



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:49 PM GMT

PDB ID : 4PZE
Title : Crystal structure of (S)-3-hydroxybutyryl-CoA dehydrogenase PaaH1 in complex with acetoacetyl-CoA
Authors : Kim, J.; Chang, J.H.; Kim, K.J.
Deposited on : 2014-03-29
Resolution : 2.70 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 ⓘ 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 (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

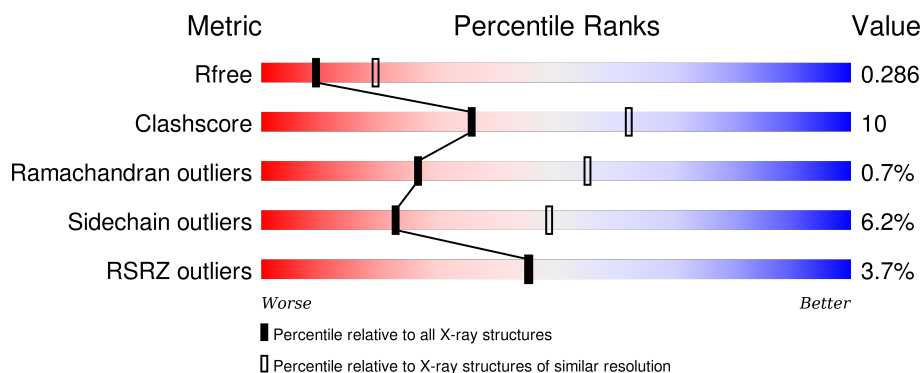
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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 $\leq 5\%$. 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	284	<div> <div>5%</div> <div>80%</div> <div>17%</div> <div>.</div> </div>
1	B	284	<div> <div>3%</div> <div>73%</div> <div>23%</div> <div>..</div> </div>
1	C	284	<div> <div>%</div> <div>82%</div> <div>15%</div> <div>.</div> </div>
1	D	284	<div> <div>5%</div> <div>81%</div> <div>17%</div> <div>.</div> </div>
1	E	284	<div> <div>7%</div> <div>71%</div> <div>27%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	284	
1	G	284	
1	H	284	
1	I	284	

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
2	CAA	A	301	-	-	-	X
2	CAA	B	301	-	-	-	X
2	CAA	C	301	-	-	-	X
2	CAA	D	301	-	-	-	X
2	CAA	E	301	-	-	-	X
2	CAA	F	301	-	-	-	X
2	CAA	G	301	-	-	-	X
2	CAA	H	301	-	-	-	X
2	CAA	I	301	-	-	-	X

2 Entry composition

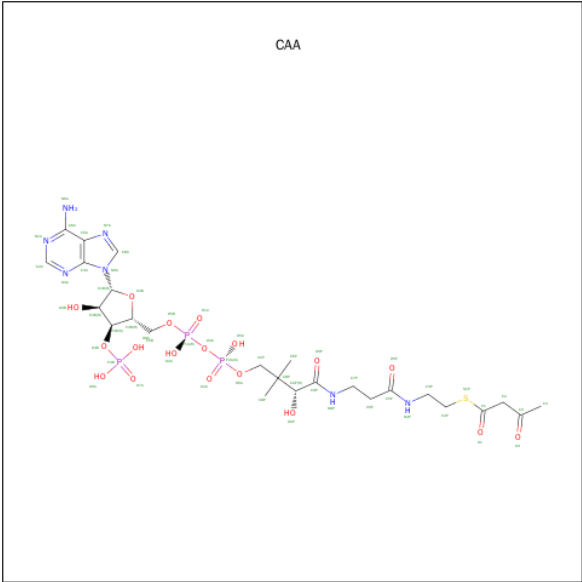
There are 3 unique types of molecules in this entry. The entry contains 19517 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 3-Hydroxyacyl-CoA dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	283	Total	C	N	O	S	0	0	0
			2102	1331	355	400	16			
1	B	283	Total	C	N	O	S	0	0	0
			2102	1331	355	400	16			
1	C	283	Total	C	N	O	S	0	0	0
			2102	1331	355	400	16			
1	D	283	Total	C	N	O	S	0	0	0
			2102	1331	355	400	16			
1	E	283	Total	C	N	O	S	0	0	0
			2102	1331	355	400	16			
1	F	283	Total	C	N	O	S	0	0	0
			2102	1331	355	400	16			
1	G	283	Total	C	N	O	S	0	0	0
			2102	1331	355	400	16			
1	H	283	Total	C	N	O	S	0	0	0
			2102	1331	355	400	16			
1	I	283	Total	C	N	O	S	0	0	0
			2102	1331	355	400	16			

- Molecule 2 is ACETOACETYL-COENZYME A (three-letter code: CAA) (formula: C₂₅H₄₀N₇O₁₈P₃S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	S	0	0
			54	25	7	18	3	1		
2	B	1	Total	C	N	O	P	S	0	0
			54	25	7	18	3	1		
2	C	1	Total	C	N	O	P	S	0	0
			54	25	7	18	3	1		
2	D	1	Total	C	N	O	P	S	0	0
			54	25	7	18	3	1		
2	E	1	Total	C	N	O	P	S	0	0
			54	25	7	18	3	1		
2	F	1	Total	C	N	O	P	S	0	0
			54	25	7	18	3	1		
2	G	1	Total	C	N	O	P	S	0	0
			54	25	7	18	3	1		
2	H	1	Total	C	N	O	P	S	0	0
			54	25	7	18	3	1		
2	I	1	Total	C	N	O	P	S	0	0
			54	25	7	18	3	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	13	Total	O	0	0
			13	13		
3	B	8	Total	O	0	0
			8	8		
3	C	20	Total	O	0	0
			20	20		

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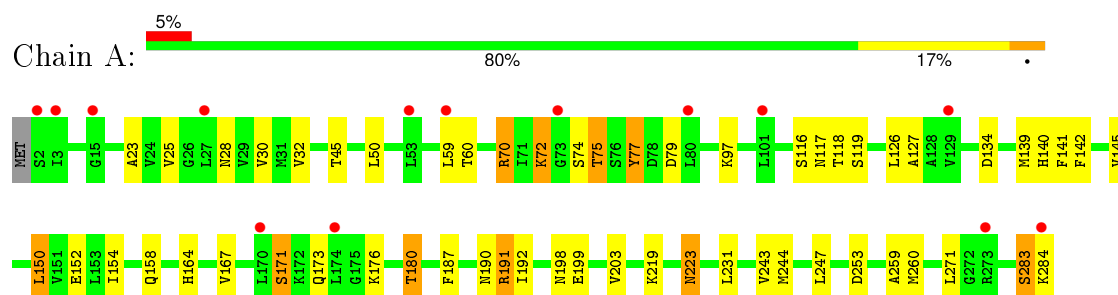
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	D	10	Total 10	O 10	0	0
3	E	15	Total 15	O 15	0	0
3	F	23	Total 23	O 23	0	0
3	G	11	Total 11	O 11	0	0
3	H	5	Total 5	O 5	0	0
3	I	8	Total 8	O 8	0	0

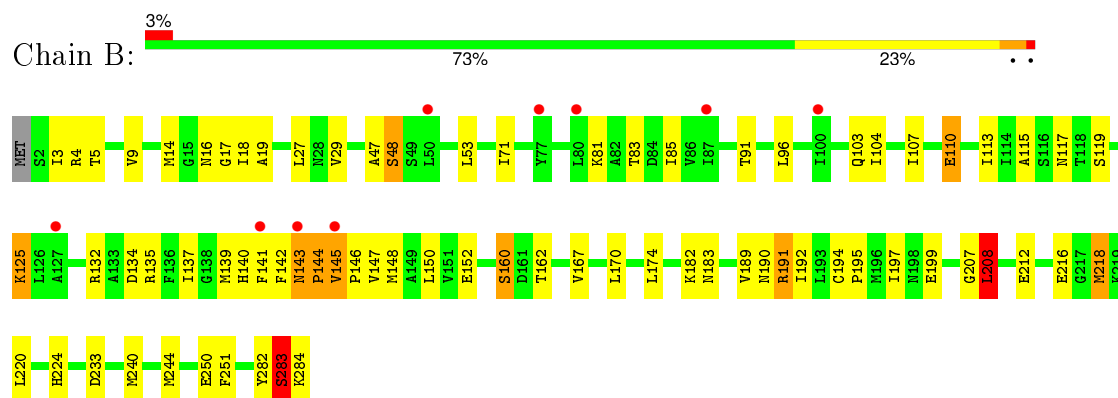
3 Residue-property plots [i](#)

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.

