



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 07:32 PM GMT

PDB ID : 1FXO
Title : THE STRUCTURAL BASIS OF THE CATALYTIC MECHANISM AND
REGULATION OF GLUCOSE-1-PHOSPHATE THYMIDYLYLTRANSFERASE (RMLA). TMP COMPLEX.
Authors : Blankenfeldt, W.; Lam, J.S.; Naismith, J.H.
Deposited on : 2000-09-26
Resolution : 1.66 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

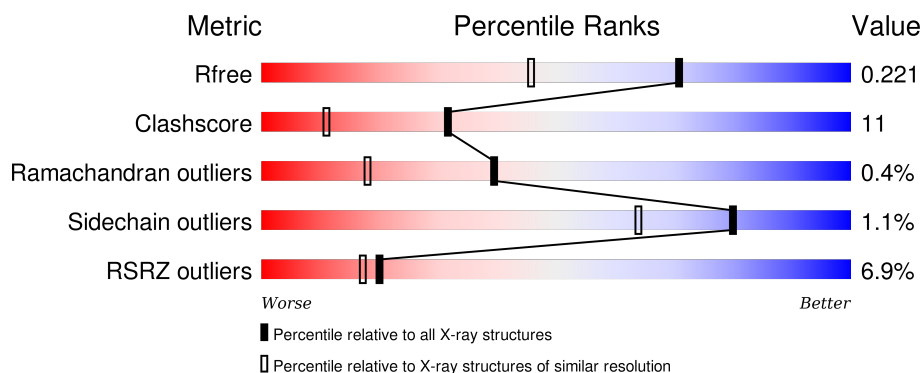
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.66 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	1226 (1.66-1.66)
Clashscore	102246	1323 (1.66-1.66)
Ramachandran outliers	100387	1295 (1.66-1.66)
Sidechain outliers	100360	1295 (1.66-1.66)
RSRZ outliers	91569	1227 (1.66-1.66)

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	293	<div> <div>5%</div> <div>83%</div> <div>15%</div> </div>
1	B	293	<div> <div>6%</div> <div>84%</div> <div>15%</div> </div>
1	C	293	<div> <div>9%</div> <div>77%</div> <div>22%</div> </div>
1	D	293	<div> <div>8%</div> <div>85%</div> <div>13%</div> </div>
1	E	293	<div> <div>11%</div> <div>81%</div> <div>18%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	293	
1	G	293	
1	H	293	

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	SO4	D	3900	-	-	X	-
2	SO4	D	5000	-	-	-	X
2	SO4	E	5700	-	-	X	-
3	TMP	A	9507	-	-	-	X
3	TMP	B	9508	-	-	-	X
3	TMP	G	9505[B]	-	-	-	X
3	TMP	G	9513	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 22771 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 GLUCOSE-1-PHOSPHATE THYMIDYLYLTRANSFERASE.

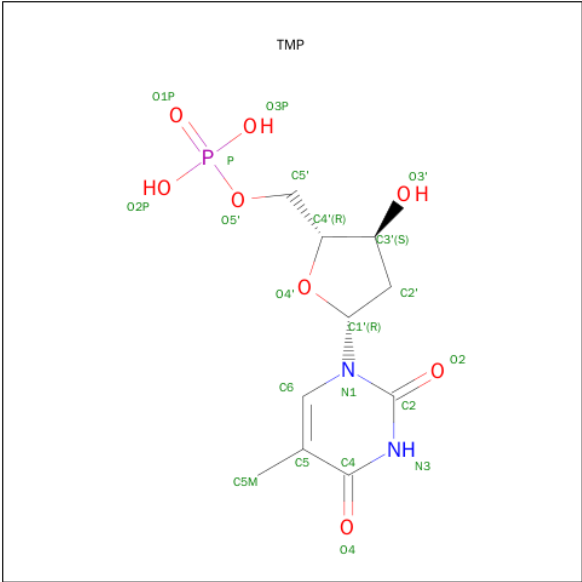
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	292	Total	C	N	O	S	0	11	0
			2376	1512	407	451	6			
1	B	293	Total	C	N	O	S	0	7	0
			2345	1495	397	446	7			
1	C	292	Total	C	N	O	S	0	14	0
			2397	1526	409	456	6			
1	D	292	Total	C	N	O	S	0	12	0
			2377	1516	400	455	6			
1	E	293	Total	C	N	O	S	0	6	0
			2337	1491	393	446	7			
1	F	293	Total	C	N	O	S	0	12	0
			2388	1523	402	456	7			
1	G	293	Total	C	N	O	S	0	6	0
			2333	1490	392	444	7			
1	H	292	Total	C	N	O	S	0	3	0
			2305	1473	388	438	6			

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

- Molecule 3 is THYMIDINE-5'-PHOSPHATE (three-letter code: TMP) (formula: C₁₀H₁₅N₂O₈P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	1
			42	20	4	16	2		
3	B	1	Total	C	N	O	P	0	1
			42	20	4	16	2		
3	C	1	Total	C	N	O	P	0	1
			42	20	4	16	2		
3	D	1	Total	C	N	O	P	0	1
			42	20	4	16	2		
3	E	1	Total	C	N	O	P	0	0
			21	10	2	8	1		
3	F	1	Total	C	N	O	P	0	1
			42	20	4	16	2		
3	G	1	Total	C	N	O	P	0	1
			42	20	4	16	2		
3	H	1	Total	C	N	O	P	0	1
			42	20	4	16	2		
3	A	1	Total	C	N	O	P	0	0
			21	10	2	8	1		
3	B	1	Total	C	N	O	P	0	0
			21	10	2	8	1		
3	C	1	Total	C	N	O	P	0	0
			21	10	2	8	1		
3	D	1	Total	C	N	O	P	0	0
			21	10	2	8	1		
3	E	1	Total	C	N	O	P	0	0
			21	10	2	8	1		
3	F	1	Total	C	N	O	P	0	0
			21	10	2	8	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	G	1	Total	C	N	O	P	0	0
			21	10	2	8	1		
3	H	1	Total	C	N	O	P	0	0
			21	10	2	8	1		

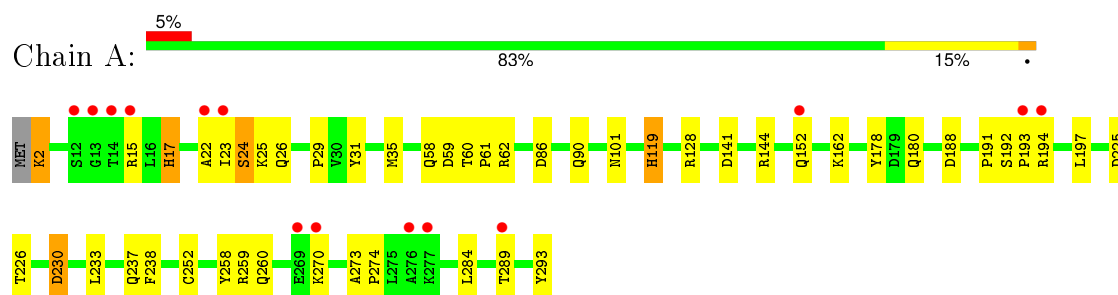
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	450	Total	O	0	0
			450	450		
4	B	486	Total	O	0	0
			486	486		
4	C	391	Total	O	0	0
			391	391		
4	D	381	Total	O	0	0
			381	381		
4	E	375	Total	O	0	0
			375	375		
4	F	399	Total	O	0	0
			399	399		
4	G	457	Total	O	0	0
			457	457		
4	H	426	Total	O	0	0
			426	426		

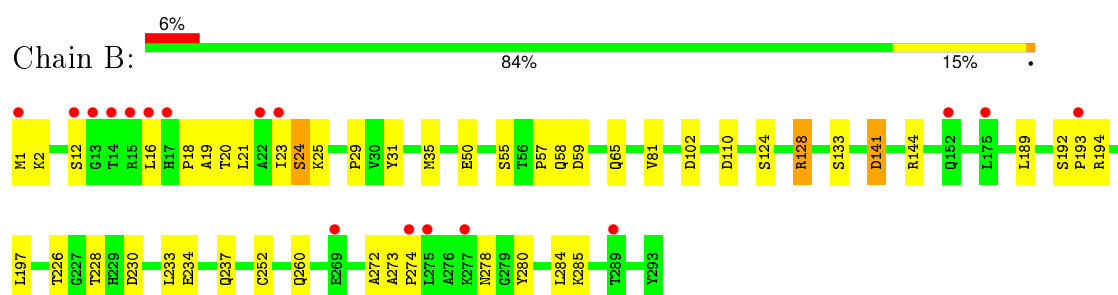
3 Residue-property plots [i](#)

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.

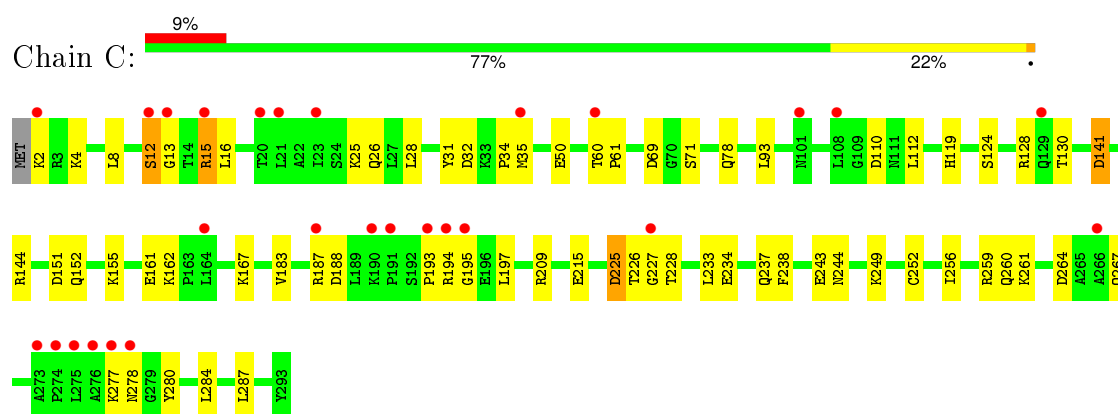
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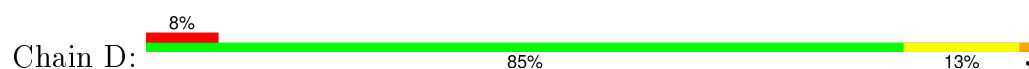
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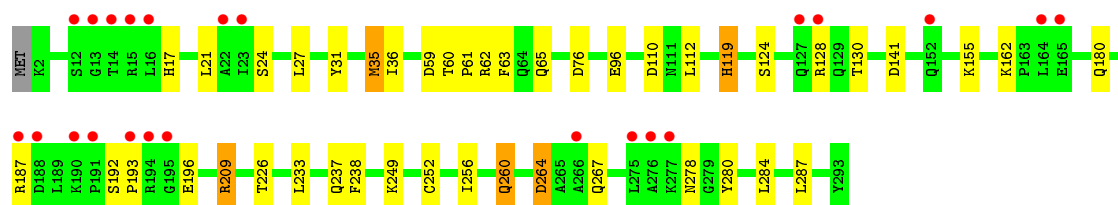


• Molecule 1: GLUCOSE-1-PHOSPHATE THYMIDYLTRANSFERASE

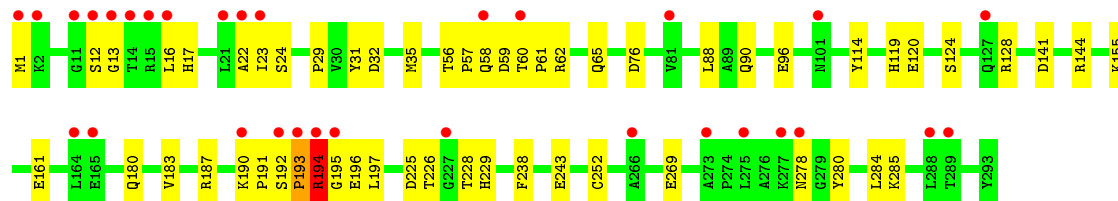
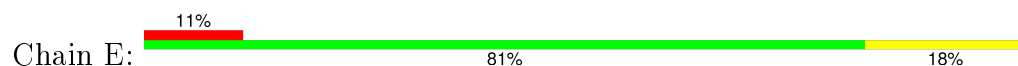


• Molecule 1: GLUCOSE-1-PHOSPHATE THYMIDYLTRANSFERASE

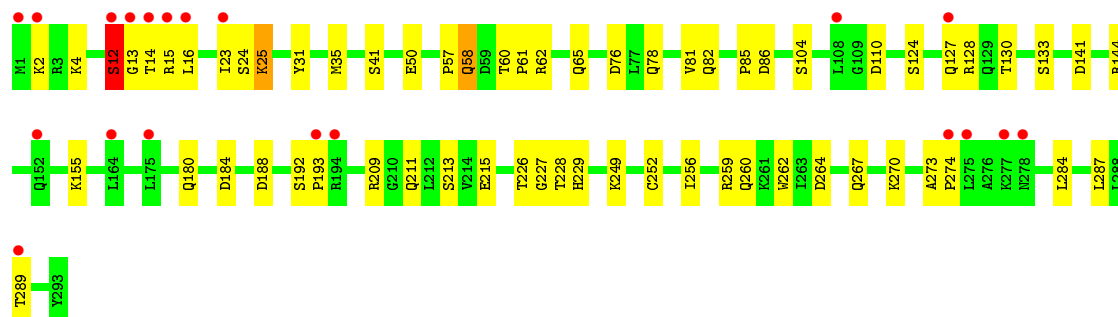
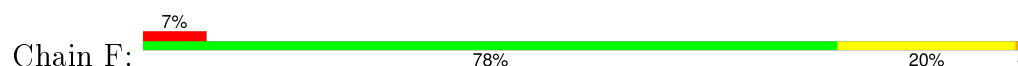




