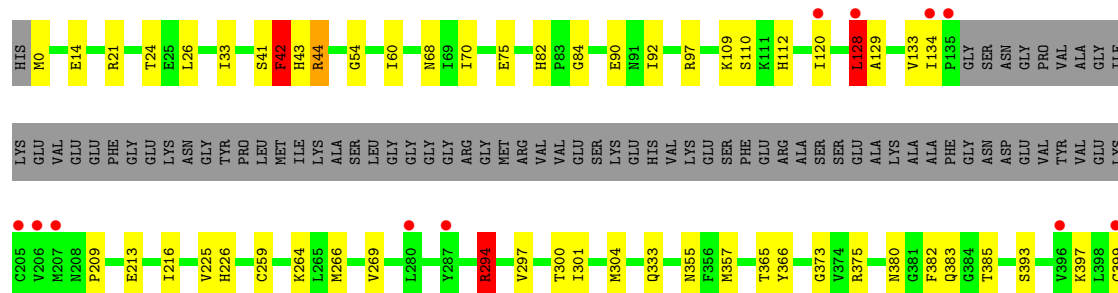
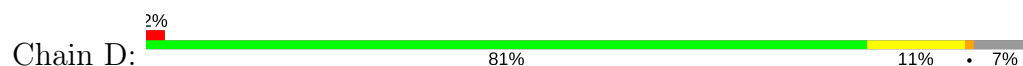




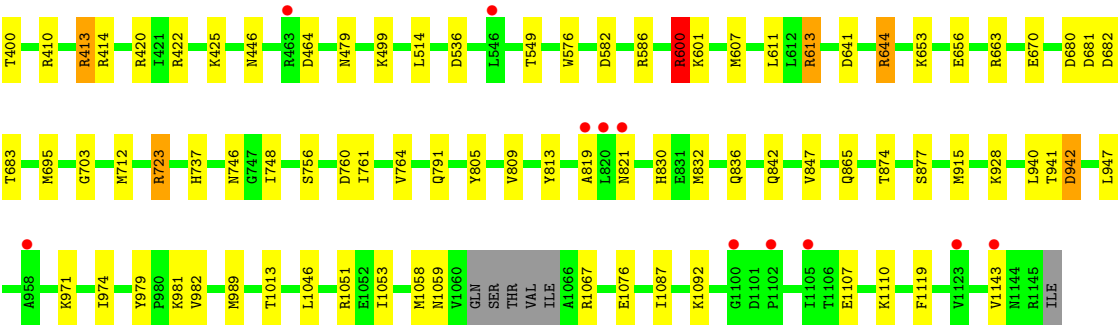
• Molecule 1: Pyruvate carboxylase



• Molecule 1: Pyruvate carboxylase







## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	96.78Å 153.30Å 221.24Å 90.00° 101.58° 90.00°	Depositor
Resolution (Å)	49.80 – 2.51 49.75 – 2.51	Depositor EDS
% Data completeness (in resolution range)	96.6 (49.80-2.51) 96.7 (49.75-2.51)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.17 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, $R_{free}$	0.195 , 0.233 0.200 , 0.236	Depositor DCC
$R_{free}$ test set	10515 reflections (5.30%)	DCC
Wilson B-factor (Å <sup>2</sup> )	47.9	Xtriage
Anisotropy	0.163	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 46.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.015 for h,-k,-h-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	34524	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.71% of the height of the origin peak. No significant pseudotranslation is detected.*

<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: FLC, MN, 2BA

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	0.80	3/8614 (0.0%)	0.87	19/11669 (0.2%)
1	B	0.68	1/8603 (0.0%)	0.85	14/11658 (0.1%)
1	C	0.68	1/8670 (0.0%)	0.84	10/11747 (0.1%)
1	D	0.81	2/8613 (0.0%)	0.88	17/11666 (0.1%)
All	All	0.75	7/34500 (0.0%)	0.86	60/46740 (0.1%)

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	1

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	213	GLU	CD-OE1	7.13	1.33	1.25
1	D	813	TYR	CE1-CZ	6.95	1.47	1.38
1	C	213	GLU	CD-OE1	6.81	1.33	1.25
1	D	213	GLU	CD-OE1	6.52	1.32	1.25
1	A	590	GLU	CG-CD	6.50	1.61	1.51
1	A	813	TYR	CE1-CZ	6.24	1.46	1.38
1	B	213	GLU	CD-OE1	5.91	1.32	1.25

All (60) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	570	MET	CA-CB-CG	-9.90	96.46	113.30
1	A	712	MET	CG-SD-CE	8.35	113.56	100.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	570	MET	CG-SD-CE	-7.50	88.21	100.20
1	D	989	MET	CG-SD-CE	-7.36	88.43	100.20
1	B	413	ARG	NE-CZ-NH1	7.00	123.80	120.30
1	A	414	ARG	NE-CZ-NH2	-6.99	116.81	120.30
1	C	294	ARG	NE-CZ-NH2	-6.95	116.83	120.30
1	B	414	ARG	NE-CZ-NH2	-6.80	116.90	120.30
1	C	294	ARG	NE-CZ-NH1	6.53	123.56	120.30
1	B	414	ARG	NE-CZ-NH1	6.49	123.55	120.30
1	C	414	ARG	NE-CZ-NH1	6.43	123.52	120.30
1	D	600	ARG	NE-CZ-NH1	6.37	123.48	120.30
1	A	294	ARG	NE-CZ-NH2	-6.30	117.15	120.30
1	D	294	ARG	NE-CZ-NH2	-6.20	117.20	120.30
1	C	414	ARG	NE-CZ-NH2	-6.18	117.21	120.30
1	D	413	ARG	NE-CZ-NH1	6.11	123.36	120.30
1	B	294	ARG	NE-CZ-NH2	-6.01	117.30	120.30
1	D	1067	ARG	NE-CZ-NH1	5.97	123.29	120.30
1	D	21	ARG	NE-CZ-NH1	5.93	123.26	120.30
1	A	712	MET	CA-CB-CG	5.90	123.33	113.30
1	D	413	ARG	NE-CZ-NH2	-5.89	117.35	120.30
1	A	414	ARG	NE-CZ-NH1	5.87	123.23	120.30
1	A	723	ARG	NE-CZ-NH1	5.80	123.20	120.30
1	A	749	TYR	CB-CG-CD1	5.79	124.47	121.00
1	D	414	ARG	NE-CZ-NH2	-5.76	117.42	120.30
1	D	600	ARG	NE-CZ-NH2	-5.76	117.42	120.30
1	A	294	ARG	NE-CZ-NH1	5.71	123.16	120.30
1	B	600	ARG	NE-CZ-NH1	5.71	123.15	120.30
1	D	613	ARG	NE-CZ-NH1	5.70	123.15	120.30
1	C	413	ARG	NE-CZ-NH1	5.70	123.15	120.30
1	C	613	ARG	NE-CZ-NH1	5.67	123.14	120.30
1	D	294	ARG	NE-CZ-NH1	5.64	123.12	120.30
1	D	723	ARG	NE-CZ-NH2	-5.56	117.52	120.30
1	C	42	PHE	CB-CA-C	5.55	121.51	110.40
1	A	1051	ARG	NE-CZ-NH2	-5.53	117.54	120.30
1	A	1009	ARG	NE-CZ-NH2	-5.51	117.55	120.30
1	D	414	ARG	NE-CZ-NH1	5.47	123.03	120.30
1	B	0	MET	CG-SD-CE	-5.46	91.46	100.20
1	D	128	LEU	CA-CB-CG	5.37	127.65	115.30
1	D	42	PHE	CB-CA-C	5.37	121.14	110.40
1	B	413	ARG	NE-CZ-NH2	-5.37	117.62	120.30
1	A	100	GLN	CB-CA-C	-5.34	99.72	110.40
1	B	1051	ARG	NE-CZ-NH2	-5.33	117.63	120.30
1	A	600	ARG	NE-CZ-NH1	5.33	122.97	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	1051	ARG	NE-CZ-NH2	-5.32	117.64	120.30
1	B	294	ARG	NE-CZ-NH1	5.30	122.95	120.30
1	A	413	ARG	NE-CZ-NH1	5.30	122.95	120.30
1	A	712	MET	CB-CG-SD	5.29	128.28	112.40
1	C	413	ARG	NE-CZ-NH2	-5.29	117.66	120.30
1	A	367	ARG	NE-CZ-NH2	-5.28	117.66	120.30
1	B	989	MET	CG-SD-CE	-5.28	91.75	100.20
1	D	1051	ARG	NE-CZ-NH2	-5.23	117.69	120.30
1	A	613	ARG	NE-CZ-NH1	5.21	122.91	120.30
1	B	42	PHE	CB-CA-C	5.17	120.74	110.40
1	C	216	ILE	CG1-CB-CG2	-5.16	100.04	111.40
1	A	600	ARG	NE-CZ-NH2	-5.07	117.77	120.30
1	B	600	ARG	NE-CZ-NH2	-5.07	117.77	120.30
1	A	42	PHE	CB-CA-C	5.07	120.53	110.40
1	D	1051	ARG	NE-CZ-NH1	5.03	122.82	120.30
1	A	413	ARG	NE-CZ-NH2	-5.01	117.80	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	682	ASP	Peptide