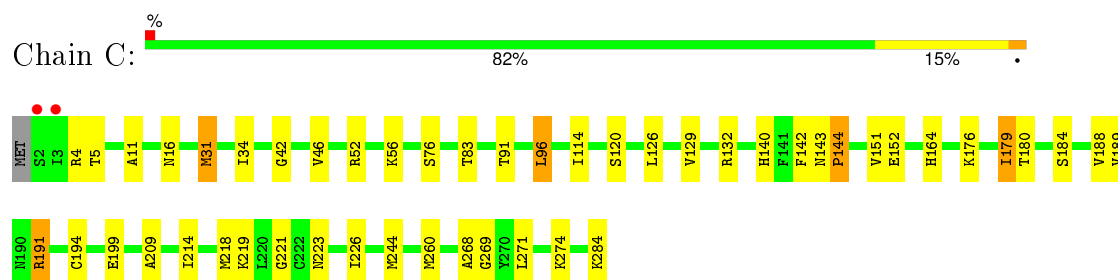
- Molecule 1: 3-Hydroxyacyl-CoA dehydrogenase



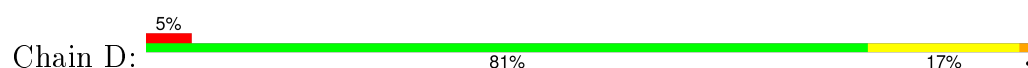
- Molecule 1: 3-Hydroxyacyl-CoA dehydrogenase

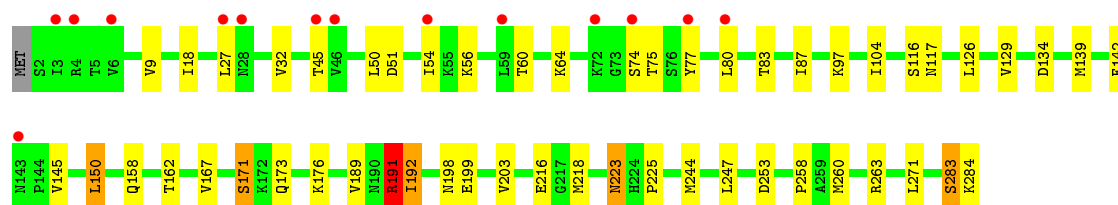


- Molecule 1: 3-Hydroxyacyl-CoA dehydrogenase

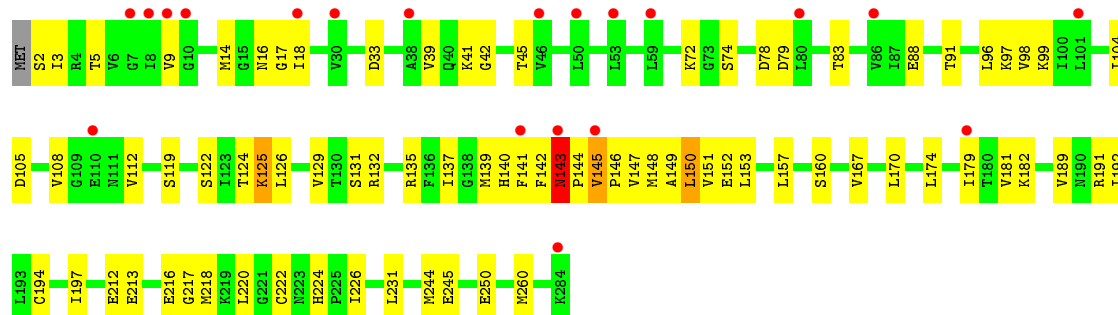


- Molecule 1: 3-Hydroxyacyl-CoA dehydrogenase

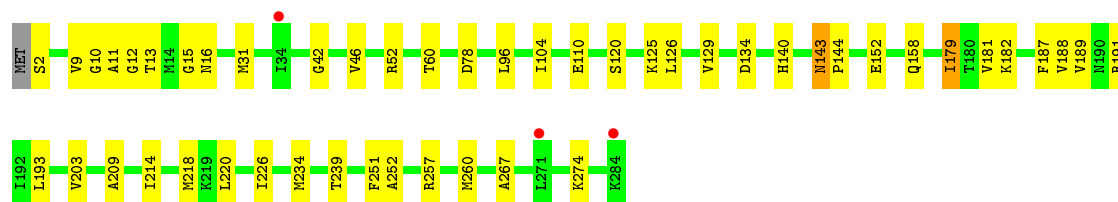
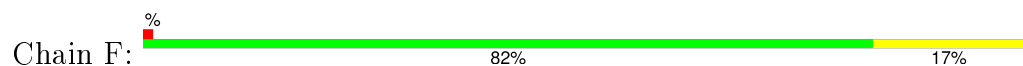




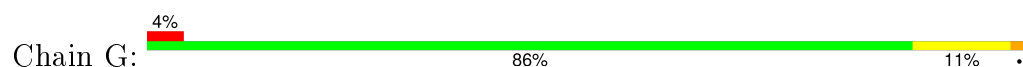
• Molecule 1: 3-Hydroxyacyl-CoA dehydrogenase



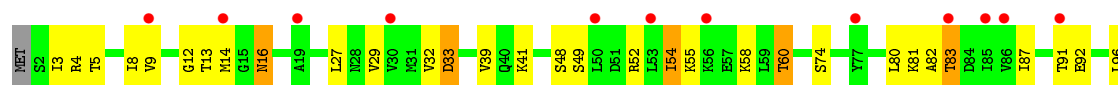
• Molecule 1: 3-Hydroxyacyl-CoA dehydrogenase

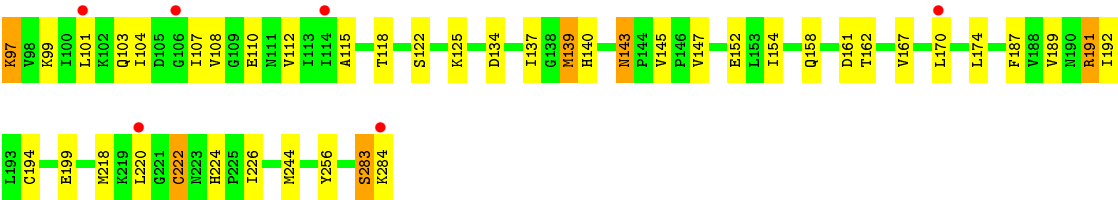


• Molecule 1: 3-Hydroxyacyl-CoA dehydrogenase

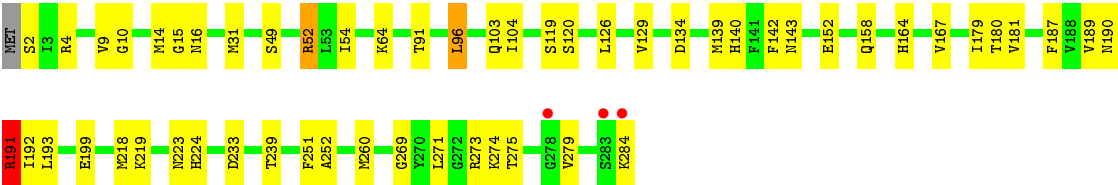
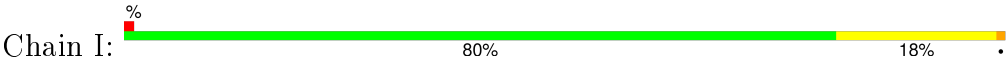


• Molecule 1: 3-Hydroxyacyl-CoA dehydrogenase





● Molecule 1: 3-Hydroxyacyl-CoA dehydrogenase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	234.24Å 135.37Å 97.36Å 90.00° 90.09° 90.00°	Depositor
Resolution (Å)	50.00 – 2.70 32.78 – 2.70	Depositor EDS
% Data completeness (in resolution range)	90.7 (50.00-2.70) 90.5 (32.78-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.23 (at 2.68Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.210 , 0.285 0.215 , 0.286	Depositor DCC
R_{free} test set	3802 reflections (5.29%)	DCC
Wilson B-factor (Å ²)	52.2	Xtriage
Anisotropy	0.726	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 35.1	EDS
Estimated twinning fraction	0.023 for -1/2*h+3/2*k,1/2*h+1/2*k,-l 0.024 for -1/2*h-3/2*k,-1/2*h+1/2*k,-l 0.449 for 1/2*h+3/2*k,1/2*h-1/2*k,-l 0.449 for 1/2*h-3/2*k,-1/2*h-1/2*k,-l 0.023 for -h,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 75743 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	19517	wwPDB-VP
Average B, all atoms (Å ²)	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.20% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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: CAA

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	0.55	0/2128	0.77	4/2879 (0.1%)
1	B	0.53	0/2128	0.78	6/2879 (0.2%)
1	C	0.59	0/2128	0.77	2/2879 (0.1%)
1	D	0.53	0/2128	0.74	4/2879 (0.1%)
1	E	0.57	0/2128	0.76	1/2879 (0.0%)
1	F	0.61	0/2128	0.75	0/2879
1	G	0.53	0/2128	0.73	2/2879 (0.1%)
1	H	0.53	0/2128	0.72	0/2879
1	I	0.60	0/2128	0.75	1/2879 (0.0%)
All	All	0.56	0/19152	0.75	20/25911 (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
1	B	0	2
1	C	0	1
1	D	0	1
1	G	0	1
All	All	0	6

There are no bond length outliers.