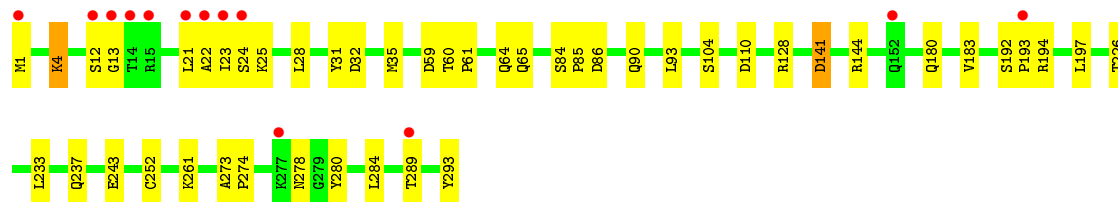
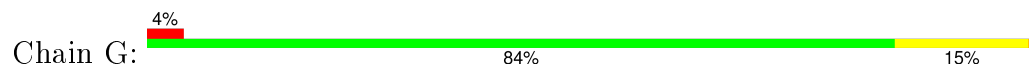
• Molecule 1: GLUCOSE-1-PHOSPHATE THYMIDYLTRANSFERASE



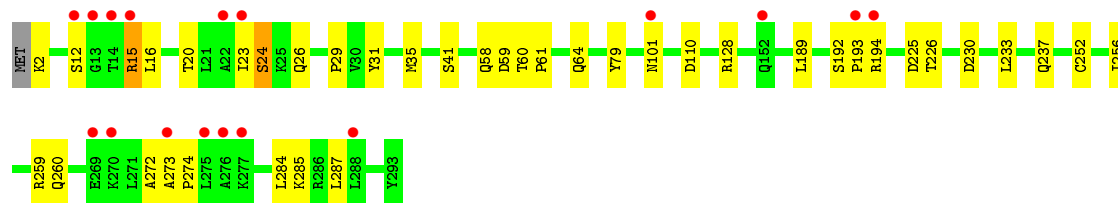
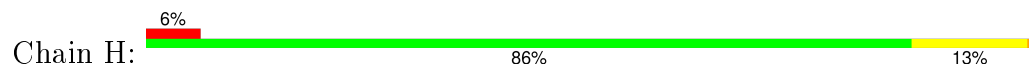
• Molecule 1: GLUCOSE-1-PHOSPHATE THYMIDYLTRANSFERASE



• Molecule 1: GLUCOSE-1-PHOSPHATE THYMIDYLTRANSFERASE



• Molecule 1: GLUCOSE-1-PHOSPHATE THYMIDYLTRANSFERASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	71.49 Å 73.06 Å 134.74 Å 89.93° 80.92° 81.11°	Depositor
Resolution (Å)	73.00 – 1.66 32.04 – 1.66	Depositor EDS
% Data completeness (in resolution range)	94.3 (73.00-1.66) 93.7 (32.04-1.66)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.83 (at 1.66 Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.142 , 0.196 0.174 , 0.221	Depositor DCC
R_{free} test set	14903 reflections (5.30%)	DCC
Wilson B-factor (Å ²)	17.5	Xtriage
Anisotropy	0.099	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 60.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 296555 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	22771	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.24% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: TMP, SO4

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.02	4/2427 (0.2%)	0.97	5/3290 (0.2%)
1	B	1.03	1/2395 (0.0%)	1.01	6/3247 (0.2%)
1	C	0.97	0/2448	0.97	4/3318 (0.1%)
1	D	0.96	1/2427 (0.0%)	0.97	7/3291 (0.2%)
1	E	0.95	2/2387 (0.1%)	0.95	2/3237 (0.1%)
1	F	1.03	1/2438 (0.0%)	0.99	7/3305 (0.2%)
1	G	1.07	5/2383 (0.2%)	1.02	5/3233 (0.2%)
1	H	1.00	1/2355 (0.0%)	0.96	4/3195 (0.1%)
All	All	1.00	15/19260 (0.1%)	0.98	40/26116 (0.2%)

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	2
1	D	0	2
1	E	0	2
All	All	0	6

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	128	ARG	CZ-NH2	-7.54	1.23	1.33
1	B	31	TYR	CD2-CE2	-6.79	1.29	1.39
1	E	114	TYR	CD2-CE2	6.63	1.49	1.39
1	A	128	ARG	CZ-NH2	-6.58	1.24	1.33
1	D	238	PHE	CE2-CZ	-6.44	1.25	1.37
1	A	293	TYR	CE1-CZ	-6.07	1.30	1.38
1	E	238	PHE	CE2-CZ	-6.00	1.25	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	258	TYR	CD1-CE1	-5.99	1.30	1.39
1	H	128	ARG	CZ-NH2	-5.93	1.25	1.33
1	G	4	LYS	CG-CD	-5.91	1.32	1.52
1	G	64	GLN	CB-CG	-5.83	1.36	1.52
1	F	127	GLN	CB-CG	5.68	1.67	1.52
1	G	128	ARG	CB-CG	-5.46	1.37	1.52
1	G	293	TYR	CE1-CZ	-5.25	1.31	1.38
1	A	178	TYR	CE1-CZ	-5.23	1.31	1.38

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	194	ARG	NE-CZ-NH2	-8.21	116.20	120.30
1	F	12	SER	N-CA-C	-6.98	92.14	111.00
1	G	194	ARG	NE-CZ-NH1	6.64	123.62	120.30
1	G	128	ARG	NE-CZ-NH2	-6.64	116.98	120.30
1	B	141	ASP	CB-CG-OD2	6.60	124.24	118.30
1	D	110	ASP	CB-CG-OD1	6.48	124.13	118.30
1	D	141	ASP	CB-CG-OD2	6.47	124.13	118.30
1	H	225	ASP	N-CA-CB	-6.31	99.23	110.60
1	A	259	ARG	NE-CZ-NH2	-6.15	117.22	120.30
1	G	194	ARG	NE-CZ-NH2	-6.15	117.22	120.30
1	B	194	ARG	NE-CZ-NH1	6.05	123.33	120.30
1	F	76	ASP	CB-CG-OD1	5.99	123.69	118.30
1	F	188	ASP	CB-CG-OD2	5.99	123.69	118.30
1	C	259	ARG	NE-CZ-NH1	5.99	123.29	120.30
1	A	230	ASP	CB-CG-OD1	5.94	123.65	118.30
1	B	102	ASP	CB-CG-OD2	5.90	123.61	118.30
1	C	151	ASP	CB-CG-OD1	5.90	123.61	118.30
1	D	76	ASP	CB-CG-OD2	5.88	123.59	118.30
1	A	259	ARG	NE-CZ-NH1	5.87	123.23	120.30
1	F	184	ASP	CB-CG-OD2	5.86	123.58	118.30
1	F	25	LYS	CD-CE-NZ	5.78	124.98	111.70
1	H	128	ARG	NE-CZ-NH2	-5.65	117.47	120.30
1	E	225	ASP	CB-CG-OD1	5.53	123.28	118.30
1	D	35[A]	MET	CG-SD-CE	5.50	109.00	100.20
1	D	35[B]	MET	CG-SD-CE	5.50	109.00	100.20
1	B	230	ASP	CB-CG-OD1	5.44	123.20	118.30
1	A	188	ASP	CB-CG-OD2	5.36	123.12	118.30
1	C	188	ASP	CB-CG-OD2	5.34	123.11	118.30
1	E	76	ASP	CB-CG-OD1	5.30	123.07	118.30
1	A	225	ASP	N-CA-CB	-5.25	101.15	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	194	ARG	NE-CZ-NH2	-5.24	117.68	120.30
1	H	230	ASP	CB-CG-OD1	5.23	123.01	118.30
1	F	86	ASP	CB-CG-OD2	5.21	122.98	118.30
1	D	264	ASP	CB-CG-OD2	5.16	122.94	118.30
1	B	128	ARG	NE-CZ-NH1	-5.14	117.73	120.30
1	C	141	ASP	CB-CG-OD1	5.10	122.89	118.30
1	F	259	ARG	NE-CZ-NH1	5.08	122.84	120.30
1	G	86	ASP	CB-CG-OD1	5.04	122.83	118.30
1	D	209	ARG	NE-CZ-NH2	-5.01	117.79	120.30
1	G	141	ASP	CB-CG-OD1	5.01	122.81	118.30

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	119[A]	HIS	Sidechain
1	A	17	HIS	Sidechain
1	D	119	HIS	Sidechain
1	D	17	HIS	Sidechain
1	E	17	HIS	Sidechain
1	E	229	HIS	Sidechain

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	2376	0	2348	60	0
1	B	2345	0	2328	58	0
1	C	2397	0	2369	70	0
1	D	2377	0	2353	40	0
1	E	2337	0	2317	54	0
1	F	2388	0	2368	71	0
1	G	2333	0	2320	57	0
1	H	2305	0	2289	44	0
2	A	5	0	0	0	0
2	C	10	0	0	2	0
2	D	25	0	0	2	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	15	0	0	3	0
2	F	5	0	0	1	0
2	G	5	0	0	0	0
3	A	63	0	38	1	0
3	B	63	0	39	2	0
3	C	63	0	39	6	0
3	D	63	0	39	2	0
3	E	42	0	26	2	0
3	F	63	0	39	8	0
3	G	63	0	39	3	0
3	H	63	0	39	3	0
4	A	450	0	0	15	1
4	B	486	0	0	13	2
4	C	391	0	0	29	0
4	D	381	0	0	15	5
4	E	375	0	0	21	1
4	F	399	0	0	23	2
4	G	457	0	0	13	1
4	H	426	0	0	5	3
All	All	22771	0	18990	411	8

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 11.