## 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	8447	0	8377	79	0
1	B	8436	0	8357	76	0
1	C	8501	0	8419	89	0
1	D	8446	0	8392	83	0
2	A	13	0	5	4	0
2	B	13	0	5	5	0
2	C	13	0	5	1	0
2	D	13	0	5	2	0
3	A	1	0	0	0	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	1	0	0	0	0
4	A	88	0	46	0	0
4	C	44	0	23	0	0
5	A	163	0	0	14	0
5	B	79	0	0	5	0
5	C	82	0	0	7	0
5	D	182	0	0	12	0
All	All	34524	0	33634	318	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 5.

All (318) 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:A:97:ARG:HD3	5:A:2174:HOH:O	1.53	1.08
1:C:125:GLN:OE1	5:C:1359:HOH:O	1.83	0.95
1:C:945:GLY:HA2	1:C:948:MET:HE2	1.51	0.91
1:A:723:ARG:HD3	5:A:2115:HOH:O	1.71	0.90
1:B:582:ASP:OD2	1:B:586:ARG:NH1	2.08	0.87
1:A:582:ASP:OD2	1:A:586:ARG:NH1	2.08	0.86
1:D:582:ASP:OD2	1:D:586:ARG:NH1	2.07	0.86
1:C:582:ASP:OD2	1:C:586:ARG:NH1	2.08	0.85
1:A:499:LYS:HA	5:A:2163:HOH:O	1.76	0.85
1:C:420:ARG:NH1	2:C:1202:FLC:OA1	2.12	0.82
1:C:82:HIS:HD2	1:C:84:GLY:H	1.28	0.81
1:D:82:HIS:HD2	1:D:84:GLY:H	1.29	0.80
1:B:663:ARG:NH1	1:B:703:GLY:O	2.13	0.79
1:B:82:HIS:HD2	1:B:84:GLY:H	1.29	0.79
1:C:663:ARG:NH1	1:C:703:GLY:O	2.17	0.78
1:A:82:HIS:HD2	1:A:84:GLY:H	1.30	0.78
1:A:663:ARG:NH1	1:A:703:GLY:O	2.17	0.77
1:D:663:ARG:NH1	1:D:703:GLY:O	2.17	0.77
1:B:1145:ARG:O	5:B:2162:HOH:O	2.02	0.77
1:C:710:LYS:HG2	1:C:712:MET:HE3	1.67	0.76
1:A:304:MET:HE1	1:A:399:CYS:HB3	1.68	0.76
1:B:570:MET:HE3	1:B:573:PHE:CE1	2.21	0.76
1:C:120:ILE:HD12	1:C:124:GLU:OE2	1.85	0.76
1:A:1047:ASN:HD22	2:A:2001:FLC:HG1	1.49	0.76
1:C:304:MET:HE1	1:C:399:CYS:HB3	1.68	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:304:MET:HE1	1:D:399:CYS:HB3	1.68	0.75
1:B:304:MET:HE1	1:B:399:CYS:HB3	1.70	0.73
1:C:756:SER:OG	5:C:1323:HOH:O	2.05	0.73
1:D:830:HIS:HD2	1:D:832:MET:H	1.38	0.71
1:C:351:ASP:OD2	1:C:425:LYS:HD2	1.92	0.70
1:D:723:ARG:HD3	5:D:2214:HOH:O	1.90	0.70
1:C:54:GLY:H	1:C:68:ASN:HD22	1.41	0.69
1:A:502:TYR:OH	1:B:75:GLU:OE1	2.04	0.68
1:D:42:PHE:HB3	1:D:382:PHE:CE1	2.27	0.68
1:C:42:PHE:HB3	1:C:382:PHE:CE1	2.28	0.68
1:A:226:HIS:H	1:A:333:GLN:HE22	1.41	0.68
1:C:226:HIS:H	1:C:333:GLN:HE22	1.40	0.68
1:C:297:VAL:HG23	5:C:1303:HOH:O	1.94	0.68
1:A:42:PHE:HB3	1:A:382:PHE:CE1	2.29	0.67
1:A:830:HIS:HD2	1:A:832:MET:H	1.43	0.67
1:C:945:GLY:HA2	1:C:948:MET:CE	2.25	0.67
1:C:304:MET:CE	1:C:399:CYS:HB3	2.25	0.67
1:A:304:MET:CE	1:A:399:CYS:HB3	2.25	0.67
1:C:120:ILE:CD1	1:C:124:GLU:OE2	2.44	0.66
1:B:42:PHE:HB3	1:B:382:PHE:CE1	2.30	0.66
1:C:534:LEU:O	1:C:570:MET:HE3	1.95	0.66
1:C:268:ASN:ND2	5:C:1359:HOH:O	2.28	0.66
1:B:479:ASN:HD21	1:B:1058:MET:H	1.43	0.66
1:B:54:GLY:H	1:B:68:ASN:HD22	1.42	0.65
1:C:120:ILE:O	1:C:124:GLU:HG3	1.96	0.65
1:B:226:HIS:H	1:B:333:GLN:HE22	1.44	0.65
1:B:1049:GLN:HE22	2:B:2001:FLC:HG2	1.61	0.65
1:B:304:MET:CE	1:B:399:CYS:HB3	2.27	0.64
1:C:830:HIS:HD2	1:C:832:MET:H	1.45	0.64
1:C:118:ASP:HB2	1:C:121:LYS:HD3	1.77	0.64
1:A:90:GLU:OE2	1:A:294:ARG:HD3	1.98	0.64
1:D:54:GLY:H	1:D:68:ASN:HD22	1.44	0.64
1:B:830:HIS:HD2	1:B:832:MET:H	1.42	0.64
1:B:0:MET:CE	1:B:26:LEU:HD22	2.28	0.64
1:B:1049:GLN:NE2	2:B:2001:FLC:HG2	2.12	0.64
1:D:304:MET:CE	1:D:399:CYS:HB3	2.27	0.64
1:A:54:GLY:H	1:A:68:ASN:HD22	1.43	0.64
1:D:226:HIS:H	1:D:333:GLN:HE22	1.43	0.63
1:B:14:GLU:CD	1:B:397:LYS:HE3	2.19	0.63
1:B:362:ARG:NH1	5:B:2163:HOH:O	2.32	0.63
1:D:479:ASN:HD21	1:D:1058:MET:H	1.45	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:366:TYR:H	1:B:383:GLN:HE21	1.47	0.63
1:B:90:GLU:OE2	1:B:294:ARG:HD3	1.99	0.63
1:C:90:GLU:OE2	1:C:294:ARG:HD3	1.98	0.62
1:D:514:LEU:HD22	1:D:607:MET:CE	2.29	0.62
1:D:366:TYR:H	1:D:383:GLN:HE21	1.48	0.62
1:B:570:MET:CE	1:B:573:PHE:CE1	2.83	0.62
1:C:14:GLU:CD	1:C:397:LYS:HE3	2.20	0.62
1:B:54:GLY:H	1:B:68:ASN:ND2	1.98	0.62
1:C:514:LEU:HD22	1:C:607:MET:CE	2.30	0.61
1:A:479:ASN:HD21	1:A:1058:MET:H	1.49	0.61
1:B:514:LEU:HD22	1:B:607:MET:CE	2.31	0.61
1:B:746:ASN:HD22	1:C:748:ILE:HG21	1.66	0.60
1:A:24:THR:O	1:B:413:ARG:NH2	2.35	0.60
1:C:54:GLY:H	1:C:68:ASN:ND2	1.98	0.60
1:C:24:THR:O	1:D:413:ARG:NH2	2.35	0.60
1:D:499:LYS:HB3	5:D:2166:HOH:O	2.02	0.60
1:B:0:MET:HE2	1:B:26:LEU:HD22	1.83	0.60
1:D:90:GLU:OE2	1:D:294:ARG:HD3	2.01	0.60
1:D:464:ASP:N	1:D:464:ASP:OD1	2.34	0.60
1:C:366:TYR:H	1:C:383:GLN:HE21	1.50	0.59
1:D:1087:ILE:HD11	1:D:1107:GLU:HB2	1.84	0.59
1:A:41:SER:OG	1:A:43:HIS:HD2	1.86	0.59
1:C:1087:ILE:HD11	1:C:1107:GLU:HB2	1.84	0.59
1:C:918:ILE:HD13	1:C:918:ILE:C	2.23	0.59
1:A:54:GLY:H	1:A:68:ASN:ND2	2.00	0.59
1:D:54:GLY:H	1:D:68:ASN:ND2	2.00	0.59
1:D:14:GLU:CD	1:D:397:LYS:HE3	2.23	0.58
1:C:118:ASP:HB2	1:C:121:LYS:CD	2.34	0.58
1:A:14:GLU:CD	1:A:397:LYS:HE3	2.24	0.58
1:A:297:VAL:HG23	5:A:2155:HOH:O	2.04	0.58
1:C:413:ARG:NH2	1:D:24:THR:O	2.36	0.58
1:B:420:ARG:NH1	2:B:2001:FLC:OG2	2.36	0.57
1:A:366:TYR:H	1:A:383:GLN:HE21	1.52	0.57
1:A:413:ARG:NH2	1:B:24:THR:O	2.37	0.57
1:B:1087:ILE:HD11	1:B:1107:GLU:HB2	1.85	0.57
1:C:786:VAL:O	1:C:791:GLN:NE2	2.38	0.57
1:D:294:ARG:NH2	5:D:2157:HOH:O	2.36	0.57