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	208	LEU	CB-CA-C	10.38	129.91	110.20
1	A	253	ASP	CB-CG-OD1	9.28	126.65	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	283	SER	CB-CA-C	8.47	126.19	110.10
1	C	184	SER	CB-CA-C	7.36	124.08	110.10
1	D	253	ASP	CB-CG-OD1	6.88	124.49	118.30
1	D	191	ARG	NE-CZ-NH2	-6.59	117.01	120.30
1	B	218	MET	CG-SD-CE	-6.15	90.36	100.20
1	B	143	ASN	C-N-CD	6.07	141.14	128.40
1	B	145	VAL	C-N-CD	6.05	141.10	128.40
1	E	145	VAL	C-N-CD	6.02	141.05	128.40
1	D	191	ARG	NE-CZ-NH1	5.75	123.18	120.30
1	D	253	ASP	CB-CG-OD2	-5.55	113.31	118.30
1	G	191	ARG	NE-CZ-NH2	-5.46	117.57	120.30
1	A	191	ARG	NE-CZ-NH2	-5.45	117.58	120.30
1	B	208	LEU	C-N-CA	5.42	135.25	121.70
1	G	191	ARG	NE-CZ-NH1	5.39	123.00	120.30
1	I	191	ARG	NE-CZ-NH2	-5.37	117.62	120.30
1	A	191	ARG	NE-CZ-NH1	5.18	122.89	120.30
1	A	118	THR	CB-CA-C	5.15	125.50	111.60
1	C	31	MET	CG-SD-CE	-5.06	92.10	100.20

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	142	PHE	Peptide
1	B	208	LEU	Peptide
1	B	283	SER	Peptide
1	C	142	PHE	Peptide
1	D	142	PHE	Peptide
1	G	142	PHE	Peptide

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	2102	0	2187	33	0
1	B	2102	0	2187	69	0
1	C	2102	0	2187	38	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	2102	0	2187	43	0
1	E	2102	0	2187	81	0
1	F	2102	0	2187	36	0
1	G	2102	0	2187	37	0
1	H	2102	0	2187	51	0
1	I	2102	0	2187	42	0
2	A	54	0	36	2	0
2	B	54	0	36	1	0
2	C	54	0	36	2	0
2	D	54	0	36	0	0
2	E	54	0	36	1	0
2	F	54	0	36	9	0
2	G	54	0	36	1	0
2	H	54	0	36	1	0
2	I	54	0	36	10	0
3	A	13	0	0	1	0
3	B	8	0	0	1	0
3	C	20	0	0	2	0
3	D	10	0	0	2	0
3	E	15	0	0	4	0
3	F	23	0	0	2	0
3	G	11	0	0	0	0
3	H	5	0	0	1	0
3	I	8	0	0	2	0
All	All	19517	0	20007	384	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 10.