All (411) 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:D:24:SER:CB	1:D:27:LEU:HD12	1.51	1.39
1:D:24:SER:HB3	1:D:27:LEU:CD1	1.53	1.36
1:C:287:LEU:HD12	4:C:9821:HOH:O	1.37	1.22
1:G:141:ASP:OD2	1:G:144:ARG:HD3	1.48	1.14
1:F:78:GLN:NE2	4:F:9901:HOH:O	1.78	1.13
1:G:180:GLN:OE1	4:G:9964:HOH:O	1.76	1.02
3:H:9506[A]:TMP:O5'	3:H:9506[A]:TMP:H2'2	1.66	0.96
1:H:26:GLN:HB3	4:H:9751:HOH:O	1.65	0.96
1:A:119[B]:HIS:HE1	4:A:9721:HOH:O	1.46	0.95
1:E:23:ILE:HG21	1:F:23:ILE:CD1	1.97	0.94
1:F:57:PRO:HG3	1:F:81[A]:VAL:HG11	1.48	0.94
1:C:244:ASN:HB3	4:C:9754:HOH:O	1.68	0.93
1:H:24:SER:HB2	1:H:59:ASP:OD2	1.68	0.92
1:E:141:ASP:OD2	1:E:144:ARG:HD3	1.71	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:155:LYS:HE3	4:D:9625:HOH:O	1.71	0.90
1:F:2:LYS:NZ	1:F:50:GLU:OE1	2.05	0.89
1:C:60:THR:HG23	4:C:9688:HOH:O	1.71	0.89
1:B:141:ASP:OD2	1:B:144:ARG:HD3	1.71	0.89
2:E:5700:SO4:O3	4:E:9813:HOH:O	1.90	0.88
1:A:23:ILE:CD1	1:B:23:ILE:HG21	2.03	0.88
1:B:141:ASP:OD1	4:B:9608:HOH:O	1.91	0.88
1:F:141:ASP:OD2	1:F:144:ARG:HD3	1.74	0.88
1:C:35[A]:MET:SD	1:C:226:THR:OG1	2.33	0.87
1:E:23:ILE:HG21	1:F:23:ILE:HD13	1.57	0.87
1:G:23:ILE:HG21	1:H:23:ILE:CD1	2.05	0.86
1:G:65:GLN:HE22	1:H:58:GLN:HE22	1.19	0.86
3:G:9505[A]:TMP:O5'	3:G:9505[A]:TMP:H2'2	1.76	0.86
1:C:209:ARG:HG3	4:C:9897:HOH:O	1.76	0.86
1:G:22:ALA:HA	4:G:9927:HOH:O	1.76	0.86
1:G:65:GLN:HE22	1:H:58:GLN:NE2	1.74	0.85
1:A:23:ILE:HD11	1:B:23:ILE:HG21	1.58	0.85
3:B:9500[A]:TMP:H2'2	3:B:9500[A]:TMP:O5'	1.76	0.85
1:F:215[B]:GLU:OE1	4:F:9884:HOH:O	1.94	0.85
1:F:15:ARG:HD3	1:F:227:GLY:O	1.76	0.85
1:A:119[B]:HIS:CE1	4:A:9721:HOH:O	2.24	0.84
1:G:22:ALA:HB3	4:G:9928:HOH:O	1.77	0.84
1:C:71:SER:OG	4:C:9894:HOH:O	1.91	0.84
1:A:152:GLN:HG3	4:A:9952:HOH:O	1.78	0.83
2:D:3900:SO4:O4	4:D:9713:HOH:O	1.95	0.83
1:G:233[A]:LEU:HD11	1:H:237:GLN:HG3	1.62	0.82
1:C:155[A]:LYS:HE3	4:C:9720:HOH:O	1.78	0.82
1:C:78:GLN:OE1	4:C:9532:HOH:O	1.98	0.81
4:B:9794:HOH:O	1:E:155:LYS:HE3	1.81	0.81
1:E:23:ILE:CG2	1:F:23:ILE:HD11	2.12	0.80
1:C:141:ASP:OD2	1:C:144[A]:ARG:HD3	1.80	0.80
1:G:23:ILE:CG2	1:H:23:ILE:HD11	2.10	0.80
1:G:23:ILE:CD1	1:H:23:ILE:HG21	2.12	0.79
1:F:270:LYS:NZ	4:F:9895:HOH:O	2.14	0.79
1:G:65:GLN:NE2	1:H:58:GLN:HE22	1.80	0.79
1:A:192:SER:HB2	1:A:193:PRO:HD2	1.62	0.79
1:G:23:ILE:HD11	1:H:23:ILE:HG21	1.63	0.78
1:G:23:ILE:HD13	1:H:23:ILE:HD13	1.66	0.78
1:E:23:ILE:CG2	1:F:23:ILE:CD1	2.60	0.78
1:F:249:LYS:HE3	4:F:9788:HOH:O	1.82	0.78
1:G:237:GLN:HE21	1:H:237:GLN:HE22	1.32	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:141:ASP:OD1	4:G:9634:HOH:O	2.02	0.78
3:D:9502[A]:TMP:O5'	3:D:9502[A]:TMP:H2'2	1.82	0.78
1:F:12:SER:HA	1:F:85:PRO:HG3	1.66	0.77
1:G:93:LEU:HD23	4:G:9949:HOH:O	1.85	0.77
1:E:192:SER:OG	1:E:193:PRO:HD2	1.85	0.77
1:B:55[A]:SER:OG	4:B:9981:HOH:O	2.01	0.74
1:G:261:LYS:NZ	4:G:9956:HOH:O	2.19	0.74
1:A:24:SER:HB2	1:A:59:ASP:OD2	1.88	0.74
1:G:23:ILE:HG21	1:H:23:ILE:HD13	1.68	0.74
1:H:24:SER:CB	1:H:59:ASP:OD2	2.35	0.73
1:A:23:ILE:HD11	1:B:23:ILE:CG2	2.17	0.73
1:E:193:PRO:O	1:E:195:GLY:N	2.20	0.73
1:F:25:LYS:HE3	3:F:9504[B]:TMP:O3'	1.88	0.73
1:G:233[A]:LEU:HD11	1:H:237:GLN:CG	2.19	0.73
3:E:9503:TMP:O2P	4:E:9747:HOH:O	2.05	0.73
1:E:90:GLN:HG3	1:E:197:LEU:HD12	1.71	0.72
1:F:289:THR:OG1	4:F:9911:HOH:O	2.07	0.72
1:C:28:LEU:O	1:C:35[A]:MET:HB2	1.90	0.72
1:E:195:GLY:O	4:E:9700:HOH:O	2.08	0.72
1:A:23:ILE:HG21	1:B:23:ILE:HD11	1.71	0.72
1:C:26:GLN:O	4:C:9893:HOH:O	2.08	0.71
1:A:35[B]:MET:SD	1:A:226:THR:HG21	2.30	0.71
1:G:289:THR:OG1	4:G:9910:HOH:O	2.08	0.71
1:A:2:LYS:HB2	4:A:9768:HOH:O	1.90	0.71
1:A:23:ILE:HG21	1:B:23:ILE:CD1	2.21	0.70
1:F:155[A]:LYS:HE3	4:F:9728:HOH:O	1.90	0.70
1:G:23:ILE:HG21	1:H:23:ILE:HD11	1.70	0.70
1:A:141:ASP:OD1	4:A:9614:HOH:O	2.09	0.70
1:D:209:ARG:HD3	4:D:9569:HOH:O	1.91	0.69
1:C:256:ILE:O	1:C:260:GLN:HG3	1.91	0.69
1:G:35[B]:MET:SD	1:G:226:THR:OG1	2.50	0.69
1:H:192:SER:HB2	1:H:193:PRO:HD2	1.74	0.69
1:F:124:SER:OG	4:F:9883:HOH:O	1.94	0.69
1:A:119[B]:HIS:CD2	1:A:119[B]:HIS:C	2.65	0.69
3:F:9504[B]:TMP:P	4:F:9748:HOH:O	2.50	0.69
1:E:23:ILE:CD1	1:F:23:ILE:HG21	2.22	0.69
1:F:12:SER:CA	1:F:85:PRO:HG3	2.22	0.69
1:E:193:PRO:C	1:E:195:GLY:N	2.46	0.69
1:C:225:ASP:OD1	1:C:227:GLY:N	2.25	0.68
1:C:26:GLN:HA	1:C:35[B]:MET:HG2	1.76	0.68
1:A:86:ASP:OD2	4:A:9948:HOH:O	2.11	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:269:GLU:OE1	4:E:9712:HOH:O	2.10	0.68
1:A:237[B]:GLN:HG3	1:B:233:LEU:HD11	1.75	0.68
1:G:23:ILE:CG2	1:H:23:ILE:CD1	2.70	0.67
1:G:65:GLN:HG2	4:H:9757:HOH:O	1.93	0.67
1:B:197:LEU:HD13	4:B:9934:HOH:O	1.93	0.67
1:D:264:ASP:OD1	1:D:267:GLN:HG3	1.94	0.67
1:B:252[B]:CYS:SG	1:B:284:LEU:HD21	2.35	0.67
1:A:289:THR:OG1	4:A:9875:HOH:O	2.11	0.67
1:C:26:GLN:HB3	4:C:9591:HOH:O	1.95	0.67
1:E:24:SER:HB2	1:E:59:ASP:OD2	1.94	0.66
1:H:101:ASN:HB3	4:H:9929:HOH:O	1.96	0.66
1:A:141:ASP:OD2	1:A:144:ARG:HD3	1.93	0.66
1:E:183:VAL:O	1:E:187:ARG:HG3	1.96	0.66
3:C:9501[B]:TMP:O3P	4:C:9622:HOH:O	2.13	0.66
1:C:26:GLN:O	1:C:35[B]:MET:HB3	1.96	0.65
1:E:120:GLU:OE1	4:E:9805:HOH:O	2.14	0.65
1:H:189:LEU:CD2	4:H:9903:HOH:O	2.45	0.65
1:D:21:LEU:O	4:D:9650:HOH:O	2.13	0.65
1:G:23:ILE:HG23	1:H:23:ILE:HD11	1.78	0.65
1:D:180:GLN:OE1	4:D:9660:HOH:O	2.15	0.65
3:D:9502[B]:TMP:O3P	4:D:9644:HOH:O	2.15	0.65
1:F:12:SER:OG	1:F:13:GLY:N	2.30	0.65
1:E:23:ILE:HD13	1:F:23:ILE:HG21	1.77	0.64
1:B:197:LEU:HB3	4:B:9934:HOH:O	1.96	0.64
1:H:252[B]:CYS:SG	1:H:284:LEU:HD21	2.37	0.64
1:A:252[B]:CYS:SG	1:A:284:LEU:HD21	2.37	0.64
1:F:130[A]:THR:HG23	4:F:9878:HOH:O	1.97	0.64
1:E:124:SER:OG	4:E:9773:HOH:O	2.15	0.64
1:G:183:VAL:HG13	4:G:9949:HOH:O	1.98	0.63
1:A:23:ILE:HD13	1:B:23:ILE:HG21	1.79	0.63
3:F:9504[B]:TMP:H2'2	3:F:9504[B]:TMP:O5'	1.99	0.63
1:E:23:ILE:HG12	1:F:23:ILE:HG12	1.81	0.63
1:D:130[A]:THR:HG22	2:D:4800:SO4:O1	1.99	0.62
1:F:12:SER:HB3	4:F:9646:HOH:O	1.97	0.62
3:H:9506[A]:TMP:C2'	3:H:9506[A]:TMP:O5'	2.46	0.62
1:A:233:LEU:HD11	1:B:237[B]:GLN:HG3	1.80	0.62
1:C:2:LYS:NZ	1:C:50:GLU:OE1	2.28	0.62
1:A:90:GLN:HG2	1:A:197:LEU:HD12	1.81	0.62
1:E:35[A]:MET:SD	1:E:226:THR:OG1	2.57	0.62
1:H:35[A]:MET:SD	1:H:226:THR:OG1	2.57	0.61
1:B:2:LYS:HD3	4:B:9752:HOH:O	2.01	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:133:SER:HB3	1:F:215[B]:GLU:OE1	2.01	0.61
1:G:23:ILE:HD11	1:H:23:ILE:CG2	2.30	0.60
1:E:1:MET:CE	1:E:180:GLN:HE22	2.14	0.60
1:A:23:ILE:CD1	1:B:23:ILE:CG2	2.77	0.60
1:A:23:ILE:CG2	1:B:23:ILE:HD11	2.31	0.60
1:C:237[A]:GLN:HG2	1:D:233[A]:LEU:HD21	1.83	0.60
3:F:9504[A]:TMP:H2'2	3:F:9504[A]:TMP:O5'	2.01	0.60
1:E:88:LEU:HD11	4:E:9752:HOH:O	2.02	0.60
1:A:101:ASN:HB2	4:A:9951:HOH:O	2.00	0.60
1:A:180:GLN:OE1	4:A:9953:HOH:O	2.17	0.60
1:F:256:ILE:O	1:F:260:GLN:HG3	2.01	0.60
1:F:155[B]:LYS:HE3	4:F:9793:HOH:O	2.00	0.60
1:C:237[A]:GLN:HG3	1:D:233[A]:LEU:HD11	1.83	0.60
1:E:191:PRO:HD2	4:E:9592:HOH:O	2.02	0.60
1:D:128:ARG:NE	4:D:9590:HOH:O	2.33	0.60
1:A:119[B]:HIS:CD2	1:A:119[B]:HIS:O	2.55	0.60
1:C:278:ASN:OD1	1:C:280:TYR:N	2.34	0.59
1:C:12:SER:OG	1:C:13:GLY:N	2.35	0.59
1:B:237[A]:GLN:HG2	1:D:237[A]:GLN:HG2	1.85	0.59
1:B:278:ASN:OD1	1:B:280:TYR:N	2.35	0.59
1:D:256:ILE:O	1:D:260:GLN:HG3	2.03	0.58
1:E:23:ILE:HG21	1:F:23:ILE:HD11	1.74	0.58
1:D:249:LYS:HE3	4:D:9867:HOH:O	2.03	0.58
1:C:261:LYS:NZ	4:C:9841:HOH:O	2.37	0.58
1:F:192:SER:HB2	1:F:193:PRO:HD2	1.85	0.58
1:E:23:ILE:HG23	1:F:23:ILE:HD11	1.86	0.58
1:F:128:ARG:HD2	4:F:9888:HOH:O	2.03	0.58
3:F:9504[B]:TMP:O1P	4:F:9748:HOH:O	2.17	0.58
1:E:128:ARG:HD2	4:E:9633:HOH:O	2.03	0.58
1:A:23:ILE:HG22	1:A:24:SER:O	2.04	0.57
1:F:15:ARG:HG2	1:F:16:LEU:HG	1.85	0.57
1:E:278:ASN:OD1	1:E:280:TYR:N	2.37	0.57
1:H:273:ALA:HB3	1:H:274:PRO:HD3	1.87	0.57
1:C:15:ARG:HB3	4:C:9855:HOH:O	2.04	0.57
1:F:130[A]:THR:HG22	2:F:6700:SO4:O2	2.05	0.57
1:B:58:GLN:OE1	4:B:9984:HOH:O	2.18	0.57
1:A:23:ILE:HD13	1:B:23:ILE:HD13	1.86	0.56
1:G:1:MET:N	4:G:9576:HOH:O	2.26	0.56
1:C:16:LEU:HD21	1:C:228:THR:HA	1.87	0.56
1:H:192:SER:HB2	1:H:193:PRO:CD	2.35	0.56
1:A:58:GLN:OE1	1:A:62:ARG:NH1	2.37	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:65:GLN:HG3	4:D:9626:HOH:O	2.05	0.56
3:E:9503:TMP:H5'1	4:E:9752:HOH:O	2.05	0.56
1:A:270:LYS:HE2	4:A:9908:HOH:O	2.04	0.56
1:F:215[A]:GLU:HG3	4:F:9884:HOH:O	2.06	0.56
1:C:124[A]:SER:OG	4:C:9780:HOH:O	2.17	0.56
1:B:2:LYS:NZ	1:B:50:GLU:OE1	2.23	0.56
1:H:273:ALA:HB3	1:H:274:PRO:CD	2.35	0.55
1:G:24:SER:HB2	1:G:59:ASP:OD2	2.06	0.55
1:D:162[A]:LYS:NZ	4:D:9827:HOH:O	2.24	0.55
1:B:24:SER:HB2	1:B:59:ASP:OD2	2.06	0.55
1:C:141:ASP:OD1	4:C:9629:HOH:O	2.18	0.55
1:F:252[B]:CYS:SG	1:F:284:LEU:HD21	2.47	0.55
1:G:192:SER:HB2	1:G:193:PRO:HD2	1.88	0.55
1:B:1:MET:CE	4:E:9553:HOH:O	2.55	0.55
1:F:57:PRO:HD3	1:F:81[A]:VAL:HG13	1.89	0.55
1:H:24:SER:N	4:H:9905:HOH:O	2.30	0.55
1:E:12:SER:HA	4:E:9831:HOH:O	2.07	0.55
1:E:35[B]:MET:SD	1:E:226:THR:HG21	2.47	0.55
1:F:35[A]:MET:SD	1:F:226:THR:OG1	2.65	0.55
1:C:93:LEU:HD23	4:C:9761:HOH:O	2.07	0.55
3:G:9505[A]:TMP:O5'	3:G:9505[A]:TMP:C2'	2.52	0.54
1:A:23:ILE:HG12	1:B:23:ILE:HG12	1.89	0.54
1:C:112:LEU:C	1:C:112:LEU:HD23	2.28	0.54
1:D:209:ARG:HH11	1:D:209:ARG:HG3	1.71	0.54
1:F:15:ARG:HG2	1:F:16:LEU:N	2.21	0.54
1:D:24:SER:CB	1:D:27:LEU:CD1	2.39	0.54
1:C:237[A]:GLN:CG	1:D:233[A]:LEU:HD11	2.37	0.54
1:C:2:LYS:HE2	1:C:4:LYS:HE3	1.90	0.54
1:F:209[A]:ARG:NH2	1:F:211:GLN:HE22	2.06	0.53
1:G:23:ILE:HD13	1:H:23:ILE:HG21	1.88	0.53
1:A:162:LYS:NZ	1:A:194[B]:ARG:HH12	2.07	0.53
1:E:22:ALA:C	1:E:23:ILE:HG13	2.28	0.53
1:D:128:ARG:HD2	4:D:9590:HOH:O	2.09	0.53
1:F:50:GLU:HG3	4:F:9901:HOH:O	2.09	0.53
1:E:192:SER:OG	1:E:193:PRO:CD	2.55	0.53
1:G:273:ALA:HB3	1:G:274:PRO:CD	2.39	0.53
1:A:25:LYS:HE2	4:A:9692:HOH:O	2.07	0.53
1:G:23:ILE:HG22	1:G:24:SER:O	2.09	0.53
1:C:162:LYS:NZ	4:C:9681:HOH:O	2.42	0.53
1:C:225:ASP:C	1:C:225:ASP:OD1	2.46	0.53
1:A:192:SER:CB	1:A:193:PRO:HD2	2.38	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:90:GLN:CG	1:E:197:LEU:HD12	2.37	0.52
1:H:23:ILE:HG22	1:H:24:SER:O	2.09	0.52
1:C:249:LYS:HE3	4:C:9802:HOH:O	2.08	0.52
1:C:119[B]:HIS:C	1:C:119[B]:HIS:CD2	2.83	0.52
1:F:130[B]:THR:HG22	4:F:9878:HOH:O	2.10	0.52
1:D:252[B]:CYS:SG	1:D:284:LEU:HD21	2.51	0.51
1:E:58:GLN:HG2	1:E:62:ARG:NH1	2.25	0.51
1:E:193:PRO:O	1:E:194:ARG:C	2.49	0.51
1:H:60:THR:HB	1:H:61:PRO:HD3	1.92	0.51
1:E:119:HIS:ND1	4:E:9798:HOH:O	2.33	0.51
1:A:162:LYS:NZ	1:A:194[B]:ARG:NH1	2.58	0.51
1:C:28:LEU:O	1:C:35[A]:MET:HE3	2.10	0.51
1:C:25:LYS:O	1:C:28:LEU:N	2.29	0.51
1:C:183:VAL:HG13	4:C:9761:HOH:O	2.11	0.51
1:D:209:ARG:HH11	1:D:209:ARG:CG	2.24	0.51
1:B:110:ASP:CG	3:B:9500[A]:TMP:H3'	2.31	0.51
1:A:35[A]:MET:SD	1:A:226:THR:OG1	2.66	0.51
1:C:234:GLU:OE2	4:C:9856:HOH:O	2.19	0.50
1:D:192:SER:HB2	1:D:193:PRO:HD2	1.92	0.50
1:B:128:ARG:NH2	2:E:4700:SO4:O2	2.45	0.50
1:B:57:PRO:HG3	1:B:81:VAL:CG1	2.41	0.50
1:C:130[A]:THR:HG22	2:C:3800:SO4:O4	2.11	0.50
1:B:35[A]:MET:SD	1:B:226:THR:OG1	2.69	0.50
1:F:209[A]:ARG:HH21	1:F:211:GLN:HE22	1.60	0.50
1:B:19:ALA:O	4:B:9743:HOH:O	2.19	0.50
1:B:189:LEU:CD2	4:B:9936:HOH:O	2.60	0.50
1:C:233:LEU:HD12	1:D:233[A]:LEU:CD1	2.41	0.50
4:C:9579:HOH:O	1:D:233[B]:LEU:HD23	2.12	0.50
1:F:81[A]:VAL:CG1	1:F:82:GLN:N	2.75	0.49
1:D:196:GLU:HG3	4:D:9725:HOH:O	2.11	0.49
1:C:60:THR:CG2	4:C:9688:HOH:O	2.46	0.49
1:D:128:ARG:CD	4:D:9590:HOH:O	2.60	0.49
1:F:229:HIS:HE1	4:F:9642:HOH:O	1.94	0.49
1:D:35[B]:MET:SD	1:D:226:THR:OG1	2.67	0.49
1:D:36:ILE:HD12	1:D:63:PHE:CE2	2.48	0.49
1:G:252[B]:CYS:SG	1:G:284:LEU:HD21	2.53	0.49
1:E:285:LYS:HE2	4:E:9649:HOH:O	2.11	0.49
1:A:24:SER:OG	1:A:26:GLN:OE1	2.31	0.49
1:B:57:PRO:HG3	1:B:81:VAL:HG11	1.93	0.49
1:C:34:PRO:HB3	4:C:9635:HOH:O	2.13	0.49
1:C:233:LEU:CD1	1:D:233[A]:LEU:HD12	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:110:ASP:OD2	3:F:9504[A]:TMP:H3'	2.13	0.48
1:G:273:ALA:HB3	1:G:274:PRO:HD3	1.95	0.48
1:A:60:THR:HB	1:A:61:PRO:HD3	1.95	0.48
1:G:25:LYS:O	1:G:35[A]:MET:HE3	2.13	0.48
1:A:194[B]:ARG:O	1:A:194[B]:ARG:HG3	2.13	0.48
1:E:23:ILE:HG23	1:F:23:ILE:CD1	2.43	0.48
1:E:193:PRO:C	1:E:195:GLY:H	2.15	0.48
1:D:59:ASP:OD1	1:D:62:ARG:NH1	2.47	0.48
1:B:192:SER:HB2	1:B:193:PRO:CD	2.43	0.48
1:D:287:LEU:HG	4:D:9747:HOH:O	2.14	0.48
1:C:25:LYS:HE3	3:C:9501[B]:TMP:O3'	2.14	0.47
1:E:161:GLU:O	1:E:194:ARG:NH2	2.47	0.47
1:G:25:LYS:HB3	1:G:25:LYS:HE2	1.74	0.47
1:A:17:HIS:O	4:A:9887:HOH:O	2.20	0.47
1:A:58:GLN:HE22	1:B:65:GLN:HE22	1.63	0.47
1:C:252[B]:CYS:SG	1:C:284:LEU:HD21	2.54	0.47
1:C:161:GLU:O	1:C:194:ARG:NH2	2.46	0.47
1:G:24:SER:HB2	1:G:59:ASP:CG	2.35	0.47
1:E:60:THR:HB	1:E:61:PRO:HD3	1.97	0.47
3:A:8500[A]:TMP:H2'2	3:A:8500[A]:TMP:O5'	2.15	0.47
1:B:20:THR:HA	1:B:23:ILE:O	2.15	0.47
1:A:60:THR:N	1:A:61:PRO:CD	2.77	0.47
1:B:133:SER:HB3	4:B:9803:HOH:O	2.15	0.47
1:C:197:LEU:HD13	4:C:9834:HOH:O	2.13	0.47
1:A:237[B]:GLN:CG	1:B:233:LEU:HD11	2.44	0.47
1:B:18:PRO:HA	1:B:21:LEU:HG	1.96	0.47
1:H:20:THR:HA	1:H:23:ILE:O	2.16	0.46
1:C:60:THR:N	1:C:61:PRO:HD2	2.29	0.46
1:B:189:LEU:HD23	4:B:9936:HOH:O	2.14	0.46
1:C:25:LYS:CE	3:C:9501[B]:TMP:O3'	2.64	0.46
1:G:141:ASP:OD2	1:G:144:ARG:CD	2.39	0.46
1:C:144[B]:ARG:NH1	4:C:9783:HOH:O	2.48	0.46
1:F:58:GLN:NE2	4:F:9639:HOH:O	2.48	0.46
1:B:234:GLU:HA	1:B:237[B]:GLN:HE21	1.80	0.46
1:C:277:LYS:N	1:C:277:LYS:HD2	2.30	0.46
1:A:23:ILE:HD13	1:B:23:ILE:CD1	2.46	0.46
1:B:124[A]:SER:OG	4:B:9558:HOH:O	2.20	0.46
1:F:213[A]:SER:OG	1:F:215[A]:GLU:OE2	2.33	0.46
1:B:141:ASP:OD2	1:B:144:ARG:CD	2.53	0.45
1:H:64:GLN:HG2	1:H:79:TYR:CG	2.52	0.45
1:E:23:ILE:CD1	1:F:23:ILE:CG2	2.94	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:167:LYS:HE3	4:C:9724:HOH:O	2.15	0.45
1:E:1:MET:HE1	1:E:180:GLN:HE22	1.82	0.45
1:F:16:LEU:HD21	1:F:228:THR:HA	1.97	0.45
1:B:1:MET:HE2	4:E:9553:HOH:O	2.16	0.45
1:F:180:GLN:HG3	4:F:9606:HOH:O	2.16	0.45
1:G:233[A]:LEU:HD12	1:H:233:LEU:CD1	2.47	0.45
1:D:119:HIS:HD2	4:D:9809:HOH:O	1.98	0.45
1:F:23:ILE:HG22	1:F:24:SER:O	2.17	0.45
1:A:233:LEU:HD12	1:B:233:LEU:CD1	2.46	0.45
1:B:1:MET:HE3	4:E:9553:HOH:O	2.16	0.45
1:F:273:ALA:HB3	1:F:274:PRO:HD3	1.98	0.45
1:A:23:ILE:CD1	1:B:23:ILE:HG12	2.47	0.45
1:G:192:SER:HB2	1:G:193:PRO:CD	2.47	0.45
1:F:4:LYS:HE2	4:F:9687:HOH:O	2.17	0.45
1:F:81[A]:VAL:HG12	1:F:82:GLN:N	2.29	0.44
1:G:25:LYS:O	1:G:35[A]:MET:CE	2.65	0.44
1:E:128:ARG:NE	4:E:9633:HOH:O	2.50	0.44
1:D:112:LEU:HD23	1:D:112:LEU:C	2.36	0.44
1:H:110:ASP:OD2	3:H:9506[A]:TMP:H3'	2.17	0.44
1:F:287:LEU:HG	4:F:9671:HOH:O	2.17	0.44
1:H:26:GLN:HA	1:H:35[B]:MET:HG2	1.98	0.44
1:C:25:LYS:HG3	4:C:9562:HOH:O	2.16	0.44
1:A:162:LYS:HZ2	1:A:194[B]:ARG:NH1	2.15	0.44
1:B:192:SER:HB2	1:B:193:PRO:HD2	1.98	0.44
1:D:24:SER:HB3	1:D:27:LEU:HD12	0.62	0.44
1:G:22:ALA:CB	4:G:9928:HOH:O	2.48	0.44
1:D:60:THR:HB	1:D:61:PRO:HD3	1.99	0.44
1:C:193:PRO:C	1:C:195:GLY:H	2.21	0.44
1:F:57:PRO:HD3	1:F:81[A]:VAL:CG1	2.47	0.44
1:E:1:MET:CE	1:E:180:GLN:NE2	2.80	0.44
1:E:96:GLU:OE2	4:E:9884:HOH:O	2.21	0.44
1:H:272:ALA:HB1	1:H:285:LYS:HG3	2.00	0.44
1:B:23:ILE:HG22	1:B:24:SER:O	2.18	0.43
1:C:69:ASP:OD1	4:C:9894:HOH:O	2.21	0.43
1:A:233:LEU:CD1	1:B:233:LEU:HD12	2.49	0.43
1:B:16:LEU:HD21	1:B:228:THR:HA	2.00	0.43
1:A:237[B]:GLN:HG2	1:B:233:LEU:HD21	1.99	0.43
1:F:264:ASP:OD1	1:F:267:GLN:HG3	2.18	0.43
1:A:273:ALA:N	1:A:274:PRO:HD2	2.33	0.43
1:E:32:ASP:OD2	1:E:243:GLU:OE1	2.37	0.43
1:F:60:THR:HB	1:F:61:PRO:HD3	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:13:GLY:HA3	4:G:9810:HOH:O	2.17	0.43
1:F:141:ASP:OD2	1:F:144:ARG:CD	2.58	0.43
3:C:9501[A]:TMP:H2'2	3:C:9501[A]:TMP:O5'	2.17	0.43
1:C:278:ASN:OD1	1:C:278:ASN:C	2.56	0.43
1:C:193:PRO:C	1:C:195:GLY:N	2.72	0.43
1:C:28:LEU:O	1:C:35[B]:MET:HB2	2.19	0.43
1:F:25:LYS:CE	3:F:9504[B]:TMP:O3'	2.63	0.43
1:E:128:ARG:CD	4:E:9633:HOH:O	2.64	0.43
1:F:141:ASP:CG	1:F:144:ARG:HD3	2.38	0.43
1:G:32:ASP:OD2	1:G:243:GLU:OE1	2.36	0.43
1:F:25:LYS:NZ	4:F:9768:HOH:O	2.51	0.42
1:A:22:ALA:C	1:A:23:ILE:HG13	2.38	0.42
1:C:8:LEU:HG	3:C:9501[A]:TMP:O2	2.18	0.42
1:E:61:PRO:O	1:E:65:GLN:HG3	2.19	0.42
1:C:233:LEU:CD1	1:D:233[A]:LEU:CD1	2.97	0.42
1:G:4:LYS:O	1:G:104:SER:HA	2.20	0.42
2:E:5700:SO4:O2	1:F:62:ARG:NH2	2.47	0.42
1:C:187:ARG:HG3	4:C:9761:HOH:O	2.18	0.42
1:C:152:GLN:HG3	2:C:4000:SO4:O3	2.19	0.42
1:C:110:ASP:CG	3:C:9501[A]:TMP:H3'	2.40	0.42
1:C:233:LEU:HD11	1:D:237[B]:GLN:HG3	2.00	0.42
1:F:260:GLN:NE2	1:F:262:TRP:CH2	2.87	0.42
1:G:60:THR:HB	1:G:61:PRO:HD3	2.02	0.42
1:E:13:GLY:HA3	4:E:9853:HOH:O	2.19	0.42
1:F:57:PRO:CG	1:F:81[A]:VAL:HG11	2.33	0.42
1:A:29:PRO:HG2	4:A:9835:HOH:O	2.20	0.42
3:F:9504[A]:TMP:O5'	3:F:9504[A]:TMP:C2'	2.67	0.42
1:E:252[B]:CYS:SG	1:E:284:LEU:HD21	2.60	0.42
1:B:29:PRO:HG2	4:B:9843:HOH:O	2.20	0.42
1:B:273:ALA:HB3	1:B:274:PRO:CD	2.50	0.41
1:E:56:THR:HB	1:E:57:PRO:HD2	2.01	0.41
1:G:28:LEU:HD22	1:H:29:PRO:HD2	2.02	0.41
1:G:180:GLN:HG2	4:G:9718:HOH:O	2.19	0.41
1:G:23:ILE:HG12	1:H:23:ILE:HG12	2.02	0.41
1:F:15:ARG:CD	1:F:227:GLY:O	2.60	0.41
1:A:23:ILE:HD13	1:B:23:ILE:CG1	2.50	0.41
1:A:192:SER:HB2	1:A:193:PRO:CD	2.43	0.41
1:H:15:ARG:HG2	1:H:16:LEU:HD23	2.02	0.41
1:B:25:LYS:HE2	1:B:25:LYS:HB3	1.89	0.41
1:D:278:ASN:OD1	1:D:280:TYR:N	2.53	0.41
1:H:41:SER:HB2	1:H:256:ILE:CD1	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:41:SER:HB2	1:F:256:ILE:CD1	2.51	0.41
1:C:264:ASP:OD1	1:C:267:GLN:HG3	2.21	0.41
1:A:230:ASP:CG	4:A:9906:HOH:O	2.58	0.41
1:G:90:GLN:CG	1:G:197:LEU:HD12	2.50	0.41
4:E:9740:HOH:O	1:F:65:GLN:HG2	2.21	0.41
1:H:192:SER:CB	1:H:193:PRO:CD	2.98	0.41
1:H:259:ARG:NH2	1:H:287:LEU:HD22	2.36	0.41
1:G:278:ASN:OD1	1:G:280:TYR:N	2.52	0.41
1:E:192:SER:HB3	1:E:196:GLU:N	2.36	0.41
1:A:191:PRO:HD3	4:A:9889:HOH:O	2.21	0.41
1:A:238:PHE:CE1	1:C:238:PHE:CE1	3.09	0.41
1:C:25:LYS:HE3	1:C:110:ASP:OD2	2.21	0.40
1:C:32:ASP:OD2	1:C:243:GLU:OE1	2.39	0.40
1:A:23:ILE:CG1	1:B:23:ILE:HG12	2.51	0.40
1:G:110:ASP:CG	3:G:9505[A]:TMP:H3'	2.42	0.40
1:D:96:GLU:OE1	1:D:187:ARG:NH1	2.53	0.40
1:E:16:LEU:HD21	1:E:228:THR:HA	2.03	0.40
1:G:21:LEU:HA	1:G:21:LEU:HD23	1.87	0.40
1:F:4:LYS:O	1:F:104:SER:HA	2.21	0.40
1:B:272:ALA:HB1	1:B:285:LYS:HG3	2.03	0.40
1:G:23:ILE:CD1	1:H:23:ILE:CG2	2.92	0.40
1:C:60:THR:CB	4:C:9688:HOH:O	2.69	0.40
1:F:128:ARG:NE	4:F:9888:HOH:O	2.54	0.40
1:G:193:PRO:N	4:G:9835:HOH:O	2.54	0.40
1:A:194[B]:ARG:O	1:A:194[B]:ARG:CG	2.69	0.40
1:E:190:LYS:HA	1:E:191:PRO:HD3	1.88	0.40
1:G:84[A]:SER:OG	1:G:85:PRO:HD2	2.22	0.40
1:C:128[B]:ARG:NH2	1:C:215:GLU:OE2	2.54	0.40