1:A:1087:ILE:HD11	1:A:1107:GLU:HB2	1.85	0.57
1:C:479:ASN:HD21	1:C:1058:MET:H	1.52	0.57
1:B:567:LEU:HB3	1:B:570:MET:HE2	1.85	0.57
1:C:41:SER:OG	1:C:43:HIS:HD2	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1067:ARG:HG2	5:C:1319:HOH:O	2.04	0.56
1:C:1076:GLU:HG2	1:C:1143:VAL:O	2.06	0.56
1:C:674:CYS:SG	1:C:712:MET:HE1	2.46	0.56
1:B:1076:GLU:HG2	1:B:1143:VAL:O	2.06	0.56
1:C:109:LYS:H	1:C:112:HIS:HD2	1.53	0.56
1:B:464:ASP:N	1:B:464:ASP:OD1	2.37	0.56
1:B:786:VAL:O	1:B:791:GLN:NE2	2.40	0.55
1:A:301:ILE:HA	1:A:304:MET:HE3	1.87	0.55
1:C:99:GLU:OE1	1:C:110:SER:OG	2.24	0.55
1:C:514:LEU:HD22	1:C:607:MET:HE2	1.87	0.55
1:D:514:LEU:HD22	1:D:607:MET:HE2	1.87	0.55
1:A:1076:GLU:HG2	1:A:1143:VAL:O	2.06	0.55
1:D:1076:GLU:HG2	1:D:1143:VAL:O	2.06	0.55
1:B:109:LYS:H	1:B:112:HIS:HD2	1.55	0.54
1:C:301:ILE:HA	1:C:304:MET:HE3	1.89	0.54
1:C:502:TYR:OH	1:D:75:GLU:OE1	2.17	0.54
1:A:748:ILE:HG21	1:D:746:ASN:HD22	1.72	0.54
1:B:514:LEU:HD22	1:B:607:MET:HE2	1.89	0.54
1:C:674:CYS:SG	1:C:712:MET:CE	2.96	0.54
1:B:748:ILE:HG21	1:C:746:ASN:HD22	1.72	0.54
1:C:847:VAL:HG12	1:C:847:VAL:O	2.08	0.54
1:C:913:PHE:HD1	1:C:918:ILE:HD11	1.71	0.54
1:D:41:SER:OG	1:D:43:HIS:HD2	1.91	0.54
1:A:1067:ARG:HG2	5:A:2135:HOH:O	2.07	0.54
1:B:942:ASP:N	1:B:942:ASP:OD1	2.41	0.53
1:A:99:GLU:OE1	1:A:110:SER:OG	2.25	0.53
1:D:301:ILE:HA	1:D:304:MET:HE3	1.90	0.53
1:B:41:SER:OG	1:B:43:HIS:HD2	1.92	0.53
1:B:663:ARG:HA	5:B:2137:HOH:O	2.07	0.53
1:B:820:LEU:HD23	1:B:820:LEU:N	2.23	0.53
1:A:746:ASN:HD22	1:D:748:ILE:HG21	1.74	0.53
1:A:681:ASP:OD1	1:A:683:THR:HB	2.08	0.53
1:D:300:THR:HG22	1:D:375:ARG:NH2	2.24	0.53
1:D:847:VAL:O	1:D:847:VAL:HG12	2.08	0.53
1:A:847:VAL:HG12	1:A:847:VAL:O	2.08	0.53
1:A:847:VAL:O	1:A:847:VAL:CG1	2.57	0.53
1:B:301:ILE:HA	1:B:304:MET:HE3	1.90	0.52
1:B:681:ASP:OD1	1:B:683:THR:HB	2.08	0.52
1:C:847:VAL:CG1	1:C:847:VAL:O	2.57	0.52
1:D:681:ASP:OD1	1:D:683:THR:HB	2.08	0.52
1:D:847:VAL:O	1:D:847:VAL:CG1	2.57	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1046:LEU:C	1:C:1046:LEU:HD23	2.30	0.52
1:A:1046:LEU:C	1:A:1046:LEU:HD23	2.30	0.52
1:D:109:LYS:H	1:D:112:HIS:HD2	1.56	0.52
1:B:14:GLU:CD	1:B:397:LYS:CE	2.79	0.51
1:C:623:TYR:N	1:C:948:MET:HE1	2.26	0.51
1:B:847:VAL:O	1:B:847:VAL:HG12	2.09	0.51
1:C:681:ASP:OD1	1:C:683:THR:HB	2.10	0.51
1:B:300:THR:HG22	1:B:375:ARG:NH2	2.26	0.51
1:B:567:LEU:HB3	1:B:570:MET:CE	2.41	0.51
1:B:847:VAL:O	1:B:847:VAL:CG1	2.58	0.51
1:C:710:LYS:HG2	1:C:712:MET:CE	2.38	0.51
1:D:0:MET:CE	1:D:26:LEU:HD22	2.40	0.51
1:A:109:LYS:H	1:A:112:HIS:HD2	1.59	0.50
1:A:133:VAL:HG12	1:A:134:ILE:N	2.27	0.50
1:A:380:ASN:O	1:A:385:THR:HG21	2.12	0.50
1:A:915:MET:HE2	5:A:2210:HOH:O	2.12	0.50
1:C:380:ASN:O	1:C:385:THR:HG21	2.11	0.50
1:A:935:LYS:HE2	5:A:2209:HOH:O	2.12	0.50
1:D:133:VAL:HG12	1:D:134:ILE:N	2.27	0.50
1:D:836:GLN:OE1	1:D:877:SER:HB2	2.12	0.50
1:A:836:GLN:OE1	1:A:877:SER:HB2	2.12	0.50
1:D:410:ARG:NH2	5:D:2101:HOH:O	2.36	0.50
1:B:836:GLN:OE1	1:B:877:SER:HB2	2.12	0.50
1:D:14:GLU:CD	1:D:397:LYS:CE	2.81	0.50
1:C:14:GLU:CD	1:C:397:LYS:CE	2.80	0.49
1:A:1047:ASN:ND2	2:A:2001:FLC:HG1	2.24	0.49
1:A:653:LYS:O	1:A:656:GLU:HG2	2.13	0.49
1:B:133:VAL:HG12	1:B:134:ILE:N	2.27	0.49
1:D:479:ASN:ND2	1:D:1058:MET:H	2.11	0.49
1:D:297:VAL:HG23	5:D:2157:HOH:O	2.13	0.49
1:D:380:ASN:O	1:D:385:THR:HG21	2.12	0.49
1:C:674:CYS:CB	1:C:712:MET:HE1	2.42	0.49
1:B:373:GLY:O	1:B:400:THR:HA	2.13	0.49
1:B:653:LYS:O	1:B:656:GLU:HG2	2.13	0.48
1:A:819:ALA:HB3	5:A:2202:HOH:O	2.13	0.48
1:D:499:LYS:HG3	5:D:2167:HOH:O	2.13	0.48
1:A:464:ASP:N	1:A:464:ASP:OD2	2.38	0.48
1:D:216:ILE:HG13	1:D:266:MET:HG3	1.95	0.48
1:C:653:LYS:O	1:C:656:GLU:HG2	2.13	0.48
1:C:836:GLN:OE1	1:C:877:SER:HB2	2.13	0.48
1:B:380:ASN:O	1:B:385:THR:HG21	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:14:GLU:CG	1:B:397:LYS:HE3	2.44	0.48
1:D:300:THR:HG22	1:D:375:ARG:CZ	2.44	0.48
1:A:14:GLU:CD	1:A:397:LYS:CE	2.83	0.47
1:B:479:ASN:ND2	1:B:1058:MET:H	2.11	0.47
1:C:365:THR:HB	1:C:422:ARG:HB2	1.96	0.47
1:B:82:HIS:CD2	1:B:84:GLY:H	2.20	0.47
1:B:33:ILE:O	1:B:43:HIS:HE1	1.96	0.47
1:C:373:GLY:O	1:C:400:THR:HA	2.14	0.47
1:D:653:LYS:O	1:D:656:GLU:HG2	2.14	0.47
1:A:979:TYR:HB3	1:A:982:VAL:HG22	1.97	0.47
1:C:600:ARG:HD3	1:C:600:ARG:HA	1.63	0.47
1:D:14:GLU:CG	1:D:397:LYS:HE3	2.45	0.47
1:B:1046:LEU:HD23	1:B:1046:LEU:C	2.34	0.47
1:D:942:ASP:OD1	1:D:942:ASP:N	2.47	0.47
2:A:2001:FLC:OG2	2:A:2001:FLC:CBC	2.59	0.47
1:C:14:GLU:CG	1:C:397:LYS:HE3	2.45	0.47
1:D:128:LEU:HD12	1:D:128:LEU:O	2.15	0.47
1:A:294:ARG:NH2	5:A:2155:HOH:O	2.48	0.47
1:B:1047:ASN:HD22	2:B:2001:FLC:HG1	1.80	0.47
1:C:133:VAL:HG12	1:C:134:ILE:N	2.29	0.47
1:D:365:THR:HB	1:D:422:ARG:HB2	1.97	0.47
1:C:300:THR:HG22	1:C:375:ARG:CZ	2.45	0.46
1:D:819:ALA:N	5:D:2216:HOH:O	2.46	0.46
1:D:979:TYR:HB3	1:D:982:VAL:HG22	1.97	0.46
1:A:373:GLY:O	1:A:400:THR:HA	2.15	0.46
1:A:600:ARG:NH2	1:A:641:ASP:OD2	2.48	0.46
2:D:2001:FLC:OA1	2:D:2001:FLC:CBC	2.61	0.46
1:C:121:LYS:HA	1:C:124:GLU:CD	2.36	0.46