All (384) 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:142:PHE:CE1	1:B:150:LEU:HD23	1.66	1.29
1:B:142:PHE:CZ	1:B:150:LEU:HD23	1.82	1.13
1:E:140:HIS:HD2	1:E:152:GLU:OE1	1.49	0.95
1:E:144:PRO:HG2	1:E:147:VAL:HB	1.46	0.95
1:B:144:PRO:HG2	1:B:148:MET:HG2	1.50	0.92
1:E:17:GLY:C	1:E:145:VAL:HG21	1.92	0.90
1:B:14:MET:CE	1:B:141:PHE:O	2.21	0.88
1:B:14:MET:HE2	1:B:141:PHE:O	1.74	0.86
1:E:144:PRO:HD2	1:E:148:MET:HG2	1.55	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:144:PRO:HD2	1:B:148:MET:HG2	1.58	0.85
1:B:144:PRO:CD	1:B:148:MET:HG2	2.07	0.85
1:B:144:PRO:CG	1:B:148:MET:HG2	2.05	0.85
1:C:176:LYS:HE2	3:C:406:HOH:O	1.76	0.84
1:E:17:GLY:C	1:E:145:VAL:CG2	2.47	0.83
1:E:17:GLY:HA3	1:E:145:VAL:CG2	2.10	0.82
1:E:140:HIS:HB3	1:E:152:GLU:HB2	1.61	0.81
1:E:141:PHE:CG	1:E:145:VAL:HG12	2.14	0.81
1:H:218:MET:SD	3:I:404:HOH:O	2.40	0.79
1:D:218:MET:HA	1:D:218:MET:HE2	1.65	0.78
1:G:194:CYS:C	1:G:244:MET:HE1	2.04	0.78
1:E:143:ASN:HB3	1:E:144:PRO:HD3	1.66	0.77
1:B:283:SER:CA	1:B:284:LYS:HB3	2.13	0.77
1:E:141:PHE:CD2	1:E:145:VAL:HG12	2.19	0.77
1:B:144:PRO:HB2	1:B:147:VAL:HB	1.65	0.77
1:B:142:PHE:HE1	1:B:150:LEU:HD23	1.41	0.77
1:E:5:THR:HG22	1:E:83:THR:HG22	1.65	0.77
1:E:140:HIS:CD2	1:E:152:GLU:OE1	2.36	0.76
1:E:192:ILE:HD12	1:F:218:MET:HE3	1.68	0.76
1:B:283:SER:HA	1:B:284:LYS:HB3	1.68	0.75
1:E:17:GLY:CA	1:E:145:VAL:CG2	2.65	0.74
1:E:18:ILE:N	1:E:145:VAL:HG21	2.03	0.74
1:B:142:PHE:CZ	1:B:150:LEU:CD2	2.68	0.73
1:B:144:PRO:HD2	1:B:148:MET:CG	2.19	0.73
1:H:39:VAL:HG21	1:H:74:SER:O	1.90	0.71
1:F:16:ASN:HA	1:F:31:MET:HE3	1.74	0.70
1:E:17:GLY:HA3	1:E:145:VAL:HG22	1.73	0.70
1:B:17:GLY:C	1:B:145:VAL:HG11	2.11	0.70
1:B:14:MET:HE1	1:B:141:PHE:O	1.92	0.69
1:C:176:LYS:CE	3:C:406:HOH:O	2.36	0.69
1:I:152:GLU:HA	1:I:179:ILE:HG22	1.75	0.69
1:C:16:ASN:HA	1:C:31:MET:HE3	1.75	0.68
1:E:149:ALA:O	1:F:220:LEU:HD13	1.93	0.68
1:D:189:VAL:HA	1:G:218:MET:CE	2.25	0.67
1:E:141:PHE:CB	1:E:145:VAL:HG12	2.24	0.67
1:G:195:PRO:HA	1:G:244:MET:HE3	1.77	0.67
1:C:126:LEU:O	1:C:129:VAL:HG22	1.95	0.67
1:A:244:MET:HE2	1:A:244:MET:HA	1.76	0.67
1:H:80:LEU:O	1:H:82:ALA:N	2.27	0.66
1:D:117:ASN:HA	1:D:139:MET:O	1.96	0.66
1:I:140:HIS:CE1	2:I:301:CAA:H4'1	2.31	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:192:ILE:HD12	1:I:218:MET:HE3	1.76	0.65
1:E:141:PHE:HB3	1:E:145:VAL:HG12	1.79	0.65
1:B:191:ARG:NH1	1:C:199:GLU:OE2	2.30	0.65
1:E:143:ASN:CB	1:E:144:PRO:HD3	2.26	0.64
1:D:244:MET:HA	1:D:244:MET:HE2	1.79	0.64
1:D:216:GLU:OE1	1:G:177:TYR:CE1	2.51	0.64
1:H:199:GLU:OE2	1:I:191:ARG:NH1	2.31	0.64
1:C:56:LYS:NZ	2:C:301:CAA:O2B	2.31	0.63
1:G:117:ASN:HA	1:G:139:MET:O	1.98	0.63
1:E:39:VAL:HG21	1:E:74:SER:O	1.98	0.63
1:E:144:PRO:HB2	1:E:146:PRO:HD2	1.81	0.63
1:B:283:SER:HA	1:B:284:LYS:CB	2.27	0.62
1:I:16:ASN:HA	1:I:31:MET:HE3	1.81	0.62
1:H:14:MET:SD	1:H:143:ASN:ND2	2.72	0.62
1:I:140:HIS:CE1	2:I:301:CAA:C4	2.83	0.62
1:B:140:HIS:HB3	1:B:152:GLU:HB2	1.80	0.62
1:B:142:PHE:CE1	1:B:150:LEU:CD2	2.62	0.62
1:E:143:ASN:HB3	1:E:144:PRO:CD	2.28	0.61
1:F:234:MET:HE3	2:F:301:CAA:H121	1.83	0.61
1:B:192:ILE:HD12	1:C:218:MET:HE3	1.81	0.61
1:D:199:GLU:CG	1:G:192:ILE:HG22	2.30	0.61
1:C:152:GLU:HA	1:C:179:ILE:CG2	2.30	0.61
1:I:49:SER:O	1:I:52:ARG:NH1	2.33	0.61
1:B:17:GLY:HA3	1:B:145:VAL:CG1	2.31	0.60
1:E:137:ILE:HG21	1:E:167:VAL:HG21	1.82	0.60
1:H:96:LEU:O	1:H:99:LYS:N	2.34	0.60
1:H:191:ARG:NH1	1:I:199:GLU:OE2	2.35	0.60
1:G:198:ASN:HB2	1:G:244:MET:HE3	1.83	0.60
1:B:9:VAL:HG21	1:B:104:ILE:HD11	1.82	0.60
1:C:151:VAL:O	1:C:179:ILE:HG22	2.02	0.59
1:F:9:VAL:HG21	1:F:104:ILE:HD11	1.85	0.59
1:E:98:VAL:HG22	1:E:129:VAL:HG21	1.85	0.59
1:E:14:MET:CE	1:E:141:PHE:HB2	2.32	0.59
1:E:189:VAL:HA	1:F:218:MET:CE	2.32	0.58
1:I:190:ASN:HD21	2:I:301:CAA:C4	2.16	0.58
1:B:17:GLY:C	1:B:145:VAL:CG1	2.72	0.58
2:I:301:CAA:H51A	2:I:301:CAA:C8A	2.34	0.58
1:I:152:GLU:HA	1:I:179:ILE:CG2	2.33	0.58
1:G:194:CYS:O	1:G:244:MET:CE	2.52	0.58
1:I:140:HIS:HE1	2:I:301:CAA:C4	2.17	0.58
1:C:194:CYS:HB3	1:C:244:MET:HE3	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:194:CYS:HB3	1:E:244:MET:CE	2.33	0.58
1:D:244:MET:HE2	1:D:247:LEU:HD12	1.86	0.57
1:E:3:ILE:HG21	1:E:170:LEU:HD12	1.85	0.57
1:B:3:ILE:O	1:B:27:LEU:HD21	2.04	0.57
1:H:5:THR:HG22	1:H:83:THR:HG22	1.85	0.57
1:C:152:GLU:HA	1:C:179:ILE:HG22	1.86	0.57
1:F:126:LEU:O	1:F:129:VAL:HG22	2.04	0.57
1:E:144:PRO:CG	1:E:147:VAL:HB	2.28	0.56
1:B:117:ASN:HA	1:B:139:MET:O	2.05	0.56
1:D:145:VAL:O	1:D:176:LYS:NZ	2.39	0.56
1:H:140:HIS:HB3	1:H:152:GLU:HB2	1.87	0.56
1:E:142:PHE:O	1:E:143:ASN:C	2.44	0.56
1:A:283:SER:O	1:A:284:LYS:HB2	2.06	0.56
1:E:17:GLY:CA	1:E:145:VAL:HG21	2.35	0.55
1:E:14:MET:HE1	1:E:141:PHE:HB2	1.87	0.55
1:B:191:ARG:HD3	3:B:404:HOH:O	2.06	0.55
1:B:19:ALA:HB1	1:B:29:VAL:HG11	1.88	0.55
1:B:140:HIS:CB	1:B:152:GLU:HB2	2.36	0.55
1:I:219:LYS:O	1:I:223:ASN:HA	2.07	0.55
1:E:17:GLY:C	1:E:145:VAL:HG23	2.27	0.55
1:B:5:THR:HG22	1:B:83:THR:HG22	1.89	0.55
1:C:209:ALA:HB3	1:C:214:ILE:HD11	1.88	0.55
1:H:137:ILE:HG21	1:H:167:VAL:HG21	1.89	0.55
1:D:27:LEU:HD21	1:D:173:GLN:HE22	1.72	0.54
1:C:140:HIS:HD2	1:C:152:GLU:OE1	1.89	0.54
1:I:9:VAL:HG21	1:I:104:ILE:HD11	1.88	0.54
1:H:191:ARG:HD3	3:H:402:HOH:O	2.08	0.54
1:E:126:LEU:O	1:E:129:VAL:HG22	2.07	0.54
1:E:143:ASN:CB	1:E:144:PRO:CD	2.86	0.54
1:E:189:VAL:HA	1:F:218:MET:HE2	1.89	0.54
1:B:132:ARG:HB3	1:B:135:ARG:HG2	1.90	0.53
1:C:91:THR:HG21	1:C:96:LEU:HB3	1.88	0.53
1:F:152:GLU:OE2	1:F:188:VAL:HB	2.08	0.53
1:A:219:LYS:O	1:A:223:ASN:HA	2.08	0.53
1:B:137:ILE:HG21	1:B:167:VAL:HG21	1.91	0.53
1:B:282:TYR:O	1:B:283:SER:HB3	2.08	0.53
1:H:189:VAL:HA	1:I:218:MET:CE	2.38	0.53
1:F:144:PRO:HD2	2:F:301:CAA:OAP	2.08	0.53
1:E:18:ILE:HG12	1:E:141:PHE:CE1	2.44	0.53
1:D:199:GLU:HB3	1:G:192:ILE:HG22	1.89	0.53
1:G:194:CYS:C	1:G:244:MET:CE	2.75	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:150:LEU:HD13	1:A:150:LEU:O	2.08	0.53
1:F:234:MET:HE3	2:F:301:CAA:CCP	2.39	0.53
1:E:91:THR:HG21	1:E:96:LEU:HD23	1.90	0.52
1:E:141:PHE:CG	1:E:145:VAL:CG1	2.90	0.52
1:A:77:TYR:CD1	1:A:77:TYR:N	2.77	0.52
1:H:189:VAL:HA	1:I:218:MET:HE2	1.91	0.52
1:I:269:GLY:O	1:I:271:LEU:HD13	2.08	0.52
1:D:258:PRO:HG2	1:D:263:ARG:NH2	2.24	0.52
1:B:283:SER:HA	1:B:284:LYS:C	2.29	0.52
1:I:119:SER:HB2	2:I:301:CAA:H4'2	1.91	0.52
1:F:140:HIS:HE1	2:F:301:CAA:H4'2	1.75	0.52
1:A:198:ASN:HD21	1:A:259:ALA:H	1.56	0.52
1:D:244:MET:CE	1:D:247:LEU:HD12	2.40	0.52
1:E:150:LEU:HG	1:E:151:VAL:N	2.25	0.52
1:B:194:CYS:HB3	1:B:244:MET:HE3	1.91	0.52
1:E:108:VAL:HG11	1:E:112:VAL:HG11	1.91	0.52
1:D:32:VAL:HG11	1:D:77:TYR:CD1	2.45	0.51
1:H:91:THR:HG21	1:H:96:LEU:HD23	1.90	0.51
1:H:3:ILE:HG21	1:H:170:LEU:HD12	1.92	0.51
1:G:50:LEU:HB3	1:G:64:LYS:HG3	1.92	0.51
1:H:9:VAL:HG21	1:H:104:ILE:HD11	1.92	0.51
1:I:140:HIS:HE1	2:I:301:CAA:C3	2.23	0.51
1:I:164:HIS:HE1	1:I:180:THR:OG1	1.94	0.51
1:A:126:LEU:O	1:A:127:ALA:C	2.49	0.51
1:F:16:ASN:HB3	1:F:31:MET:HE1	1.91	0.51
1:B:190:ASN:HD21	2:B:301:CAA:H2'1	1.75	0.51
1:A:167:VAL:O	1:A:171:SER:OG	2.29	0.51
1:D:199:GLU:HG3	1:G:192:ILE:HG22	1.92	0.51
1:D:225:PRO:HG3	1:G:223:ASN:HB3	1.92	0.51
1:E:96:LEU:O	1:E:99:LYS:N	2.43	0.51
1:E:5:THR:CG2	1:E:83:THR:HG22	2.37	0.50
2:F:301:CAA:C4	3:F:421:HOH:O	2.59	0.50
1:E:18:ILE:HG12	1:E:141:PHE:CZ	2.46	0.50
1:I:273:ARG:O	1:I:275:THR:N	2.45	0.50
1:B:207:GLY:O	1:B:208:LEU:C	2.48	0.50
2:F:301:CAA:O6A	2:F:301:CAA:OAP	2.18	0.50
1:A:260:MET:CE	3:A:404:HOH:O	2.58	0.50
1:D:244:MET:CE	1:D:244:MET:HA	2.42	0.50
1:D:167:VAL:O	1:D:171:SER:OG	2.28	0.50
1:B:115:ALA:HB1	1:B:139:MET:HE3	1.93	0.50
1:H:283:SER:HA	1:H:284:LYS:HB3	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:117:ASN:HD21	1:B:141:PHE:H	1.60	0.50
1:G:53:LEU:HD23	1:G:58:LYS:HG3	1.94	0.50
1:A:117:ASN:HD21	1:A:141:PHE:H	1.60	0.50
1:H:115:ALA:HB1	1:H:139:MET:HE3	1.94	0.50
1:H:8:ILE:HG22	1:H:8:ILE:O	2.11	0.50
1:E:141:PHE:C	1:E:142:PHE:CD1	2.86	0.49
1:I:139:MET:CE	1:I:167:VAL:HG13	2.41	0.49
1:D:54:ILE:HD11	1:D:64:LYS:HB2	1.94	0.49
1:D:199:GLU:CB	1:G:192:ILE:HG22	2.42	0.49
1:F:152:GLU:HA	1:F:179:ILE:HG22	1.93	0.49
1:E:218:MET:CE	1:F:189:VAL:HA	2.43	0.49
1:I:251:PHE:O	1:I:252:ALA:HB3	2.13	0.49
1:B:194:CYS:HB3	1:B:244:MET:CE	2.42	0.49
1:A:140:HIS:HD2	1:A:152:GLU:OE1	1.94	0.49
1:C:11:ALA:HA	1:C:31:MET:CE	2.43	0.49
1:E:72:LYS:NZ	3:E:415:HOH:O	2.45	0.49
1:D:192:ILE:HG13	1:G:218:MET:SD	2.53	0.48
1:A:243:VAL:HG12	1:A:244:MET:CE	2.42	0.48
1:A:117:ASN:HA	1:A:139:MET:O	2.13	0.48
1:B:17:GLY:CA	1:B:145:VAL:CG1	2.91	0.48
1:E:245:GLU:OE1	1:E:245:GLU:HA	2.13	0.48
1:E:141:PHE:CD2	1:E:145:VAL:CG1	2.93	0.48
1:B:18:ILE:N	1:B:145:VAL:HG11	2.28	0.48
1:C:209:ALA:HB3	1:C:214:ILE:CD1	2.43	0.48