All (8) 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)
4:D:9860:HOH:O	4:E:9857:HOH:O[1_655]	1.93	0.27
4:D:9569:HOH:O	4:H:9651:HOH:O[1_565]	2.01	0.19
4:D:9563:HOH:O	4:H:9651:HOH:O[1_565]	2.15	0.05
4:A:9763:HOH:O	4:F:9762:HOH:O[1_566]	2.15	0.05
2:D:3900:SO4:O2	4:B:9956:HOH:O[1_655]	2.16	0.04
4:F:9619:HOH:O	4:G:9811:HOH:O[1_455]	2.17	0.03
4:B:9978:HOH:O	4:D:9669:HOH:O[1_455]	2.18	0.02
4:D:9775:HOH:O	4:H:9697:HOH:O[1_565]	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	301/293 (103%)	296 (98%)	4 (1%)	1 (0%)	46	24
1	B	298/293 (102%)	292 (98%)	6 (2%)	0	100	100
1	C	304/293 (104%)	296 (97%)	7 (2%)	1 (0%)	46	24
1	D	302/293 (103%)	297 (98%)	4 (1%)	1 (0%)	46	24
1	E	297/293 (101%)	291 (98%)	3 (1%)	3 (1%)	19	3
1	F	303/293 (103%)	298 (98%)	3 (1%)	2 (1%)	26	7
1	G	297/293 (101%)	293 (99%)	3 (1%)	1 (0%)	46	24
1	H	293/293 (100%)	287 (98%)	5 (2%)	1 (0%)	46	24
All	All	2395/2344 (102%)	2350 (98%)	35 (2%)	10 (0%)	39	18