1:A:300:THR:HG22	1:A:375:ARG:NH2	2.30	0.46
1:D:1046:LEU:HD23	1:D:1046:LEU:C	2.36	0.46
1:D:971:LYS:HA	1:D:974:ILE:HG22	1.97	0.46
1:B:979:TYR:HB3	1:B:982:VAL:HG22	1.97	0.46
1:D:33:ILE:O	1:D:43:HIS:HE1	1.98	0.46
1:B:819:ALA:N	5:B:2147:HOH:O	2.49	0.46
1:D:82:HIS:CD2	1:D:84:GLY:H	2.20	0.46
1:B:300:THR:HG22	1:B:375:ARG:CZ	2.46	0.46
1:C:979:TYR:HB3	1:C:982:VAL:HG22	1.98	0.45
1:B:365:THR:HB	1:B:422:ARG:HB2	1.97	0.45
1:A:712:MET:HG2	1:A:873:VAL:HB	1.99	0.45
1:B:611:LEU:HD12	1:B:644:ARG:HG2	1.99	0.45
1:C:33:ILE:O	1:C:43:HIS:HE1	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:226:HIS:CD2	1:D:259:CYS:HB3	2.52	0.45
1:D:373:GLY:O	1:D:400:THR:HA	2.16	0.45
1:C:300:THR:HG22	1:C:375:ARG:NH2	2.32	0.45
1:D:600:ARG:HD3	1:D:600:ARG:HA	1.64	0.45
1:A:112:HIS:HE1	1:A:269:VAL:O	2.00	0.44
1:A:346:ARG:HB2	5:A:2236:HOH:O	2.17	0.44
1:A:365:THR:HB	1:A:422:ARG:HB2	1.99	0.44
1:A:97:ARG:HG3	1:A:97:ARG:HH11	1.82	0.44
1:D:819:ALA:O	1:D:821:ASN:ND2	2.51	0.44
1:D:819:ALA:HB3	5:D:2216:HOH:O	2.18	0.44
1:B:746:ASN:ND2	1:C:748:ILE:HG21	2.32	0.44
1:D:613:ARG:NH2	5:D:2251:HOH:O	2.50	0.44
1:B:44:ARG:O	1:B:44:ARG:HG2	2.17	0.44
1:B:600:ARG:HD3	1:B:600:ARG:HA	1.65	0.44
1:A:500:ILE:N	5:A:2163:HOH:O	2.38	0.44
1:B:680:ASP:OD1	1:B:723:ARG:NH1	2.51	0.44
1:D:601:LYS:HE3	5:D:2140:HOH:O	2.17	0.44
1:A:33:ILE:O	1:A:43:HIS:HE1	2.00	0.44
1:B:600:ARG:NH2	1:B:641:ASP:OD2	2.51	0.44
1:C:112:HIS:HE1	1:C:269:VAL:O	2.00	0.44
1:A:14:GLU:CG	1:A:397:LYS:HE3	2.48	0.44
1:B:112:HIS:HE1	1:B:269:VAL:O	2.01	0.44
1:C:1092:LYS:HB2	1:C:1092:LYS:HE2	1.73	0.44
1:C:97:ARG:HG3	1:C:97:ARG:HH11	1.83	0.44
1:A:300:THR:HG22	1:A:375:ARG:CZ	2.47	0.43
1:A:600:ARG:HA	1:A:600:ARG:HD3	1.64	0.43
1:D:420:ARG:NH1	2:D:2001:FLC:OA1	2.47	0.43
1:D:499:LYS:CG	5:D:2167:HOH:O	2.66	0.43
1:D:611:LEU:HD12	1:D:644:ARG:HG2	2.00	0.43
1:A:734:VAL:HG12	5:A:2146:HOH:O	2.19	0.43
1:B:118:ASP:HB3	1:B:121:LYS:CD	2.47	0.43
1:D:97:ARG:HG3	1:D:97:ARG:HH11	1.83	0.43
1:A:1067:ARG:CD	5:A:2135:HOH:O	2.66	0.43
1:C:600:ARG:NH2	1:C:641:ASP:OD2	2.51	0.43
1:D:670:GLU:OE1	1:D:737:HIS:ND1	2.51	0.43
1:A:819:ALA:O	1:A:821:ASN:ND2	2.51	0.43
1:B:819:ALA:HB3	5:B:2147:HOH:O	2.18	0.43
1:B:819:ALA:O	1:B:821:ASN:ND2	2.52	0.43
1:C:680:ASP:OD1	1:C:723:ARG:NH1	2.51	0.43
1:D:536:ASP:HA	1:D:764:VAL:O	2.19	0.43
1:A:44:ARG:O	1:A:44:ARG:HG2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:44:ARG:HG2	1:C:44:ARG:O	2.18	0.42
1:C:674:CYS:SG	1:C:712:MET:HE2	2.59	0.42
1:C:712:MET:HB3	1:C:712:MET:HE3	1.87	0.42
1:D:112:HIS:HE1	1:D:269:VAL:O	2.01	0.42
1:A:369:THR:HG22	1:A:418:GLU:HG2	2.02	0.42
1:C:123:LYS:HD2	1:C:133:VAL:CG1	2.49	0.42
1:D:680:ASP:OD1	1:D:723:ARG:NH1	2.53	0.42
1:A:680:ASP:OD1	1:A:723:ARG:NH1	2.53	0.42
1:A:942:ASP:N	1:A:942:ASP:OD1	2.52	0.42
1:A:83:PRO:HB2	1:A:89:SER:HA	2.02	0.42
1:C:369:THR:HG22	1:C:418:GLU:HG2	2.02	0.42
1:D:1013:THR:HG22	5:D:2274:HOH:O	2.19	0.42
1:D:760:ASP:C	1:D:761:ILE:HG13	2.40	0.42
1:C:60:ILE:HB	5:C:1305:HOH:O	2.19	0.42
1:D:0:MET:HE3	1:D:26:LEU:HD22	2.01	0.42
1:D:600:ARG:NH2	1:D:641:ASP:OD2	2.52	0.41
1:A:420:ARG:NH1	2:A:2001:FLC:OG2	2.52	0.41
1:B:570:MET:CE	1:B:573:PHE:HE1	2.33	0.41
1:C:819:ALA:O	1:C:821:ASN:ND2	2.53	0.41
1:A:44:ARG:CG	1:A:44:ARG:HH11	2.33	0.41
2:B:2001:FLC:CBC	2:B:2001:FLC:OG2	2.68	0.41
1:D:805:TYR:CZ	1:D:809:VAL:HG21	2.56	0.41
1:D:97:ARG:NH1	1:D:97:ARG:HG3	2.36	0.41
1:C:479:ASN:ND2	1:C:1058:MET:H	2.16	0.41
1:C:1067:ARG:CD	5:C:1319:HOH:O	2.68	0.41
1:C:129:ALA:O	1:C:264:LYS:HD3	2.21	0.41
1:D:129:ALA:O	1:D:264:LYS:HD3	2.21	0.41
1:D:44:ARG:CG	1:D:44:ARG:HH11	2.34	0.41
1:A:830:HIS:CD2	1:A:832:MET:HG3	2.56	0.41
1:A:312:GLN:HE22	1:B:410:ARG:HH21	1.69	0.41
1:C:209:PRO:O	1:C:446:ASN:HB2	2.21	0.41
1:A:777:SER:HB3	5:A:2111:HOH:O	2.21	0.41
1:B:670:GLU:OE1	1:B:737:HIS:ND1	2.50	0.41
1:A:226:HIS:CD2	1:A:259:CYS:HB3	2.55	0.40
1:A:974:ILE:HD13	1:A:974:ILE:N	2.36	0.40
1:D:209:PRO:O	1:D:446:ASN:HB2	2.21	0.40
1:A:479:ASN:ND2	1:A:1058:MET:H	2.17	0.40
1:A:901:GLY:O	1:A:935:LYS:NZ	2.54	0.40
1:D:0:MET:HE1	1:D:26:LEU:HD22	2.03	0.40
1:C:58:LYS:H	1:C:58:LYS:HG3	1.67	0.40
1:C:682:ASP:N	1:C:682:ASP:OD1	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:611:LEU:HD12	1:A:644:ARG:HG2	2.03	0.40
1:B:226:HIS:CD2	1:B:259:CYS:HB3	2.57	0.40
1:C:934:LEU:HA	1:C:934:LEU:HD23	1.84	0.40
1:D:44:ARG:O	1:D:44:ARG:HG2	2.19	0.40
1:D:682:ASP:OD1	1:D:682:ASP:N	2.53	0.40
1:A:129:ALA:O	1:A:264:LYS:HD3	2.21	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1066/1148 (93%)	1026 (96%)	40 (4%)	0	100	100
1	B	1068/1148 (93%)	1027 (96%)	41 (4%)	0	100	100
1	C	1075/1148 (94%)	1034 (96%)	41 (4%)	0	100	100
1	D	1066/1148 (93%)	1021 (96%)	45 (4%)	0	100	100
All	All	4275/4592 (93%)	4108 (96%)	167 (4%)	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	919/983 (94%)	879 (96%)	40 (4%)	33	57
1	B	916/983 (93%)	882 (96%)	34 (4%)	39	66
1	C	924/983 (94%)	889 (96%)	35 (4%)	38	64
1	D	921/983 (94%)	884 (96%)	37 (4%)	36	62
All	All	3680/3932 (94%)	3534 (96%)	146 (4%)	36	62