1:F:181:VAL:HG11	1:F:187:PHE:HB3	1.95	0.48
1:E:213:GLU:O	1:F:179:ILE:HD11	2.14	0.48
1:G:28:ASN:HD22	1:G:70:ARG:HG3	1.79	0.48
1:E:9:VAL:HG21	1:E:104:ILE:HD11	1.96	0.48
1:D:189:VAL:HA	1:G:218:MET:HE1	1.94	0.48
1:B:117:ASN:ND2	1:B:141:PHE:H	2.11	0.48
1:A:145:VAL:O	1:A:176:LYS:NZ	2.47	0.48
1:H:192:ILE:HD12	1:I:218:MET:CE	2.44	0.48
1:D:218:MET:HE3	1:G:189:VAL:HG22	1.94	0.47
1:D:191:ARG:HD2	1:G:203:VAL:HG22	1.96	0.47
1:E:145:VAL:N	1:E:146:PRO:CD	2.77	0.47
1:H:154:ILE:HG21	1:H:187:PHE:CE1	2.50	0.47
1:I:126:LEU:O	1:I:129:VAL:HG22	2.14	0.47
1:D:150:LEU:O	1:D:150:LEU:HD13	2.14	0.47
1:C:268:ALA:HB2	1:E:124:THR:HG23	1.95	0.47
1:F:234:MET:HB3	2:F:301:CAA:H142	1.95	0.47
1:H:91:THR:HG21	1:H:96:LEU:CD2	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:103:GLN:O	1:B:107:ILE:HD12	2.15	0.47
1:B:189:VAL:HA	1:C:218:MET:CE	2.45	0.47
1:C:164:HIS:HE1	1:C:180:THR:OG1	1.98	0.47
1:E:132:ARG:HB3	1:E:135:ARG:HG2	1.96	0.47
1:A:59:LEU:O	1:A:60:THR:HG23	2.15	0.47
1:D:218:MET:HE1	1:G:189:VAL:HG13	1.96	0.46
1:C:140:HIS:HE1	2:C:301:CAA:H4'2	1.79	0.46
1:B:218:MET:CE	1:C:189:VAL:HA	2.45	0.46
1:C:152:GLU:OE2	1:C:188:VAL:HB	2.16	0.46
1:E:144:PRO:HD2	1:E:148:MET:CG	2.37	0.46
1:F:11:ALA:HA	1:F:31:MET:CE	2.44	0.46
1:C:16:ASN:HB3	1:C:31:MET:HE1	1.98	0.46
1:G:283:SER:O	1:G:284:LYS:HB2	2.14	0.46
1:H:103:GLN:O	1:H:107:ILE:HD12	2.15	0.46
1:H:222:CYS:SG	1:I:193:LEU:HD13	2.56	0.46
1:E:122:SER:HB3	1:E:125:LYS:HG3	1.96	0.46
1:C:5:THR:HG22	1:C:83:THR:HG22	1.97	0.46
1:E:189:VAL:HA	1:F:218:MET:HE1	1.98	0.46
1:H:218:MET:HE1	1:I:189:VAL:HA	1.98	0.46
1:H:107:ILE:O	1:H:107:ILE:CG2	2.64	0.46
1:F:209:ALA:HB3	1:F:214:ILE:HD11	1.98	0.46
1:F:42:GLY:O	1:F:46:VAL:HG23	2.15	0.46
1:I:91:THR:HG21	1:I:96:LEU:HB3	1.97	0.46
1:D:189:VAL:HA	1:G:218:MET:HE3	1.96	0.45
1:D:51:ASP:HA	1:D:54:ILE:HD12	1.97	0.45
1:A:23:ALA:C	1:A:25:VAL:H	2.19	0.45
1:I:139:MET:HE1	1:I:167:VAL:HG13	1.98	0.45
1:E:212:GLU:O	1:E:216:GLU:HG2	2.16	0.45
1:H:97:LYS:O	1:H:101:LEU:HG	2.15	0.45
1:H:91:THR:HG21	1:H:96:LEU:HG	1.99	0.45
1:E:218:MET:HE1	1:F:189:VAL:HA	1.98	0.45
1:H:194:CYS:HB3	1:H:244:MET:CE	2.46	0.45
1:B:17:GLY:CA	1:B:145:VAL:HG11	2.46	0.45
1:A:283:SER:O	1:A:284:LYS:CB	2.65	0.45
1:C:11:ALA:HA	1:C:31:MET:HE1	1.99	0.45
1:F:143:ASN:HD21	2:F:301:CAA:H31	1.81	0.45
1:C:194:CYS:CB	1:C:244:MET:HE3	2.46	0.45
1:E:72:LYS:CE	3:E:415:HOH:O	2.65	0.45
1:B:134:ASP:O	1:B:160:SER:HB3	2.17	0.45
1:D:97:LYS:HE3	1:D:116:SER:OG	2.16	0.45
1:F:209:ALA:HB3	1:F:214:ILE:CD1	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:18:ILE:HG21	1:D:87:ILE:HD13	1.97	0.45
1:B:145:VAL:N	1:B:146:PRO:CD	2.80	0.45
1:E:144:PRO:C	1:E:146:PRO:CD	2.86	0.45
1:B:251:PHE:HA	1:F:260:MET:CE	2.47	0.45
1:B:85:ILE:HG13	1:B:113:ILE:O	2.17	0.44
1:B:233:ASP:OD2	1:B:282:TYR:OH	2.21	0.44
1:H:108:VAL:HG12	1:H:112:VAL:HB	1.99	0.44
1:H:218:MET:HE3	1:I:192:ILE:CD1	2.47	0.44
1:E:105:ASP:CG	1:E:131:SER:HG	2.20	0.44
1:D:126:LEU:O	1:D:129:VAL:HG22	2.17	0.44
1:I:142:PHE:HD2	2:I:301:CAA:H31	1.83	0.44
1:A:154:ILE:HD13	1:A:187:PHE:CE2	2.53	0.44
1:F:10:GLY:O	1:F:15:GLY:HA3	2.18	0.44
1:E:96:LEU:O	1:E:97:LYS:C	2.55	0.44
1:A:97:LYS:HE3	1:A:116:SER:OG	2.18	0.44
1:D:223:ASN:HB3	1:G:225:PRO:HG3	1.99	0.44
1:E:150:LEU:HD11	1:E:179:ILE:CG1	2.48	0.44
1:H:32:VAL:HG12	1:H:33:ASP:N	2.32	0.44
1:H:4:ARG:O	1:H:27:LEU:HD23	2.18	0.43
1:I:260:MET:CE	3:I:403:HOH:O	2.65	0.43
1:H:8:ILE:HD12	1:H:29:VAL:HG13	2.00	0.43
1:F:260:MET:CE	3:F:405:HOH:O	2.65	0.43
1:D:134:ASP:HA	1:D:158:GLN:O	2.18	0.43
1:A:134:ASP:HA	1:A:158:GLN:O	2.18	0.43
1:D:218:MET:SD	1:G:192:ILE:HG13	2.59	0.43
1:B:47:ALA:O	1:B:48:SER:C	2.56	0.43
1:C:260:MET:HE1	1:E:250:GLU:O	2.18	0.43
1:F:134:ASP:HA	1:F:158:GLN:O	2.18	0.43
1:B:212:GLU:O	1:B:216:GLU:HG2	2.18	0.43
1:B:189:VAL:HA	1:C:218:MET:HE2	2.00	0.43
1:I:54:ILE:HD11	1:I:64:LYS:HB2	2.00	0.43
1:D:260:MET:HE1	3:D:404:HOH:O	2.18	0.43
1:G:50:LEU:HA	1:G:53:LEU:HD12	2.01	0.43
1:A:244:MET:CE	1:A:244:MET:HA	2.47	0.43
1:H:107:ILE:O	1:H:107:ILE:HG22	2.18	0.43
1:H:147:VAL:HG11	2:H:301:CAA:C4B	2.49	0.43
1:A:164:HIS:HE1	1:A:180:THR:OG1	2.02	0.43
1:I:134:ASP:HA	1:I:158:GLN:O	2.18	0.43
1:E:216:GLU:O	1:E:217:GLY:C	2.55	0.43
1:H:49:SER:O	1:H:52:ARG:N	2.52	0.43
1:C:269:GLY:C	1:C:271:LEU:HD13	2.39	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:142:PHE:CD2	2:G:301:CAA:H31	2.54	0.43
1:G:198:ASN:HD21	1:G:259:ALA:H	1.67	0.43
1:A:231:LEU:HD11	2:A:301:CAA:H72	2.00	0.43
1:C:114:ILE:HG13	1:C:132:ARG:HD2	2.00	0.43
1:D:198:ASN:ND2	1:D:244:MET:HG3	2.34	0.42
1:B:197:ILE:HB	1:B:240:MET:HE1	2.01	0.42
1:E:119:SER:HA	1:E:140:HIS:CE1	2.54	0.42
1:B:250:GLU:O	1:F:260:MET:HE1	2.19	0.42
1:E:222:CYS:SG	1:F:193:LEU:HD13	2.59	0.42
1:A:30:VAL:HA	1:A:72:LYS:O	2.19	0.42
1:B:139:MET:HG2	1:B:141:PHE:CE2	2.54	0.42
1:D:218:MET:CE	1:D:218:MET:HA	2.42	0.42
1:G:117:ASN:HD21	1:G:141:PHE:H	1.67	0.42
1:A:190:ASN:ND2	2:A:301:CAA:S1P	2.71	0.42
1:A:28:ASN:ND2	1:A:70:ARG:HG3	2.34	0.42
1:D:56:LYS:O	1:D:56:LYS:CG	2.67	0.42
1:E:197:ILE:HD11	1:E:231:LEU:HD23	2.01	0.42
1:H:12:GLY:O	1:H:13:THR:C	2.56	0.42
1:H:192:ILE:HB	1:I:218:MET:HE1	2.01	0.42
1:B:3:ILE:HD13	1:B:170:LEU:HD12	2.02	0.42
1:A:23:ALA:C	1:A:25:VAL:N	2.73	0.42
1:D:203:VAL:CG2	1:G:191:ARG:HD2	2.49	0.42
1:H:134:ASP:HA	1:H:158:GLN:O	2.20	0.42
1:A:244:MET:CE	1:A:247:LEU:HD12	2.49	0.42
2:I:301:CAA:H2'1	2:I:301:CAA:C3P	2.50	0.42
1:E:91:THR:HG21	1:E:96:LEU:CD2	2.50	0.42
1:H:108:VAL:HG11	1:H:112:VAL:HG11	2.02	0.42
1:E:260:MET:CE	3:E:401:HOH:O	2.66	0.42
1:G:145:VAL:N	1:G:146:PRO:CD	2.83	0.42
1:F:12:GLY:O	1:F:13:THR:C	2.58	0.42
1:B:191:ARG:O	1:B:195:PRO:HG2	2.20	0.42
1:G:117:ASN:O	1:G:118:THR:HB	2.19	0.42
1:H:218:MET:CE	1:I:189:VAL:HA	2.49	0.42
1:A:32:VAL:HG11	1:A:77:TYR:CD2	2.54	0.42
1:E:150:LEU:HD11	1:E:179:ILE:HG13	2.02	0.42
1:C:268:ALA:HB2	1:E:124:THR:CG2	2.49	0.42
1:D:260:MET:CE	3:D:404:HOH:O	2.67	0.42
1:E:157:LEU:HD23	1:E:157:LEU:HA	1.91	0.42
1:D:9:VAL:HG21	1:D:104:ILE:HD11	2.02	0.42
1:B:29:VAL:HB	1:B:71:ILE:HA	2.01	0.41
1:H:87:ILE:HG12	1:H:115:ALA:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:269:GLY:O	1:C:271:LEU:HD13	2.20	0.41
1:H:191:ARG:NH1	1:H:256:TYR:OH	2.48	0.41
1:I:269:GLY:C	1:I:271:LEU:HD13	2.40	0.41
1:I:181:VAL:HG11	1:I:187:PHE:HB3	2.01	0.41
1:B:125:LYS:HG2	1:F:267:ALA:HB1	2.02	0.41
1:F:11:ALA:HA	1:F:31:MET:HE1	2.03	0.41
1:A:244:MET:HE2	1:A:247:LEU:HD12	2.03	0.41
1:H:32:VAL:CG1	1:H:33:ASP:N	2.84	0.41
1:G:173:GLN:C	1:G:175:GLY:H	2.23	0.41
1:C:143:ASN:HB2	1:C:144:PRO:CD	2.50	0.41
1:E:17:GLY:HA3	1:E:145:VAL:HG21	1.96	0.41
1:A:244:MET:CA	1:A:244:MET:HE2	2.47	0.41
1:A:199:GLU:O	1:A:203:VAL:HG23	2.19	0.41
1:B:91:THR:HG21	1:B:96:LEU:HG	2.02	0.41
1:D:218:MET:HE3	1:G:189:VAL:HA	2.03	0.41
1:I:103:GLN:HE21	1:I:103:GLN:HB2	1.71	0.41
1:E:42:GLY:O	1:E:45:THR:N	2.54	0.41
1:I:233:ASP:CG	1:I:279:VAL:H	2.24	0.41
1:B:150:LEU:HD22	1:C:221:GLY:CA	2.51	0.41
1:G:283:SER:O	1:G:284:LYS:CB	2.69	0.41
1:I:14:MET:CE	1:I:143:ASN:HB3	2.50	0.41
1:I:10:GLY:O	1:I:15:GLY:HA3	2.20	0.41
1:H:96:LEU:O	1:H:97:LYS:C	2.59	0.41
1:B:182:LYS:O	1:B:183:ASN:C	2.59	0.41
1:H:54:ILE:HD13	1:H:60:THR:C	2.41	0.41
1:I:190:ASN:HD21	2:I:301:CAA:H4'2	1.84	0.40
1:E:260:MET:HE1	3:E:401:HOH:O	2.20	0.40
1:H:122:SER:HB3	1:H:125:LYS:HG3	2.02	0.40
1:B:115:ALA:CB	1:B:139:MET:HE3	2.52	0.40
1:D:218:MET:CE	1:G:189:VAL:HA	2.51	0.40
2:F:301:CAA:C2P	2:F:301:CAA:C6P	2.97	0.40
1:G:7:GLY:N	1:G:85:ILE:O	2.38	0.40
1:H:92:GLU:OE2	1:H:118:THR:HA	2.21	0.40
1:A:74:SER:OG	1:A:75:THR:N	2.54	0.40
1:D:80:LEU:O	1:D:83:THR:OG1	2.31	0.40
1:B:141:PHE:CD1	1:B:145:VAL:HG23	2.57	0.40
1:B:17:GLY:HA3	1:B:145:VAL:HG11	2.00	0.40
1:H:12:GLY:O	1:H:16:ASN:OD1	2.39	0.40
2:E:301:CAA:H2B	2:E:301:CAA:N3A	2.36	0.40
1:F:251:PHE:O	1:F:252:ALA:HB3	2.21	0.40
1:E:181:VAL:HG12	1:E:182:LYS:O	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:16:ASN:CA	1:C:31:MET:HE3	2.49	0.40
1:E:191:ARG:HE	1:F:203:VAL:HG22	1.86	0.40
1:B:199:GLU:OE2	1:C:191:ARG:NH1	2.53	0.40
1:E:74:SER:OG	1:E:79:ASP:OD2	2.33	0.40
1:C:42:GLY:O	1:C:46:VAL:HG23	2.21	0.40
1:C:219:LYS:O	1:C:223:ASN:HA	2.22	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	281/284 (99%)	253 (90%)	27 (10%)	1 (0%)	39	69
1	B	281/284 (99%)	241 (86%)	37 (13%)	3 (1%)	17	42
1	C	281/284 (99%)	263 (94%)	15 (5%)	3 (1%)	17	42
1	D	281/284 (99%)	262 (93%)	18 (6%)	1 (0%)	39	69
1	E	281/284 (99%)	250 (89%)	30 (11%)	1 (0%)	39	69
1	F	281/284 (99%)	265 (94%)	13 (5%)	3 (1%)	17	42
1	G	281/284 (99%)	262 (93%)	18 (6%)	1 (0%)	39	69
1	H	281/284 (99%)	253 (90%)	26 (9%)	2 (1%)	26	55
1	I	281/284 (99%)	262 (93%)	17 (6%)	2 (1%)	26	55
All	All	2529/2556 (99%)	2311 (91%)	201 (8%)	17 (1%)	26	55