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	12	SER
1	E	194	ARG
1	F	31	TYR
1	H	31	TYR
1	A	31	TYR
1	C	31	TYR
1	D	31	TYR
1	E	31	TYR
1	E	193	PRO
1	G	31	TYR

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	250/240 (104%)	246 (98%)	4 (2%)	70	48
1	B	247/240 (103%)	244 (99%)	3 (1%)	78	60
1	C	253/240 (105%)	250 (99%)	3 (1%)	78	60
1	D	251/240 (105%)	248 (99%)	3 (1%)	78	60
1	E	246/240 (102%)	244 (99%)	2 (1%)	86	76
1	F	252/240 (105%)	250 (99%)	2 (1%)	86	76
1	G	246/240 (102%)	245 (100%)	1 (0%)	93	89
1	H	242/240 (101%)	237 (98%)	5 (2%)	61	34
All	All	1987/1920 (104%)	1964 (99%)	23 (1%)	80	60

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	LYS
1	A	15	ARG
1	A	24	SER
1	A	260	GLN
1	B	12	SER
1	B	24	SER
1	B	260	GLN
1	C	12	SER
1	C	15	ARG
1	C	225	ASP
1	D	124[A]	SER
1	D	124[B]	SER
1	D	260	GLN
1	E	29	PRO
1	E	194	ARG
1	F	14	THR
1	F	58	GLN
1	G	12	SER
1	H	2	LYS
1	H	12	SER
1	H	15	ARG
1	H	24	SER
1	H	260	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	17	HIS
1	B	65	GLN
1	C	17	HIS
1	C	260	GLN
1	C	282	GLN
1	E	58	GLN
1	E	119	HIS
1	F	58	GLN
1	F	282	GLN
1	G	17	HIS
1	G	58	GLN
1	G	65	GLN
1	G	119	HIS
1	G	180	GLN
1	G	237	GLN
1	H	17	HIS
1	H	119	HIS
1	H	180	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

36 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	SO4	A	3700	-	4,4,4	0.53	0	6,6,6	0.97	0
3	TMP	A	8500[A]	-	17,22,22	2.02	5 (29%)	22,33,33	2.65	10 (45%)
3	TMP	A	8500[B]	-	17,22,22	2.04	5 (29%)	22,33,33	2.84	10 (45%)
3	TMP	A	9507	-	17,22,22	1.38	2 (11%)	22,33,33	1.89	4 (18%)
3	TMP	B	9500[A]	-	17,22,22	2.19	6 (35%)	22,33,33	4.39	11 (50%)
3	TMP	B	9500[B]	-	17,22,22	2.07	6 (35%)	22,33,33	2.69	8 (36%)
3	TMP	B	9508	-	17,22,22	1.42	2 (11%)	22,33,33	2.69	7 (31%)
2	SO4	C	3800	-	4,4,4	0.16	0	6,6,6	0.41	0
2	SO4	C	4000	-	4,4,4	1.07	0	6,6,6	0.81	0
3	TMP	C	9501[A]	-	17,22,22	2.14	5 (29%)	22,33,33	4.25	12 (54%)
3	TMP	C	9501[B]	-	17,22,22	1.97	5 (29%)	22,33,33	3.45	10 (45%)
3	TMP	C	9509	-	17,22,22	1.55	5 (29%)	22,33,33	2.84	6 (27%)
2	SO4	D	3900	-	4,4,4	0.67	0	6,6,6	0.49	0
2	SO4	D	4800	-	4,4,4	0.08	0	6,6,6	0.25	0
2	SO4	D	5000	-	4,4,4	0.31	0	6,6,6	0.42	0
2	SO4	D	5100	-	4,4,4	0.72	0	6,6,6	1.12	0
2	SO4	D	5200	-	4,4,4	0.26	0	6,6,6	0.37	0
3	TMP	D	9502[A]	-	17,22,22	2.13	5 (29%)	22,33,33	4.29	11 (50%)
3	TMP	D	9502[B]	-	17,22,22	2.10	6 (35%)	22,33,33	2.79	5 (22%)
3	TMP	D	9510	-	17,22,22	1.37	2 (11%)	22,33,33	2.57	6 (27%)
2	SO4	E	4700	-	4,4,4	0.14	0	6,6,6	0.69	0
2	SO4	E	5700	-	4,4,4	0.44	0	6,6,6	0.24	0
2	SO4	E	5800	-	4,4,4	0.30	0	6,6,6	0.36	0
3	TMP	E	9503	-	17,22,22	2.11	4 (23%)	22,33,33	3.79	10 (45%)
3	TMP	E	9511	-	17,22,22	1.88	6 (35%)	22,33,33	2.81	9 (40%)
2	SO4	F	6700	-	4,4,4	0.19	0	6,6,6	0.32	0
3	TMP	F	9504[A]	-	17,22,22	2.10	4 (23%)	22,33,33	3.00	7 (31%)
3	TMP	F	9504[B]	-	17,22,22	1.97	4 (23%)	22,33,33	3.09	7 (31%)
3	TMP	F	9512	-	17,22,22	1.12	2 (11%)	22,33,33	2.19	5 (22%)
2	SO4	G	7700	-	4,4,4	0.59	0	6,6,6	0.31	0
3	TMP	G	9505[A]	-	17,22,22	2.04	6 (35%)	22,33,33	4.37	11 (50%)
3	TMP	G	9505[B]	-	17,22,22	1.90	5 (29%)	22,33,33	3.26	11 (50%)
3	TMP	G	9513	-	17,22,22	1.25	1 (5%)	22,33,33	2.69	8 (36%)
3	TMP	H	9506[A]	-	17,22,22	2.20	7 (41%)	22,33,33	4.18	10 (45%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	TMP	H	9506[B]	-	17,22,22	2.06	6 (35%)	22,33,33	4.57	13 (59%)
3	TMP	H	9514	-	17,22,22	1.59	4 (23%)	22,33,33	2.03	3 (13%)