All (146) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	-1	HIS
1	A	42	PHE
1	A	44	ARG
1	A	70	ILE
1	A	92	ILE
1	A	96	ARG
1	A	110	SER
1	A	119	LYS
1	A	120	ILE
1	A	225	VAL
1	A	294	ARG
1	A	326	GLN
1	A	355	ASN
1	A	377	ASP
1	A	393	SER
1	A	464	ASP
1	A	549	THR
1	A	576	TRP
1	A	600	ARG
1	A	644	ARG
1	A	682	ASP
1	A	695	MET
1	A	712	MET
1	A	756	SER
1	A	791	GLN
1	A	842	GLN
1	A	865	GLN
1	A	915	MET
1	A	928	LYS
1	A	940	LEU
1	A	941	THR
1	A	942	ASP
1	A	947	LEU

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Mol	Chain	Res	Type
1	A	981	LYS
1	A	1053	ILE
1	A	1061	GLN
1	A	1092	LYS
1	A	1109	MET
1	A	1110	LYS
1	A	1119	PHE
1	B	2	ASN
1	B	42	PHE
1	B	44	ARG
1	B	70	ILE
1	B	92	ILE
1	B	110	SER
1	B	120	ILE
1	B	121	LYS
1	B	225	VAL
1	B	294	ARG
1	B	355	ASN
1	B	377	ASP
1	B	393	SER
1	B	549	THR
1	B	576	TRP
1	B	600	ARG
1	B	644	ARG
1	B	663	ARG
1	B	682	ASP
1	B	695	MET
1	B	712	MET
1	B	756	SER
1	B	791	GLN
1	B	842	GLN
1	B	865	GLN
1	B	915	MET
1	B	940	LEU
1	B	941	THR
1	B	942	ASP
1	B	947	LEU
1	B	1053	ILE
1	B	1059	ASN
1	B	1092	LYS
1	B	1119	PHE
1	C	-1	HIS