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	110	GLU
1	C	274	LYS

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Mol	Chain	Res	Type
1	E	143	ASN
1	H	81	LYS
1	I	274	LYS
1	D	283	SER
1	F	274	LYS
1	G	59	LEU
1	A	283	SER
1	B	81	LYS
1	C	120	SER
1	H	97	LYS
1	B	144	PRO
1	F	120	SER
1	F	143	ASN
1	C	144	PRO
1	I	120	SER

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	227/228 (100%)	211 (93%)	16 (7%)	19	42
1	B	227/228 (100%)	213 (94%)	14 (6%)	23	49
1	C	227/228 (100%)	218 (96%)	9 (4%)	38	69
1	D	227/228 (100%)	213 (94%)	14 (6%)	23	49
1	E	227/228 (100%)	211 (93%)	16 (7%)	19	42
1	F	227/228 (100%)	214 (94%)	13 (6%)	25	53
1	G	227/228 (100%)	213 (94%)	14 (6%)	23	49
1	H	227/228 (100%)	205 (90%)	22 (10%)	10	23
1	I	227/228 (100%)	219 (96%)	8 (4%)	43	74
All	All	2043/2052 (100%)	1917 (94%)	126 (6%)	23	49

All (126) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	45	THR
1	A	50	LEU
1	A	70	ARG
1	A	72	LYS
1	A	75	THR
1	A	77	TYR
1	A	79	ASP
1	A	119	SER
1	A	150	LEU
1	A	171	SER
1	A	173	GLN
1	A	180	THR
1	A	191	ARG
1	A	192	ILE
1	A	223	ASN
1	A	271	LEU
1	B	4	ARG
1	B	16	ASN
1	B	48	SER
1	B	53	LEU
1	B	110	GLU
1	B	119	SER
1	B	125	LYS
1	B	143	ASN
1	B	160	SER
1	B	162	THR
1	B	174	LEU
1	B	191	ARG
1	B	220	LEU
1	B	224	HIS
1	C	4	ARG
1	C	34	ILE
1	C	52	ARG
1	C	76	SER
1	C	96	LEU
1	C	179	ILE
1	C	191	ARG
1	C	226	ILE
1	C	284	LYS
1	D	45	THR
1	D	50	LEU
1	D	60	THR
1	D	74	SER

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Mol	Chain	Res	Type
1	D	75	THR
1	D	150	LEU
1	D	162	THR
1	D	171	SER
1	D	191	ARG
1	D	192	ILE
1	D	223	ASN
1	D	271	LEU
1	D	283	SER
1	D	284	LYS
1	E	2	SER
1	E	16	ASN
1	E	33	ASP
1	E	41	LYS
1	E	78	ASP
1	E	88	GLU
1	E	125	LYS
1	E	139	MET
1	E	143	ASN
1	E	150	LEU
1	E	153	LEU
1	E	160	SER
1	E	174	LEU
1	E	220	LEU
1	E	224	HIS
1	E	226	ILE
1	F	2	SER
1	F	52	ARG
1	F	60	THR
1	F	78	ASP
1	F	96	LEU
1	F	110	GLU
1	F	125	LYS
1	F	179	ILE
1	F	182	LYS
1	F	191	ARG
1	F	226	ILE
1	F	239	THR
1	F	257	ARG
1	G	13	THR
1	G	36	ASP
1	G	45	THR