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	3700	-	-	0/0/0/0	0/0/0/0
3	TMP	A	8500[A]	-	-	0/6/22/22	0/2/2/2
3	TMP	A	8500[B]	-	-	0/6/22/22	0/2/2/2
3	TMP	A	9507	-	-	0/6/22/22	0/2/2/2
3	TMP	B	9500[A]	-	-	0/6/22/22	0/2/2/2
3	TMP	B	9500[B]	-	-	0/6/22/22	0/2/2/2
3	TMP	B	9508	-	-	0/6/22/22	0/2/2/2
2	SO4	C	3800	-	-	0/0/0/0	0/0/0/0
2	SO4	C	4000	-	-	0/0/0/0	0/0/0/0
3	TMP	C	9501[A]	-	-	0/6/22/22	0/2/2/2
3	TMP	C	9501[B]	-	-	0/6/22/22	0/2/2/2
3	TMP	C	9509	-	-	0/6/22/22	0/2/2/2
2	SO4	D	3900	-	-	0/0/0/0	0/0/0/0
2	SO4	D	4800	-	-	0/0/0/0	0/0/0/0
2	SO4	D	5000	-	-	0/0/0/0	0/0/0/0
2	SO4	D	5100	-	-	0/0/0/0	0/0/0/0
2	SO4	D	5200	-	-	0/0/0/0	0/0/0/0
3	TMP	D	9502[A]	-	-	0/6/22/22	0/2/2/2
3	TMP	D	9502[B]	-	-	0/6/22/22	0/2/2/2
3	TMP	D	9510	-	-	0/6/22/22	0/2/2/2
2	SO4	E	4700	-	-	0/0/0/0	0/0/0/0
2	SO4	E	5700	-	-	0/0/0/0	0/0/0/0
2	SO4	E	5800	-	-	0/0/0/0	0/0/0/0
3	TMP	E	9503	-	-	0/6/22/22	0/2/2/2
3	TMP	E	9511	-	-	0/6/22/22	0/2/2/2
2	SO4	F	6700	-	-	0/0/0/0	0/0/0/0
3	TMP	F	9504[A]	-	-	0/6/22/22	0/2/2/2
3	TMP	F	9504[B]	-	-	0/6/22/22	0/2/2/2
3	TMP	F	9512	-	-	0/6/22/22	0/2/2/2
2	SO4	G	7700	-	-	0/0/0/0	0/0/0/0
3	TMP	G	9505[A]	-	-	0/6/22/22	0/2/2/2
3	TMP	G	9505[B]	-	-	0/6/22/22	0/2/2/2
3	TMP	G	9513	-	-	0/6/22/22	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	TMP	H	9506[A]	-	-	0/6/22/22	0/2/2/2
3	TMP	H	9506[B]	-	-	0/6/22/22	0/2/2/2
3	TMP	H	9514	-	-	0/6/22/22	0/2/2/2

All (103) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	9511	TMP	O4'-C4'	-3.64	1.36	1.45
3	B	9508	TMP	O4'-C4'	-3.25	1.37	1.45
3	G	9505[B]	TMP	C3'-C4'	-2.93	1.44	1.53
3	B	9500[B]	TMP	C3'-C4'	-2.89	1.44	1.53
3	H	9506[B]	TMP	O4'-C4'	-2.51	1.39	1.45
3	D	9502[B]	TMP	C3'-C4'	-2.50	1.45	1.53
3	H	9514	TMP	O4'-C4'	-2.50	1.39	1.45
3	A	9507	TMP	C2'-C1'	-2.46	1.45	1.52
3	B	9500[A]	TMP	O4'-C4'	-2.40	1.39	1.45
3	H	9506[B]	TMP	C3'-C4'	-2.37	1.46	1.53
3	H	9506[A]	TMP	C3'-C4'	-2.31	1.46	1.53
3	C	9501[B]	TMP	C3'-C4'	-2.30	1.46	1.53
3	G	9505[A]	TMP	O4'-C4'	-2.26	1.39	1.45
3	D	9502[B]	TMP	C6-N1	-2.21	1.31	1.35
3	A	8500[B]	TMP	C3'-C4'	-2.21	1.46	1.53
3	G	9513	TMP	O4'-C4'	-2.20	1.39	1.45
3	H	9506[A]	TMP	O4'-C4'	-2.15	1.40	1.45
3	C	9509	TMP	O3'-C3'	-2.12	1.38	1.43
3	H	9514	TMP	P-O3P	2.00	1.61	1.54
3	C	9509	TMP	P-O3P	2.07	1.62	1.54
3	F	9512	TMP	P-O1P	2.14	1.58	1.51
3	E	9511	TMP	P-O2P	2.15	1.62	1.54
3	A	9507	TMP	P-O1P	2.22	1.58	1.51
3	E	9511	TMP	C5'-C4'	2.22	1.58	1.51
3	G	9505[B]	TMP	O4-C4	2.28	1.30	1.24
3	G	9505[A]	TMP	C2'-C3'	2.35	1.59	1.52
3	F	9512	TMP	P-O3P	2.40	1.63	1.54
3	E	9511	TMP	C6-N1	2.45	1.38	1.35
3	H	9514	TMP	P-O1P	2.49	1.59	1.51
3	D	9502[A]	TMP	C2'-C3'	2.49	1.59	1.52
3	C	9509	TMP	P-O2P	2.54	1.63	1.54
3	C	9509	TMP	C2'-C3'	2.55	1.59	1.52
3	H	9506[A]	TMP	C2'-C3'	2.57	1.59	1.52
3	B	9500[A]	TMP	C2'-C3'	2.59	1.59	1.52
3	E	9511	TMP	P-O3P	2.72	1.64	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	9510	TMP	P-O2P	2.74	1.64	1.54
3	C	9501[A]	TMP	P-O1P	2.74	1.60	1.51
3	F	9504[B]	TMP	O4-C4	2.74	1.31	1.24
3	C	9501[A]	TMP	C2'-C3'	2.78	1.60	1.52
3	B	9500[B]	TMP	O4'-C1'	2.78	1.48	1.42
3	B	9500[B]	TMP	O4-C4	2.82	1.31	1.24
3	B	9508	TMP	O4-C4	2.84	1.31	1.24
3	G	9505[A]	TMP	O4-C4	2.86	1.31	1.24
3	F	9504[B]	TMP	P-O1P	2.94	1.60	1.51
3	F	9504[A]	TMP	P-O1P	2.96	1.60	1.51
3	D	9502[B]	TMP	P-O1P	2.96	1.60	1.51
3	A	8500[A]	TMP	P-O1P	2.99	1.61	1.51
3	E	9503	TMP	P-O1P	3.00	1.61	1.51
3	C	9509	TMP	O4-C4	3.02	1.31	1.24
3	E	9511	TMP	O4-C4	3.05	1.32	1.24
3	C	9501[B]	TMP	P-O1P	3.05	1.61	1.51
3	D	9502[A]	TMP	P-O1P	3.05	1.61	1.51
3	B	9500[A]	TMP	P-O1P	3.06	1.61	1.51
3	A	8500[B]	TMP	P-O1P	3.09	1.61	1.51
3	H	9514	TMP	O4-C4	3.11	1.32	1.24
3	A	8500[B]	TMP	O4-C4	3.13	1.32	1.24
3	H	9506[A]	TMP	P-O1P	3.14	1.61	1.51
3	G	9505[A]	TMP	P-O1P	3.16	1.61	1.51
3	D	9510	TMP	O4-C4	3.17	1.32	1.24
3	A	8500[A]	TMP	O4-C4	3.22	1.32	1.24
3	C	9501[A]	TMP	O4-C4	3.22	1.32	1.24
3	B	9500[A]	TMP	O4-C4	3.24	1.32	1.24
3	A	8500[A]	TMP	O3'-C3'	3.28	1.50	1.43
3	G	9505[B]	TMP	P-O3P	3.41	1.67	1.54
3	H	9506[B]	TMP	O4-C4	3.43	1.32	1.24
3	H	9506[B]	TMP	P-O1P	3.46	1.62	1.51
3	C	9501[B]	TMP	O4-C4	3.47	1.33	1.24
3	F	9504[A]	TMP	C2'-C3'	3.49	1.62	1.52
3	G	9505[B]	TMP	P-O1P	3.49	1.62	1.51
3	E	9503	TMP	O4-C4	3.54	1.33	1.24
3	D	9502[B]	TMP	O4-C4	3.57	1.33	1.24
3	B	9500[B]	TMP	P-O2P	3.64	1.67	1.54
3	H	9506[A]	TMP	O4-C4	3.66	1.33	1.24
3	G	9505[A]	TMP	P-O2P	3.66	1.67	1.54
3	A	8500[A]	TMP	P-O3P	3.72	1.68	1.54
3	H	9506[B]	TMP	P-O2P	3.82	1.68	1.54
3	B	9500[B]	TMP	P-O3P	3.86	1.68	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	9502[A]	TMP	O4-C4	3.90	1.34	1.24
3	A	8500[B]	TMP	P-O3P	3.91	1.68	1.54
3	B	9500[B]	TMP	P-O1P	3.98	1.64	1.51
3	G	9505[B]	TMP	P-O2P	4.02	1.69	1.54
3	C	9501[B]	TMP	P-O3P	4.04	1.69	1.54
3	D	9502[A]	TMP	P-O2P	4.04	1.69	1.54
3	D	9502[B]	TMP	P-O3P	4.07	1.69	1.54
3	D	9502[A]	TMP	P-O3P	4.22	1.69	1.54
3	H	9506[A]	TMP	P-O2P	4.23	1.69	1.54
3	F	9504[A]	TMP	P-O3P	4.29	1.70	1.54
3	E	9503	TMP	P-O3P	4.31	1.70	1.54
3	B	9500[A]	TMP	P-O2P	4.31	1.70	1.54
3	A	8500[A]	TMP	P-O2P	4.32	1.70	1.54
3	H	9506[A]	TMP	P-O3P	4.35	1.70	1.54
3	C	9501[A]	TMP	P-O2P	4.38	1.70	1.54
3	H	9506[B]	TMP	P-O3P	4.42	1.70	1.54
3	G	9505[A]	TMP	P-O3P	4.42	1.70	1.54
3	D	9502[B]	TMP	P-O2P	4.43	1.70	1.54
3	F	9504[A]	TMP	P-O2P	4.44	1.70	1.54
3	C	9501[A]	TMP	P-O3P	4.45	1.70	1.54
3	F	9504[B]	TMP	P-O2P	4.48	1.70	1.54
3	F	9504[B]	TMP	P-O3P	4.54	1.71	1.54
3	E	9503	TMP	P-O2P	4.61	1.71	1.54
3	C	9501[B]	TMP	P-O2P	4.63	1.71	1.54
3	B	9500[A]	TMP	P-O3P	4.69	1.71	1.54
3	A	8500[B]	TMP	P-O2P	5.00	1.72	1.54

All (194) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	9500[A]	TMP	C2'-C3'-C4'	-11.48	78.98	102.77
3	D	9502[A]	TMP	C2'-C3'-C4'	-11.45	79.05	102.77
3	G	9505[A]	TMP	C2'-C3'-C4'	-10.96	80.05	102.77
3	H	9506[A]	TMP	C2'-C3'-C4'	-10.80	80.38	102.77
3	H	9506[B]	TMP	O4'-C1'-N1	-10.58	89.40	107.72
3	C	9501[A]	TMP	C2'-C3'-C4'	-10.42	81.16	102.77
3	E	9503	TMP	C2'-C3'-C4'	-9.37	83.36	102.77
3	H	9506[B]	TMP	O4'-C1'-C2'	-8.71	88.90	106.27
3	F	9504[B]	TMP	C2'-C3'-C4'	-8.33	85.52	102.77
3	H	9506[B]	TMP	C2'-C3'-C4'	-8.27	85.63	102.77
3	F	9504[A]	TMP	C2'-C3'-C4'	-8.16	85.86	102.77
3	C	9501[B]	TMP	O4'-C1'-C2'	-7.72	90.89	106.27