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Mol	Chain	Res	Type
1	C	42	PHE
1	C	44	ARG
1	C	70	ILE
1	C	92	ILE
1	C	110	SER
1	C	119	LYS
1	C	120	ILE
1	C	121	LYS
1	C	137	SER
1	C	202	VAL
1	C	225	VAL
1	C	294	ARG
1	C	377	ASP
1	C	393	SER
1	C	549	THR
1	C	576	TRP
1	C	600	ARG
1	C	613	ARG
1	C	644	ARG
1	C	695	MET
1	C	712	MET
1	C	756	SER
1	C	791	GLN
1	C	842	GLN
1	C	865	GLN
1	C	915	MET
1	C	918	ILE
1	C	940	LEU
1	C	941	THR
1	C	947	LEU
1	C	1053	ILE
1	C	1092	LYS
1	C	1110	LYS
1	C	1119	PHE
1	D	42	PHE
1	D	44	ARG
1	D	60	ILE
1	D	70	ILE
1	D	92	ILE
1	D	110	SER
1	D	120	ILE
1	D	128	LEU

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Mol	Chain	Res	Type
1	D	225	VAL
1	D	294	ARG
1	D	355	ASN
1	D	357	MET
1	D	393	SER
1	D	425	LYS
1	D	549	THR
1	D	576	TRP
1	D	600	ARG
1	D	644	ARG
1	D	695	MET
1	D	712	MET
1	D	756	SER
1	D	791	GLN
1	D	842	GLN
1	D	865	GLN
1	D	874	THR
1	D	915	MET
1	D	928	LYS
1	D	940	LEU
1	D	941	THR
1	D	942	ASP
1	D	947	LEU
1	D	981	LYS
1	D	1053	ILE
1	D	1059	ASN
1	D	1092	LYS
1	D	1110	LYS
1	D	1119	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (62) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	43	HIS
1	A	68	ASN
1	A	82	HIS
1	A	112	HIS
1	A	223	ASN
1	A	292	ASN
1	A	312	GLN
1	A	333	GLN
1	A	383	GLN