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Mol	Chain	Res	Type
1	G	50	LEU
1	G	70	ARG
1	G	78	ASP
1	G	111	ASN
1	G	150	LEU
1	G	173	GLN
1	G	177	TYR
1	G	191	ARG
1	G	192	ILE
1	G	223	ASN
1	G	271	LEU
1	H	16	ASN
1	H	33	ASP
1	H	41	LYS
1	H	48	SER
1	H	54	ILE
1	H	55	LYS
1	H	58	LYS
1	H	60	THR
1	H	83	THR
1	H	110	GLU
1	H	139	MET
1	H	143	ASN
1	H	145	VAL
1	H	161	ASP
1	H	162	THR
1	H	174	LEU
1	H	191	ARG
1	H	220	LEU
1	H	222	CYS
1	H	224	HIS
1	H	226	ILE
1	H	283	SER
1	I	2	SER
1	I	4	ARG
1	I	52	ARG
1	I	96	LEU
1	I	191	ARG
1	I	224	HIS
1	I	239	THR
1	I	284	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (53) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	28	ASN
1	A	117	ASN
1	A	164	HIS
1	A	198	ASN
1	B	16	ASN
1	B	20	GLN
1	B	117	ASN
1	B	140	HIS
1	B	143	ASN
1	B	164	HIS
1	B	173	GLN
1	B	190	ASN
1	B	223	ASN
1	C	40	GLN
1	C	103	GLN
1	C	140	HIS
1	C	164	HIS
1	C	173	GLN
1	D	28	ASN
1	D	117	ASN
1	D	140	HIS
1	D	164	HIS
1	D	173	GLN
1	D	190	ASN
1	D	198	ASN
1	E	16	ASN
1	E	28	ASN
1	E	117	ASN
1	E	140	HIS
1	E	143	ASN
1	E	164	HIS
1	E	173	GLN
1	E	190	ASN
1	F	40	GLN
1	F	103	GLN
1	F	140	HIS
1	F	164	HIS
1	F	173	GLN
1	F	223	ASN
1	G	28	ASN
1	G	117	ASN
1	G	164	HIS

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Mol	Chain	Res	Type
1	G	190	ASN
1	G	198	ASN
1	H	164	HIS
1	H	173	GLN
1	H	190	ASN
1	H	223	ASN
1	I	40	GLN
1	I	103	GLN
1	I	140	HIS
1	I	164	HIS
1	I	223	ASN

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](#)

9 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
2	CAA	A	301	-	45,56,56	1.08	4 (8%)	58,83,83	2.06	5 (8%)
2	CAA	B	301	-	45,56,56	1.08	2 (4%)	58,83,83	2.13	6 (10%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	CAA	C	301	-	45,56,56	1.10	3 (6%)	58,83,83	1.87	8 (13%)
2	CAA	D	301	-	45,56,56	1.09	3 (6%)	58,83,83	1.83	9 (15%)
2	CAA	E	301	-	45,56,56	1.02	3 (6%)	58,83,83	1.96	8 (13%)
2	CAA	F	301	-	45,56,56	1.09	4 (8%)	58,83,83	1.93	11 (18%)
2	CAA	G	301	-	45,56,56	1.09	3 (6%)	58,83,83	1.97	12 (20%)
2	CAA	H	301	-	45,56,56	1.05	4 (8%)	58,83,83	1.85	6 (10%)
2	CAA	I	301	-	45,56,56	1.00	3 (6%)	58,83,83	2.47	11 (18%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	CAA	A	301	-	-	2/50/71/71	0/3/3/3
2	CAA	B	301	-	-	0/50/71/71	0/3/3/3
2	CAA	C	301	-	-	0/50/71/71	0/3/3/3
2	CAA	D	301	-	-	1/50/71/71	0/3/3/3
2	CAA	E	301	-	-	2/50/71/71	0/3/3/3
2	CAA	F	301	-	-	0/50/71/71	0/3/3/3
2	CAA	G	301	-	-	2/50/71/71	0/3/3/3
2	CAA	H	301	-	-	0/50/71/71	0/3/3/3
2	CAA	I	301	-	-	2/50/71/71	0/3/3/3

All (29) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	301	CAA	C1-S1P	-4.03	1.67	1.76
2	F	301	CAA	C1-S1P	-3.92	1.68	1.76
2	G	301	CAA	C1-S1P	-3.81	1.68	1.76
2	D	301	CAA	C1-S1P	-3.61	1.68	1.76
2	A	301	CAA	C1-S1P	-3.60	1.68	1.76
2	C	301	CAA	C1-S1P	-3.41	1.69	1.76
2	H	301	CAA	C1-S1P	-3.34	1.69	1.76
2	I	301	CAA	C1-S1P	-3.33	1.69	1.76
2	E	301	CAA	C1-S1P	-3.17	1.69	1.76
2	F	301	CAA	C2A-N3A	2.02	1.35	1.32
2	H	301	CAA	C2A-N3A	2.02	1.35	1.32
2	I	301	CAA	C2A-N3A	2.04	1.35	1.32
2	A	301	CAA	C2A-N3A	2.08	1.35	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	301	CAA	O4B-C1B	2.19	1.44	1.41
2	E	301	CAA	O4B-C1B	2.21	1.44	1.41
2	H	301	CAA	O4B-C1B	2.29	1.44	1.41
2	F	301	CAA	O4B-C1B	2.43	1.44	1.41
2	A	301	CAA	O4B-C1B	2.58	1.44	1.41
2	D	301	CAA	O4B-C1B	2.66	1.44	1.41
2	C	301	CAA	O4B-C1B	3.07	1.45	1.41
2	I	301	CAA	C5A-C4A	3.12	1.47	1.40
2	B	301	CAA	C5A-C4A	3.17	1.47	1.40
2	H	301	CAA	C5A-C4A	3.21	1.47	1.40
2	E	301	CAA	C5A-C4A	3.26	1.47	1.40
2	F	301	CAA	C5A-C4A	3.29	1.47	1.40
2	D	301	CAA	C5A-C4A	3.33	1.48	1.40
2	G	301	CAA	C5A-C4A	3.36	1.48	1.40
2	C	301	CAA	C5A-C4A	3.44	1.48	1.40
2	A	301	CAA	C5A-C4A	3.50	1.48	1.40