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	9505[B]	TMP	O4'-C1'-C2'	-7.53	91.26	106.27
3	A	8500[B]	TMP	O4'-C1'-C2'	-7.41	91.51	106.27
3	F	9504[B]	TMP	O4'-C1'-C2'	-7.37	91.59	106.27
3	D	9502[B]	TMP	O4'-C1'-C2'	-7.26	91.81	106.27
3	C	9509	TMP	C2'-C3'-C4'	-6.46	89.38	102.77
3	G	9513	TMP	C2'-C3'-C4'	-6.33	89.65	102.77
3	D	9502[A]	TMP	C5-C4-N3	-6.30	118.12	125.14
3	E	9511	TMP	C2'-C3'-C4'	-6.26	89.80	102.77
3	H	9506[A]	TMP	C5-C4-N3	-6.16	118.28	125.14
3	B	9508	TMP	C2'-C3'-C4'	-6.13	90.08	102.77
3	C	9501[A]	TMP	C5-C4-N3	-5.98	118.48	125.14
3	H	9506[B]	TMP	C5-C4-N3	-5.96	118.50	125.14
3	G	9505[A]	TMP	C5-C4-N3	-5.94	118.53	125.14
3	B	9500[B]	TMP	O4'-C1'-C2'	-5.84	94.63	106.27
3	D	9502[B]	TMP	C5-C4-N3	-5.62	118.88	125.14
3	C	9501[B]	TMP	C5-C4-N3	-5.57	118.93	125.14
3	G	9505[B]	TMP	C5-C4-N3	-5.53	118.98	125.14
3	H	9506[A]	TMP	O4'-C1'-N1	-5.33	98.48	107.72
3	E	9503	TMP	C5-C4-N3	-5.20	119.34	125.14
3	C	9501[B]	TMP	O4'-C1'-N1	-5.19	98.72	107.72
3	H	9514	TMP	C5-C4-N3	-5.03	119.54	125.14
3	B	9508	TMP	C5-C4-N3	-5.00	119.57	125.14
3	A	8500[A]	TMP	C2'-C3'-C4'	-4.92	92.58	102.77
3	B	9500[A]	TMP	O4'-C1'-N1	-4.88	99.27	107.72
3	B	9500[A]	TMP	C5-C4-N3	-4.77	119.82	125.14
3	G	9505[A]	TMP	O4'-C1'-N1	-4.77	99.46	107.72
3	C	9501[B]	TMP	C2'-C3'-C4'	-4.73	92.97	102.77
3	C	9501[A]	TMP	O4'-C1'-N1	-4.67	99.62	107.72
3	H	9506[B]	TMP	O3'-C3'-C2'	-4.58	95.58	110.74
3	D	9502[B]	TMP	C2'-C3'-C4'	-4.58	93.29	102.77
3	D	9510	TMP	C5-C4-N3	-4.54	120.08	125.14
3	D	9502[A]	TMP	C4'-O4'-C1'	-4.54	97.99	109.47
3	F	9504[A]	TMP	C4'-O4'-C1'	-4.54	97.99	109.47
3	E	9503	TMP	C4'-O4'-C1'	-4.45	98.23	109.47
3	B	9500[B]	TMP	C5-C4-N3	-4.42	120.21	125.14
3	A	8500[A]	TMP	O4'-C4'-C3'	-4.37	94.68	105.67
3	C	9509	TMP	C5-C4-N3	-4.29	120.36	125.14
3	G	9513	TMP	C5-C4-N3	-4.21	120.45	125.14
3	A	8500[B]	TMP	C5-C4-N3	-4.05	120.63	125.14
3	D	9502[A]	TMP	O4'-C1'-N1	-3.94	100.89	107.72
3	B	9500[A]	TMP	C4'-O4'-C1'	-3.92	99.57	109.47
3	A	8500[A]	TMP	C5-C4-N3	-3.89	120.81	125.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	9503	TMP	O4'-C1'-N1	-3.88	101.00	107.72
3	G	9505[B]	TMP	C2'-C3'-C4'	-3.85	94.79	102.77
3	G	9505[A]	TMP	C4'-O4'-C1'	-3.81	99.83	109.47
3	H	9506[A]	TMP	C4'-O4'-C1'	-3.76	99.97	109.47
3	C	9501[A]	TMP	C4'-O4'-C1'	-3.66	100.21	109.47
3	G	9505[B]	TMP	O3'-C3'-C2'	-3.46	99.30	110.74
3	A	9507	TMP	C5-C4-N3	-3.45	121.30	125.14
3	A	8500[B]	TMP	O4'-C1'-N1	-3.42	101.80	107.72
3	F	9504[A]	TMP	O4'-C1'-N1	-3.39	101.85	107.72
3	A	8500[B]	TMP	C2'-C3'-C4'	-3.31	95.92	102.77
3	B	9500[A]	TMP	O4'-C1'-C2'	-3.29	99.72	106.27
3	G	9513	TMP	O4'-C1'-N1	-3.21	102.16	107.72
3	C	9501[B]	TMP	O3'-C3'-C2'	-3.14	100.36	110.74
3	F	9512	TMP	C5-C4-N3	-3.11	121.67	125.14
3	F	9504[B]	TMP	C5-C4-N3	-3.00	121.80	125.14
3	E	9511	TMP	C5-C4-N3	-2.97	121.83	125.14
3	D	9510	TMP	O4'-C1'-C2'	-2.96	100.37	106.27
3	F	9512	TMP	O4'-C1'-C2'	-2.84	100.61	106.27
3	G	9505[A]	TMP	O4'-C1'-C2'	-2.78	100.72	106.27
3	H	9506[A]	TMP	O4'-C1'-C2'	-2.73	100.83	106.27
3	C	9501[A]	TMP	O4'-C1'-C2'	-2.65	100.98	106.27
3	A	8500[B]	TMP	O3'-C3'-C2'	-2.64	102.00	110.74
3	B	9508	TMP	O4'-C1'-N1	-2.60	103.22	107.72
3	F	9512	TMP	O4'-C1'-N1	-2.58	103.24	107.72
3	D	9510	TMP	C2'-C3'-C4'	-2.45	97.71	102.77
3	D	9502[A]	TMP	O4'-C1'-C2'	-2.42	101.45	106.27
3	E	9503	TMP	O3'-C3'-C2'	-2.42	102.75	110.74
3	F	9504[A]	TMP	C5-C4-N3	-2.39	122.47	125.14
3	A	8500[A]	TMP	O4'-C1'-C2'	-2.39	101.51	106.27
3	B	9508	TMP	O4'-C1'-C2'	-2.38	101.54	106.27
3	A	8500[A]	TMP	C5M-C5-C4	-2.37	116.99	120.05
3	E	9511	TMP	O5'-P-O1P	-2.37	101.11	107.14
3	C	9509	TMP	C4'-O4'-C1'	-2.23	103.82	109.47
3	C	9509	TMP	O5'-P-O1P	-2.23	101.46	107.14
3	H	9514	TMP	O4'-C1'-N1	-2.18	103.94	107.72
3	H	9506[B]	TMP	C5'-C4'-C3'	-2.17	100.90	114.64
3	E	9503	TMP	C5'-C4'-C3'	-2.16	100.92	114.64
3	D	9510	TMP	O4'-C1'-N1	-2.12	104.05	107.72
3	B	9500[A]	TMP	C5M-C5-C4	-2.11	117.32	120.05
3	E	9511	TMP	O4'-C1'-C2'	-2.06	102.16	106.27
3	A	9507	TMP	O4'-C1'-C2'	-2.05	102.18	106.27
3	E	9511	TMP	C4'-O4'-C1'	-2.04	104.30	109.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	9510	TMP	O5'-P-O1P	-2.03	101.97	107.14
3	G	9505[B]	TMP	O2P-P-O5'	-2.01	100.77	106.56
3	G	9513	TMP	O4'-C1'-C2'	-2.00	102.28	106.27
3	E	9511	TMP	C2'-C1'-N1	2.00	119.03	114.16
3	D	9502[A]	TMP	O3'-C3'-C4'	2.04	118.27	110.05
3	G	9505[B]	TMP	C5M-C5-C4	2.06	122.71	120.05
3	A	8500[B]	TMP	C2'-C1'-N1	2.08	119.21	114.16
3	C	9501[B]	TMP	C4'-O4'-C1'	2.08	114.72	109.47
3	H	9506[A]	TMP	O5'-C5'-C4'	2.09	116.82	109.12
3	G	9513	TMP	C3'-C2'-C1'	2.10	107.46	102.40
3	D	9502[A]	TMP	O5'-C5'-C4'	2.11	116.88	109.12
3	B	9500[B]	TMP	C3'-C2'-C1'	2.13	107.53	102.40
3	G	9505[A]	TMP	O3'-C3'-C4'	2.14	118.70	110.05
3	C	9501[A]	TMP	O2P-P-O5'	2.17	112.82	106.56
3	C	9501[A]	TMP	O5'-C5'-C4'	2.19	117.20	109.12
3	B	9508	TMP	C3'-C2'-C1'	2.20	107.70	102.40
3	F	9504[B]	TMP	O3'-C3'-C4'	2.21	118.96	110.05
3	E	9511	TMP	C3'-C2'-C1'	2.28	107.88	102.40
3	A	9507	TMP	O3'-C3'-C2'	2.33	118.45	110.74
3	C	9501[A]	TMP	C5M-C5-C6	2.36	123.37	118.62
3	B	9500[B]	TMP	C4'-O4'-C1'	2.39	115.49	109.47
3	H	9506[B]	TMP	O2P-P-O5'	2.43	113.56	106.56
3	B	9500[B]	TMP	C5M-C5-C4	2.47	123.24	120.05
3	H	9506[B]	TMP	O3P-P-O5'	2.51	113.80	106.56
3	A	8500[B]	TMP	O3P-P-O5'	2.60	114.04	106.56
3	C	9501[B]	TMP	C2'-C1'-N1	2.64	120.58	114.16
3	F	9512	TMP	C5M-C5-C4	2.67	123.49	120.05
3	A	8500[A]	TMP	C5M-C5-C6	2.71	124.08	118.62
3	G	9513	TMP	C2'-C1'-N1	2.72	120.77	114.16
3	E	9503	TMP	O2P-P-O5'	2.77	114.53	106.56
3	G	9505[A]	TMP	O3P-P-O5'	2.78	114.56	106.56
3	A	8500[B]	TMP	C3'-C2'-C1'	2.78	109.09	102.40
3	B	9500[B]	TMP	O3'-C3'-C4'	2.88	121.67	110.05
3	A	8500[A]	TMP	O3'-C3'-C4'	2.92	121.86	110.05
3	B	9500[A]	TMP	C5M-C5-C6	2.96	124.58	118.62
3	G	9505[B]	TMP	C4'-O4'-C1'	3.00	117.06	109.47
3	H	9506[B]	TMP	O3'-C3'-C4'	3.13	122.71	110.05
3	B	9500[B]	TMP	O3P-P-O5'	3.17	115.68	106.56
3	F	9504[A]	TMP	C4-N3-C2	3.24	118.05	115.25
3	H	9506[A]	TMP	C3'-C2'-C1'	3.27	110.26	102.40
3	B	9500[A]	TMP	C3'-C2'-C1'	3.32	110.39	102.40
3	D	9502[A]	TMP	C3'-C2'-C1'	3.47	110.74	102.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	9505[B]	TMP	O3P-P-O5'	3.51	116.69	106.56
3	F	9504[A]	TMP	C2'-C1'-N1	3.58	122.87	114.16
3	E	9503	TMP	C3'-C2'-C1'	3.64	111.16	102.40
3	D	9502[B]	TMP	O3'-C3'-C4'	3.73	125.11	110.05
3	C	9501[A]	TMP	C3'-C2'-C1'	3.76	111.44	102.40
3	G	9505[A]	TMP	C3'-C2'-C1'	3.83	111.61	102.40
3	A	8500[A]	TMP	C2'-C1'-N1	3.87	123.57	114.16
3	F	9504[B]	TMP	O4'-C4'-C3'	3.87	115.40	105.67
3	G	9505[B]	TMP	O3'-C3'-C4'	3.90	125.82	110.05
3	H	9506[B]	TMP	C2'-C1'-N1	4.05	124.01	114.16
3	A	8500[A]	TMP	O3'-C3'-C2'	4.14	124.44	110.74
3	F	9504[B]	TMP	C4-N3-C2	4.33	118.99	115.25
3	H	9506[B]	TMP	O4'-C4'-C3'	4.44	116.84	105.67
3	G	9505[B]	TMP	C3'-C2'-C1'	4.45	113.11	102.40
3	A	8500[A]	TMP	C4-N3-C2	4.58	119.20	115.25
3	A	8500[B]	TMP	O3'-C3'-C4'	4.60	128.63	110.05
3	C	9501[B]	TMP	O3'-C3'-C4'	4.66	128.88	110.05
3	C	9501[B]	TMP	C3'-C2'-C1'	4.92	114.23	102.40
3	B	9508	TMP	O4'-C4'-C3'	4.93	118.08	105.67
3	F	9504[B]	TMP	C3'-C2'-C1'	5.24	115.00	102.40
3	A	8500[B]	TMP	C4-N3-C2	5.24	119.77	115.25
3	C	9509	TMP	O4'-C4'-C3'	5.26	118.90	105.67
3	H	9506[B]	TMP	C3'-C2'-C1'	5.34	115.24	102.40
3	G	9513	TMP	O4'-C4'-C3'	5.38	119.19	105.67
3	G	9513	TMP	C4-N3-C2	5.51	120.01	115.25
3	A	9507	TMP	C4-N3-C2	5.66	120.14	115.25
3	E	9511	TMP	O4'-C4'-C3'	5.92	120.56	105.67
3	E	9503	TMP	C4-N3-C2	6.11	120.53	115.25
3	B	9508	TMP	C4-N3-C2	6.16	120.57	115.25
3	D	9502[B]	TMP	C4-N3-C2	6.25	120.64	115.25
3	D	9502[A]	TMP	C2'-C1'-N1	6.35	129.60	114.16
3	C	9501[A]	TMP	C2'-C1'-N1	6.41	129.74	114.16
3	H	9514	TMP	C4-N3-C2	6.47	120.84	115.25
3	C	9501[B]	TMP	C4-N3-C2	6.56	120.91	115.25
3	H	9506[A]	TMP	C2'-C1'-N1	6.58	130.16	114.16
3	B	9500[A]	TMP	C4-N3-C2	6.65	120.99	115.25
3	G	9505[B]	TMP	C4-N3-C2	6.76	121.09	115.25
3	H	9506[A]	TMP	C4-N3-C2	6.78	121.10	115.25
3	H	9506[B]	TMP	C4-N3-C2	6.81	121.13	115.25
3	D	9502[A]	TMP	C4-N3-C2	6.93	121.24	115.25
3	C	9501[A]	TMP	C4-N3-C2	6.95	121.25	115.25
3	G	9505[A]	TMP	C2'-C1'-N1	7.08	131.36	114.16