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Mol	Chain	Res	Type
1	A	415	ASN
1	A	479	ASN
1	A	746	ASN
1	A	821	ASN
1	A	830	HIS
1	B	43	HIS
1	B	68	ASN
1	B	82	HIS
1	B	112	HIS
1	B	223	ASN
1	B	292	ASN
1	B	312	GLN
1	B	333	GLN
1	B	383	GLN
1	B	415	ASN
1	B	479	ASN
1	B	529	GLN
1	B	746	ASN
1	B	821	ASN
1	B	824	GLN
1	B	830	HIS
1	B	1049	GLN
1	C	43	HIS
1	C	68	ASN
1	C	82	HIS
1	C	112	HIS
1	C	223	ASN
1	C	292	ASN
1	C	312	GLN
1	C	333	GLN
1	C	383	GLN
1	C	415	ASN
1	C	479	ASN
1	C	505	GLN
1	C	746	ASN
1	C	821	ASN
1	C	830	HIS
1	C	1049	GLN
1	D	43	HIS
1	D	68	ASN
1	D	82	HIS
1	D	112	HIS

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Mol	Chain	Res	Type
1	D	223	ASN
1	D	292	ASN
1	D	312	GLN
1	D	333	GLN
1	D	383	GLN
1	D	415	ASN
1	D	479	ASN
1	D	505	GLN
1	D	746	ASN
1	D	821	ASN
1	D	830	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 11 ligands modelled in this entry, 4 are monoatomic - leaving 7 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	FLC	A	2001	-	3,12,12	1.55	1 (33%)	3,17,17	3.07	2 (66%)
4	2BA	A	2003	-	44,50,50	1.29	1 (2%)	46,78,78	2.61	12 (26%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	2BA	A	2004	-	44,50,50	1.51	7 (15%)	46,78,78	2.65	13 (28%)
2	FLC	B	2001	-	3,12,12	1.24	0	3,17,17	2.66	1 (33%)
4	2BA	C	1201	-	44,50,50	1.16	5 (11%)	46,78,78	2.32	11 (23%)
2	FLC	C	1202	-	3,12,12	1.03	0	3,17,17	4.44	2 (66%)
2	FLC	D	2001	-	3,12,12	1.34	1 (33%)	3,17,17	2.97	1 (33%)

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	FLC	A	2001	-	-	0/6/16/16	0/0/0/0
4	2BA	A	2003	-	-	0/22/62/62	0/6/7/7
4	2BA	A	2004	-	-	0/22/62/62	0/6/7/7
2	FLC	B	2001	-	-	0/6/16/16	0/0/0/0
4	2BA	C	1201	-	-	0/22/62/62	0/6/7/7
2	FLC	C	1202	-	-	0/6/16/16	0/0/0/0
2	FLC	D	2001	-	-	0/6/16/16	0/0/0/0

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	1201	2BA	C5-N7	-2.13	1.32	1.39
4	C	1201	2BA	C2'-C1'	-2.08	1.50	1.53
4	C	1201	2BA	O4'-C1'	2.01	1.44	1.41
2	D	2001	FLC	OHB-CB	2.31	1.46	1.43
4	A	2004	2BA	C51-C41	2.39	1.45	1.40
4	A	2004	2BA	C2-N3	2.45	1.36	1.32
2	A	2001	FLC	OHB-CB	2.53	1.47	1.43
4	A	2004	2BA	C5-C4	2.61	1.46	1.40
4	A	2003	2BA	C5-C4	2.63	1.46	1.40
4	A	2004	2BA	C2'-C1'	2.89	1.58	1.53
4	C	1201	2BA	C51-C41	2.90	1.47	1.40
4	C	1201	2BA	C5-C4	3.01	1.47	1.40
4	A	2004	2BA	O2'-C2'	3.44	1.50	1.43
4	A	2004	2BA	O4'1-C1'1	4.22	1.47	1.41
4	A	2004	2BA	O4'-C1'	4.43	1.47	1.41

All (42) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	2003	2BA	N31-C21-N11	-10.40	119.80	128.86
4	A	2004	2BA	N31-C21-N11	-10.25	119.93	128.86
4	A	2003	2BA	N3-C2-N1	-9.33	120.74	128.86
4	C	1201	2BA	N31-C21-N11	-9.22	120.83	128.86
4	A	2004	2BA	N3-C2-N1	-8.59	121.38	128.86
4	C	1201	2BA	N3-C2-N1	-7.70	122.15	128.86
2	C	1202	FLC	CB-CA-CAC	-7.03	103.96	114.95
2	D	2001	FLC	CB-CA-CAC	-4.82	107.42	114.95
2	A	2001	FLC	CB-CG-CGC	-4.58	107.80	114.95
2	B	2001	FLC	CB-CG-CGC	-4.22	108.36	114.95
4	A	2004	2BA	C1'-N9-C4	-3.56	120.48	126.64
4	A	2003	2BA	C51-C61-N61	-3.28	113.77	120.47
4	A	2003	2BA	O2'1-C2'1-C3'1	-3.19	102.10	111.18
4	A	2003	2BA	C2'-C3'-C4'	-2.93	97.99	103.23
4	A	2003	2BA	C1'1-N91-C41	-2.93	121.58	126.64
4	A	2004	2BA	O2P1-P1-O3'	-2.53	96.30	106.49
4	A	2003	2BA	C4'1-O4'1-C1'1	-2.53	107.08	109.77
4	C	1201	2BA	C2'-C3'-C4'	-2.44	98.87	103.23
4	A	2004	2BA	C5-C6-N6	-2.30	115.78	120.47
4	A	2004	2BA	C1'1-N91-C41	-2.27	122.71	126.64
4	C	1201	2BA	C2'1-C3'1-C4'1	-2.18	99.33	103.23
4	C	1201	2BA	O2P1-P1-O5'1	-2.11	98.16	108.14
4	C	1201	2BA	O2'1-C2'1-C1'1	-2.05	105.20	111.61
4	A	2004	2BA	O3'1-P-O1P	-2.00	101.57	109.46
4	A	2003	2BA	O2P1-P1-O1P1	2.02	122.74	112.28
4	A	2003	2BA	C21-N11-C61	2.02	122.31	118.77
4	C	1201	2BA	O2P-P-O1P	2.07	122.98	112.28
4	A	2004	2BA	O5'-P-O1P	2.15	117.94	109.25
4	A	2004	2BA	C4'-O4'-C1'	2.21	112.12	109.77
4	C	1201	2BA	C2-N1-C6	2.32	122.82	118.77
4	A	2003	2BA	C41-C51-N71	2.49	111.81	109.41
4	A	2004	2BA	O2P1-P1-O1P1	2.49	125.18	112.28
4	A	2004	2BA	O3'1-C3'1-C4'1	2.53	119.54	110.04
2	A	2001	FLC	CB-CA-CAC	2.62	119.05	114.95
4	C	1201	2BA	C21-N11-C61	2.68	123.45	118.77
2	C	1202	FLC	CB-CG-CGC	2.84	119.38	114.95
4	C	1201	2BA	N6-C6-N1	2.99	124.69	118.77
4	C	1201	2BA	C3'-C2'-C1'	3.10	106.92	99.95
4	A	2003	2BA	N61-C61-N11	3.19	125.09	118.77
4	A	2003	2BA	O3'1-P-O1P	3.46	123.08	109.46
4	A	2004	2BA	O2'-C2'-C1'	4.45	125.54	111.61
4	A	2004	2BA	C2'-C3'-C4'	5.44	112.96	103.23