All (76) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	301	CAA	N3A-C2A-N1A	-8.95	122.04	128.89
2	G	301	CAA	N3A-C2A-N1A	-8.69	122.24	128.89
2	E	301	CAA	N3A-C2A-N1A	-8.63	122.28	128.89
2	H	301	CAA	N3A-C2A-N1A	-8.45	122.42	128.89
2	B	301	CAA	N3A-C2A-N1A	-8.33	122.51	128.89
2	D	301	CAA	N3A-C2A-N1A	-8.30	122.54	128.89
2	I	301	CAA	N3A-C2A-N1A	-8.06	122.72	128.89
2	A	301	CAA	N3A-C2A-N1A	-8.05	122.73	128.89
2	F	301	CAA	N3A-C2A-N1A	-7.92	122.83	128.89
2	B	301	CAA	O1-C1-S1P	-7.35	117.00	122.83
2	I	301	CAA	O1-C1-S1P	-4.92	118.93	122.83
2	I	301	CAA	C3P-N4P-C5P	-4.08	114.76	122.79
2	C	301	CAA	C4A-C5A-N7A	-3.94	105.85	109.48
2	D	301	CAA	P2A-O3A-P1A	-3.87	121.85	132.73
2	C	301	CAA	O1-C1-S1P	-3.87	119.77	122.83
2	D	301	CAA	C4A-C5A-N7A	-3.84	105.95	109.48
2	A	301	CAA	C4A-C5A-N7A	-3.81	105.97	109.48
2	F	301	CAA	C4A-C5A-N7A	-3.77	106.02	109.48
2	H	301	CAA	O1-C1-S1P	-3.75	119.86	122.83
2	I	301	CAA	C7P-C6P-C5P	-3.74	106.14	112.31
2	G	301	CAA	C4A-C5A-N7A	-3.63	106.14	109.48
2	G	301	CAA	C7P-C6P-C5P	-3.36	106.78	112.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	301	CAA	C4A-C5A-N7A	-3.12	106.61	109.48
2	F	301	CAA	O1-C1-S1P	-3.00	120.45	122.83
2	H	301	CAA	P2A-O3A-P1A	-2.85	124.72	132.73
2	B	301	CAA	C1B-N9A-C4A	-2.78	122.75	126.94
2	B	301	CAA	C4A-C5A-N7A	-2.75	106.94	109.48
2	H	301	CAA	C4A-C5A-N7A	-2.74	106.96	109.48
2	F	301	CAA	P2A-O3A-P1A	-2.71	125.12	132.73
2	D	301	CAA	O9P-C9P-N8P	-2.65	117.76	123.08
2	G	301	CAA	O9P-C9P-N8P	-2.50	118.06	123.08
2	E	301	CAA	O1-C1-S1P	-2.48	120.86	122.83
2	F	301	CAA	OAP-CAP-C9P	-2.37	104.94	110.38
2	G	301	CAA	O1-C1-S1P	-2.32	121.00	122.83
2	F	301	CAA	C3P-C2P-S1P	-2.16	105.59	111.36
2	C	301	CAA	C3P-C2P-S1P	-2.12	105.69	111.36
2	F	301	CAA	CAP-C9P-N8P	-2.10	111.82	116.47
2	D	301	CAA	O1-C1-S1P	-2.07	121.19	122.83
2	I	301	CAA	C2B-C1B-N9A	-2.04	111.17	114.29
2	E	301	CAA	O5P-C5P-C6P	-2.03	118.47	121.98
2	E	301	CAA	C2A-N1A-C6A	2.03	122.39	118.77
2	I	301	CAA	C3B-C2B-C1B	2.08	104.98	99.98
2	I	301	CAA	O3B-C3B-C2B	2.09	119.64	111.51
2	F	301	CAA	C1B-N9A-C4A	2.11	130.13	126.94
2	A	301	CAA	CEP-CBP-CAP	2.13	113.23	109.34
2	I	301	CAA	N6A-C6A-N1A	2.17	123.86	119.20
2	E	301	CAA	C3B-C2B-C1B	2.22	105.32	99.98
2	C	301	CAA	C4B-O4B-C1B	2.25	112.19	109.72
2	D	301	CAA	C3B-C2B-C1B	2.25	105.37	99.98
2	G	301	CAA	C7P-N8P-C9P	2.27	127.02	122.53
2	E	301	CAA	C4B-O4B-C1B	2.38	112.34	109.72
2	G	301	CAA	O5B-C5B-C4B	2.45	118.16	109.12
2	G	301	CAA	C3B-C2B-C1B	2.52	106.02	99.98
2	F	301	CAA	P3B-O3B-C3B	2.56	127.70	121.56
2	H	301	CAA	O4B-C1B-N9A	2.58	113.50	108.10
2	I	301	CAA	C2P-S1P-C1	2.62	111.44	102.09
2	C	301	CAA	O4B-C1B-N9A	2.70	113.75	108.10
2	G	301	CAA	CDP-CBP-CAP	2.71	114.29	109.34
2	D	301	CAA	O4B-C1B-N9A	2.80	113.95	108.10
2	B	301	CAA	C2P-C3P-N4P	2.82	117.99	112.36
2	D	301	CAA	C7P-N8P-C9P	2.85	128.17	122.53
2	G	301	CAA	C4B-O4B-C1B	3.04	113.06	109.72
2	I	301	CAA	C2P-C3P-N4P	3.27	118.89	112.36
2	C	301	CAA	O6A-CCP-CBP	3.27	115.80	110.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	301	CAA	CAP-C9P-N8P	3.51	124.25	116.47
2	A	301	CAA	O4B-C1B-N9A	4.50	117.53	108.10
2	C	301	CAA	C2-C1-S1P	4.94	118.42	113.50
2	F	301	CAA	CEP-CBP-CCP	5.17	115.20	108.50
2	G	301	CAA	C2-C1-S1P	5.42	118.91	113.50
2	D	301	CAA	C2-C1-S1P	5.47	118.96	113.50
2	F	301	CAA	C2-C1-S1P	5.56	119.05	113.50
2	H	301	CAA	C2-C1-S1P	6.76	120.24	113.50
2	B	301	CAA	C2-C1-S1P	8.38	121.86	113.50
2	E	301	CAA	C2-C1-S1P	8.54	122.02	113.50
2	A	301	CAA	C2-C1-S1P	9.38	122.86	113.50
2	I	301	CAA	C2-C1-S1P	12.25	125.72	113.50

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	301	CAA	C2-C1-S1P-C2P
2	E	301	CAA	O1-C1-S1P-C2P
2	G	301	CAA	P1A-O5B-C5B-C4B
2	A	301	CAA	O3-C3-C2-C1
2	A	301	CAA	C4-C3-C2-C1
2	I	301	CAA	O1-C1-S1P-C2P
2	I	301	CAA	C2-C1-S1P-C2P
2	G	301	CAA	CAP-C9P-N8P-C7P
2	D	301	CAA	CAP-C9P-N8P-C7P

There are no ring outliers.

8 monomers are involved in 27 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	CAA	2	0
2	B	301	CAA	1	0
2	C	301	CAA	2	0
2	E	301	CAA	1	0
2	F	301	CAA	9	0
2	G	301	CAA	1	0
2	H	301	CAA	1	0
2	I	301	CAA	10	0

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, 95th 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	283/284 (99%)	0.40	14 (4%)	33 32	39, 72, 119, 156	0
1	B	283/284 (99%)	0.36	9 (3%)	51 51	42, 77, 111, 128	0
1	C	283/284 (99%)	0.15	2 (0%)	89 90	43, 58, 78, 121	0
1	D	283/284 (99%)	0.39	14 (4%)	33 32	43, 72, 118, 148	0
1	E	283/284 (99%)	0.45	20 (7%)	19 17	43, 78, 110, 131	0
1	F	283/284 (99%)	0.14	3 (1%)	82 83	43, 58, 78, 125	0
1	G	283/284 (99%)	0.27	10 (3%)	48 48	42, 72, 114, 163	0
1	H	283/284 (99%)	0.44	18 (6%)	23 21	43, 77, 106, 123	0
1	I	283/284 (99%)	0.22	3 (1%)	82 83	45, 58, 78, 122	0
All	All	2547/2556 (99%)	0.31	93 (3%)	45 45	39, 64, 109, 163	0

All (93) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	284	LYS	7.5
1	A	2	SER	6.5
1	E	59	LEU	5.5
1	E	145	VAL	4.9
1	A	59	LEU	4.9
1	H	85	ILE	4.6
1	A	3	ILE	4.3
1	D	59	LEU	4.3
1	E	110	GLU	3.7
1	E	10	GLY	3.7
1	H	86	VAL	3.6
1	D	6	VAL	3.6
1	A	27	LEU	3.5
1	H	53	LEU	3.5
1	E	38	ALA	3.5

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Mol	Chain	Res	Type	RSRZ
1	E	284	LYS	3.4
1	E	50	LEU	3.4
1	A	101	LEU	3.3
1	E	53	LEU	3.3
1	B	145	VAL	3.3
1	H	14	MET	3.3
1	G	170	LEU	3.2
1	B	143	ASN	3.2
1	H	30	VAL	3.2
1	A	174	LEU	3.2
1	E	9	VAL	3.1
1	G	174	LEU	3.0
1	B	80	LEU	2.9
1	A	170	LEU	2.9
1	G	59	LEU	2.9
1	C	2	SER	2.9
1	I	283	SER	2.8
1	E	101	LEU	2.8
1	A	284	LYS	2.8
1	E	179	ILE	2.8
1	H	220	LEU	2.8
1	E	143	ASN	2.8
1	I	284	LYS	2.8
1	A	53	LEU	2.8
1	G	60	THR	2.8
1	H	77	TYR	2.8
1	A	80	LEU	2.7
1	D	3	ILE	2.7
1	D	72	LYS	2.6
1	B	100	ILE	2.6
1	G	70	ARG	2.6
1	G	72	LYS	2.6
1	D	54	ILE	2.6
1	E	7	GLY	2.5
1	F	271	LEU	2.5
1	H	170	LEU	2.5
1	D	46	VAL	2.5
1	E	46	VAL	2.5
1	F	34	ILE	2.5
1	H	106	GLY	2.5
1	D	28	ASN	2.5
1	E	8	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	127	ALA	2.4
1	D	4	ARG	2.4
1	H	101	LEU	2.4
1	I	278	GLY	2.4
1	E	80	LEU	2.4
1	E	18	ILE	2.4
1	H	19	ALA	2.4
1	D	143	ASN	2.4
1	E	141	PHE	2.4
1	D	77	TYR	2.4
1	F	284	LYS	2.3
1	D	45	THR	2.3
1	D	27	LEU	2.3
1	D	80	LEU	2.3
1	B	77	TYR	2.3
1	A	15	GLY	2.2
1	G	34	ILE	2.2
1	C	3	ILE	2.2
1	H	83	THR	2.2
1	A	273	ARG	2.2
1	B	50	LEU	2.2
1	H	50	LEU	2.2
1	H	284	LYS	2.2
1	H	56	LYS	2.1
1	E	86	VAL	2.1
1	A	129	VAL	2.1
1	D	74	SER	2.1
1	B	141	PHE	2.1
1	E	30	VAL	2.1
1	B	87	ILE	2.1
1	G	30	VAL	2.0
1	H	9	VAL	2.0
1	H	114	ILE	2.0
1	A	73	GLY	2.0
1	H	91	THR	2.0
1	G	58	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, 95th 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(\AA^2)	Q<0.9
2	CAA	A	301	54/54	0.65	0.46	5.55	97,165,223,234	0
2	CAA	C	301	54/54	0.72	0.44	4.92	109,171,188,194	0
2	CAA	F	301	54/54	0.73	0.39	4.63	109,148,195,205	0
2	CAA	H	301	54/54	0.73	0.40	4.50	98,157,180,183	0
2	CAA	B	301	54/54	0.69	0.40	3.86	85,151,185,211	0
2	CAA	I	301	54/54	0.64	0.39	3.73	98,176,207,216	0
2	CAA	D	301	54/54	0.70	0.39	3.64	72,184,201,207	0
2	CAA	G	301	54/54	0.70	0.39	3.52	83,153,206,214	0
2	CAA	E	301	54/54	0.69	0.37	2.40	81,150,198,204	0

6.5 Other polymers [i](#)

There are no such residues in this entry.