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Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	G	9505[A]	TMP	C4-N3-C2	7.17	121.45	115.25
3	F	9512	TMP	C4-N3-C2	7.34	121.59	115.25
3	B	9500[B]	TMP	C4-N3-C2	7.35	121.60	115.25
3	E	9511	TMP	C4-N3-C2	7.38	121.63	115.25
3	F	9504[A]	TMP	O4'-C4'-C3'	7.45	124.40	105.67
3	C	9509	TMP	C4-N3-C2	7.81	121.99	115.25
3	H	9506[A]	TMP	O4'-C4'-C3'	7.85	125.42	105.67
3	B	9500[A]	TMP	C2'-C1'-N1	7.87	133.31	114.16
3	D	9502[A]	TMP	O4'-C4'-C3'	8.55	127.18	105.67
3	B	9500[A]	TMP	O4'-C4'-C3'	8.78	127.76	105.67
3	G	9505[A]	TMP	O4'-C4'-C3'	8.86	127.94	105.67
3	C	9501[A]	TMP	O4'-C4'-C3'	9.01	128.33	105.67
3	D	9510	TMP	C4-N3-C2	9.03	123.05	115.25
3	E	9503	TMP	O4'-C4'-C3'	9.33	129.12	105.67

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

18 monomers are involved in 36 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	8500[A]	TMP	1	0
3	B	9500[A]	TMP	2	0
2	C	3800	SO4	1	0
2	C	4000	SO4	1	0
3	C	9501[A]	TMP	3	0
3	C	9501[B]	TMP	3	0
2	D	3900	SO4	1	1
2	D	4800	SO4	1	0
3	D	9502[A]	TMP	1	0
3	D	9502[B]	TMP	1	0
2	E	4700	SO4	1	0
2	E	5700	SO4	2	0
3	E	9503	TMP	2	0
2	F	6700	SO4	1	0
3	F	9504[A]	TMP	3	0
3	F	9504[B]	TMP	5	0
3	G	9505[A]	TMP	3	0
3	H	9506[A]	TMP	3	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	292/293 (99%)	0.15	14 (4%) 34 32	7, 12, 25, 43	0
1	B	293/293 (100%)	0.15	17 (5%) 26 23	6, 11, 26, 39	0
1	C	292/293 (99%)	0.26	27 (9%) 11 9	6, 13, 28, 42	0
1	D	292/293 (99%)	0.36	23 (7%) 15 14	7, 13, 30, 45	0
1	E	293/293 (100%)	0.54	31 (10%) 8 6	8, 15, 32, 52	0
1	F	293/293 (100%)	0.28	20 (6%) 20 18	6, 11, 29, 47	0
1	G	293/293 (100%)	0.14	13 (4%) 38 37	5, 10, 26, 40	0
1	H	292/293 (99%)	0.15	17 (5%) 26 23	8, 13, 26, 43	0
All	All	2340/2344 (99%)	0.25	162 (6%) 20 17	5, 12, 28, 52	0

All (162) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	193	PRO	9.1
1	F	13	GLY	8.9
1	E	195	GLY	8.7
1	E	12	SER	8.0
1	A	23	ILE	7.8
1	E	23	ILE	7.7
1	G	23	ILE	7.4
1	H	23	ILE	7.0
1	E	194	ARG	6.3
1	D	195	GLY	6.3
1	D	193	PRO	6.2
1	D	15	ARG	6.1
1	B	14	THR	5.9
1	H	13	GLY	5.8
1	E	164	LEU	5.6
1	B	13	GLY	5.5

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Mol	Chain	Res	Type	RSRZ
1	E	13	GLY	5.5
1	E	15	ARG	5.3
1	D	13	GLY	5.3
1	A	193	PRO	5.2
1	A	14	THR	5.1
1	G	14	THR	5.0
1	F	12	SER	4.9
1	F	14	THR	4.9
1	D	164	LEU	4.8
1	G	12	SER	4.8
1	F	193	PRO	4.6
1	E	1	MET	4.6
1	B	12	SER	4.5
1	B	23	ILE	4.4
1	C	193	PRO	4.4
1	E	14	THR	4.4
1	H	14	THR	4.3
1	A	12	SER	4.3
1	D	14	THR	4.3
1	F	277	LYS	4.2
1	G	13	GLY	4.2
1	A	13	GLY	4.0
1	E	277	LYS	4.0
1	H	22	ALA	4.0
1	E	2	LYS	3.9
1	B	1	MET	3.9
1	G	193	PRO	3.8
1	A	277	LYS	3.8
1	F	15	ARG	3.8
1	G	22	ALA	3.7
1	D	22	ALA	3.7
1	H	277	LYS	3.6
1	D	194	ARG	3.6
1	D	23	ILE	3.6
1	B	277	LYS	3.6
1	H	12	SER	3.6
1	C	277	LYS	3.6
1	F	164[A]	LEU	3.6
1	E	227	GLY	3.5
1	B	193	PRO	3.5
1	E	192	SER	3.5
1	D	277	LYS	3.4

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Mol	Chain	Res	Type	RSRZ
1	F	1	MET	3.3
1	C	194	ARG	3.3
1	H	152	GLN	3.3
1	C	195	GLY	3.2
1	D	191	PRO	3.2
1	C	273	ALA	3.2
1	C	15	ARG	3.1
1	G	277	LYS	3.1
1	B	152	GLN	3.1
1	C	164[A]	LEU	3.0
1	D	16	LEU	2.9
1	H	273	ALA	2.9
1	A	289	THR	2.9
1	C	275	LEU	2.9
1	F	275	LEU	2.9
1	F	194	ARG	2.9
1	B	289	THR	2.8
1	E	22	ALA	2.8
1	C	266	ALA	2.8
1	C	12	SER	2.7
1	B	22	ALA	2.7
1	G	289	THR	2.7
1	E	127	GLN	2.7
1	A	152	GLN	2.7
1	C	190	LYS	2.7
1	F	127	GLN	2.7
1	G	15	ARG	2.7
1	E	11	GLY	2.7
1	C	13	GLY	2.6
1	G	152	GLN	2.7
1	G	21	LEU	2.6
1	H	193	PRO	2.6
1	D	165	GLU	2.6
1	A	22	ALA	2.6
1	H	15	ARG	2.6
1	B	269	GLU	2.6
1	A	15	ARG	2.5
1	H	288	LEU	2.5
1	A	194[A]	ARG	2.5
1	D	187	ARG	2.5
1	E	16	LEU	2.5
1	B	15	ARG	2.5

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Mol	Chain	Res	Type	RSRZ
1	C	276	ALA	2.5
1	F	152	GLN	2.5
1	B	274	PRO	2.5
1	C	21	LEU	2.5
1	E	21	LEU	2.5
1	E	289	THR	2.4
1	F	175	LEU	2.4
1	D	190	LYS	2.4
1	C	227	GLY	2.4
1	D	128	ARG	2.4
1	C	101	ASN	2.4
1	E	275	LEU	2.3
1	C	23	ILE	2.3
1	E	101	ASN	2.3
1	H	276	ALA	2.3
1	C	20	THR	2.3
1	A	270	LYS	2.3
1	D	275	LEU	2.3
1	C	2	LYS	2.3
1	B	275	LEU	2.3
1	D	127	GLN	2.3
1	D	152	GLN	2.3
1	E	60	THR	2.3
1	E	81	VAL	2.2
1	E	266	ALA	2.2
1	F	16	LEU	2.2
1	F	23	ILE	2.2
1	D	276	ALA	2.2
1	B	17	HIS	2.2
1	F	278	ASN	2.2
1	C	274	PRO	2.2
1	E	58	GLN	2.2
1	H	269	GLU	2.1
1	F	108	LEU	2.1
1	C	60	THR	2.1
1	A	276	ALA	2.1
1	F	274	PRO	2.1
1	E	288	LEU	2.1
1	H	275	LEU	2.1
1	C	187	ARG	2.1
1	D	266	ALA	2.1
1	E	273	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
1	H	270	LYS	2.1
1	E	165	GLU	2.1
1	F	289	THR	2.1
1	C	129	GLN	2.1
1	D	12	SER	2.1
1	F	2	LYS	2.1
1	C	35[A]	MET	2.0
1	G	1	MET	2.0
1	G	24	SER	2.0
1	D	188	ASP	2.0
1	B	175	LEU	2.0
1	C	278	ASN	2.0
1	H	101	ASN	2.0
1	A	269	GLU	2.0
1	H	194	ARG	2.0
1	E	278	ASN	2.0
1	B	16	LEU	2.0
1	C	108	LEU	2.0
1	C	191	PRO	2.0
1	E	190	LYS	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, 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(Å ²)	Q<0.9
2	SO4	D	5000	5/5	0.87	0.28	7.79	46,53,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	TMP	B	9508	21/21	0.97	0.15	2.30	11,13,17,32	0
3	TMP	A	9507	21/21	0.97	0.12	2.14	11,13,16,19	0
3	TMP	G	9513	21/21	0.98	0.13	2.06	10,12,15,19	0
3	TMP	G	9505[B]	21/21	0.85	0.16	2.05	18,27,30,34	21
3	TMP	F	9504[B]	21/21	0.86	0.16	1.91	10,13,22,23	21
3	TMP	H	9514	21/21	0.96	0.12	1.57	12,14,17,20	0
3	TMP	D	9502[B]	21/21	0.87	0.14	1.56	23,32,38,40	21
3	TMP	H	9506[B]	21/21	0.88	0.14	1.52	22,30,39,39	21
3	TMP	B	9500[A]	21/21	0.91	0.13	1.48	11,16,27,28	21
3	TMP	B	9500[B]	21/21	0.91	0.13	1.45	17,20,25,28	21
3	TMP	C	9501[B]	21/21	0.88	0.15	1.45	18,26,40,41	21
3	TMP	C	9509	21/21	0.97	0.11	1.44	13,14,16,19	0
3	TMP	C	9501[A]	21/21	0.88	0.15	1.40	16,23,41,42	21
2	SO4	C	4000	5/5	0.92	0.17	1.34	40,42,45,48	0
2	SO4	C	3800	5/5	0.98	0.22	1.25	38,40,43,44	0
2	SO4	A	3700	5/5	0.95	0.19	1.22	35,36,40,46	0
2	SO4	G	7700	5/5	0.97	0.20	1.14	45,47,49,50	0
3	TMP	D	9502[A]	21/21	0.87	0.14	1.11	15,21,30,31	21
3	TMP	G	9505[A]	21/21	0.85	0.16	0.75	15,16,27,28	21
3	TMP	F	9512	21/21	0.96	0.11	0.72	12,13,15,17	0
3	TMP	A	8500[B]	21/21	0.88	0.14	0.63	20,24,37,37	21
3	TMP	H	9506[A]	21/21	0.88	0.14	0.61	17,20,33,35	21
3	TMP	E	9511	21/21	0.97	0.10	0.51	14,14,18,19	0
3	TMP	F	9504[A]	21/21	0.86	0.16	0.44	14,26,43,46	21
3	TMP	A	8500[A]	21/21	0.88	0.14	0.43	16,20,36,39	21
3	TMP	D	9510	21/21	0.97	0.10	0.42	11,14,16,18	0
2	SO4	D	5100	5/5	0.94	0.13	0.18	39,39,43,44	0
3	TMP	E	9503	21/21	0.83	0.13	0.18	27,34,50,51	0
2	SO4	E	4700	5/5	0.96	0.14	-0.00	34,36,37,42	0
2	SO4	E	5700	5/5	0.94	0.22	-	72,73,75,75	0
2	SO4	D	4800	5/5	0.95	0.20	-	38,42,44,45	0
2	SO4	D	3900	5/5	0.97	0.13	-	42,45,48,49	0
2	SO4	D	5200	5/5	0.94	0.23	-	41,47,49,50	0
2	SO4	E	5800	5/5	0.97	0.23	-	39,44,45,47	0
2	SO4	F	6700	5/5	0.96	0.27	-	36,42,44,45	0

6.5 Other polymers ⓘ

There are no such residues in this entry.