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	2001	FLC	4	0
2	B	2001	FLC	5	0
2	C	1202	FLC	1	0
2	D	2001	FLC	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

### 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<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	1072/1148 (93%)	-0.08	33 (3%)	49	52	17, 47, 86, 120	0
1	B	1074/1148 (93%)	0.02	43 (4%)	39	41	34, 56, 100, 128	0
1	C	1081/1148 (94%)	0.05	45 (4%)	37	39	30, 57, 98, 130	0
1	D	1072/1148 (93%)	-0.12	22 (2%)	64	66	20, 45, 84, 123	0
All	All	4299/4592 (93%)	-0.03	143 (3%)	47	50	17, 51, 94, 130	0

All (143) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	906	PHE	7.0
1	C	933	VAL	6.5
1	C	202	VAL	6.5
1	C	904	ILE	6.1
1	C	201	TYR	5.8
1	B	898	TYR	5.5
1	B	897	VAL	5.5
1	D	206	VAL	5.3
1	D	820	LEU	5.0
1	B	892	LEU	4.9
1	D	135	PRO	4.9
1	B	901	GLY	4.8
1	B	207	MET	4.8
1	C	929	LEU	4.8
1	B	205	CYS	4.7
1	C	137	SER	4.7
1	C	135	PRO	4.7
1	C	207	MET	4.3
1	A	134	ILE	4.3
1	D	280	LEU	4.3
1	A	820	LEU	4.2

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Mol	Chain	Res	Type	RSRZ
1	D	205	CYS	4.0
1	C	934	LEU	4.0
1	C	206	VAL	4.0
1	C	901	GLY	4.0
1	D	1143	VAL	3.9
1	C	903	THR	3.9
1	A	207	MET	3.9
1	B	120	ILE	3.7
1	D	207	MET	3.7
1	B	932	LEU	3.7
1	A	206	VAL	3.7
1	B	820	LEU	3.6
1	B	887	MET	3.6
1	A	821	ASN	3.6
1	C	200	VAL	3.6
1	B	906	PHE	3.5
1	C	127	LEU	3.5
1	B	204	LYS	3.5
1	A	118	ASP	3.5
1	B	135	PRO	3.5
1	C	926	PRO	3.5
1	B	128	LEU	3.5
1	B	933	VAL	3.5
1	C	134	ILE	3.4
1	A	463	ARG	3.4
1	B	929	LEU	3.3
1	A	1097	VAL	3.3
1	C	905	ASP	3.3
1	A	1092	LYS	3.2
1	D	134	ILE	3.2
1	C	205	CYS	3.2
1	A	128	LEU	3.2
1	C	203	GLU	3.2
1	D	128	LEU	3.2
1	A	1119	PHE	3.2
1	B	287	TYR	3.1
1	A	1100	GLY	3.1
1	A	1103	LEU	3.0
1	D	821	ASN	3.0
1	B	237	ARG	3.0
1	C	932	LEU	3.0
1	C	925	PHE	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	129	ALA	3.0
1	B	1100	GLY	3.0
1	D	120	ILE	2.9
1	A	1094	GLY	2.9
1	C	1096	SER	2.9
1	A	1090	VAL	2.9
1	A	1106	THR	2.9
1	A	1089	VAL	2.9
1	B	1143	VAL	2.9
1	B	893	SER	2.9
1	B	206	VAL	2.8
1	C	1089	VAL	2.8
1	B	280	LEU	2.8
1	C	374	VAL	2.7
1	A	819	ALA	2.7
1	C	899	GLU	2.7
1	C	953	PHE	2.7
1	A	1116	GLN	2.7
1	B	937	ARG	2.7
1	C	951	VAL	2.6
1	B	1094	GLY	2.6
1	B	903	THR	2.6
1	B	123	LYS	2.6
1	A	1091	VAL	2.6
1	A	280	LEU	2.6
1	C	928	LYS	2.6
1	C	136	GLY	2.6
1	C	897	VAL	2.6
1	B	894	GLU	2.6
1	C	734	VAL	2.5
1	D	399	CYS	2.5
1	B	958	ALA	2.5
1	B	463	ARG	2.5
1	B	902	ASP	2.5
1	A	208	ASN	2.5
1	B	282	GLU	2.5
1	A	1120	ASP	2.5
1	C	461	HIS	2.4
1	A	1123	VAL	2.4
1	D	463	ARG	2.4
1	D	1102	PRO	2.4
1	C	900	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	122	ALA	2.4
1	A	1104	LEU	2.4
1	B	732	VAL	2.3
1	D	396	VAL	2.3
1	B	904	ILE	2.3
1	D	1123	VAL	2.3
1	B	134	ILE	2.3
1	C	287	TYR	2.3
1	C	914	PHE	2.3
1	B	133	VAL	2.3
1	D	958	ALA	2.2
1	C	927	GLU	2.2
1	A	127	LEU	2.2
1	D	1100	GLY	2.2
1	D	287	TYR	2.2
1	B	725	ILE	2.2
1	A	287	TYR	2.2
1	B	1090	VAL	2.2
1	D	546	LEU	2.2
1	A	822	SER	2.2
1	B	867	PHE	2.1
1	C	1061	GLN	2.1
1	C	444	ASN	2.1
1	C	463	ARG	2.1
1	A	1115	ILE	2.1
1	B	238	HIS	2.1
1	D	1105	ILE	2.1
1	B	127	LEU	2.1
1	D	819	ALA	2.1
1	B	934	LEU	2.1
1	A	1122	GLU	2.1
1	C	707	LEU	2.0
1	C	1038	GLY	2.0
1	A	284	ASP	2.0
1	C	1090	VAL	2.0
1	C	937	ARG	2.0
1	B	966	TYR	2.0
1	C	1092	LYS	2.0

## 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 [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	MN	B	2002	1/1	0.79	0.16	0.63	94,94,94,94	0
3	MN	C	1203	1/1	0.98	0.15	-0.02	85,85,85,85	0
4	2BA	A	2003	44/44	0.99	0.12	-0.03	21,32,38,44	0
3	MN	D	2002	1/1	0.93	0.16	-0.08	75,75,75,75	0
4	2BA	C	1201	44/44	0.98	0.11	-0.31	33,49,59,65	0
2	FLC	B	2001	13/13	0.91	0.15	-0.39	46,53,59,69	0
2	FLC	A	2001	13/13	0.95	0.12	-0.71	43,55,59,62	0
2	FLC	D	2001	13/13	0.98	0.08	-1.33	41,46,56,59	0
3	MN	A	2002	1/1	0.87	0.14	-1.74	72,72,72,72	0
2	FLC	C	1202	13/13	0.95	0.12	-2.38	47,54,59,62	0
4	2BA	A	2004	44/44	0.89	0.16	-	35,71,86,94	0

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

There are no such residues in this entry.