



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 22, 2026 – 06:51 PM EDT

PDB ID : 2YWC / pdb_00002ywc
Title : Crystal structure of GMP synthetase from *Thermus thermophilus* in complex with XMP
Authors : Baba, S.; Kanagawa, M.; Kuramitsu, S.; Yokoyama, S.; Sampei, G.; Kawai, G.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)
Deposited on : 2007-04-20
Resolution : 2.20 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

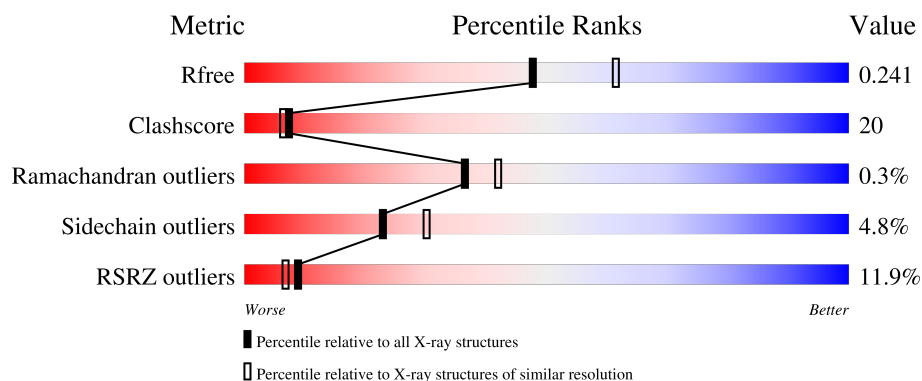
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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}	180053	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	503	5% 65% 26% 6%
1	B	503	13% 58% 30% 5% 7%
1	C	503	7% 60% 29% 7%
1	D	503	19% 48% 40% 7%

2 Entry composition [i](#)

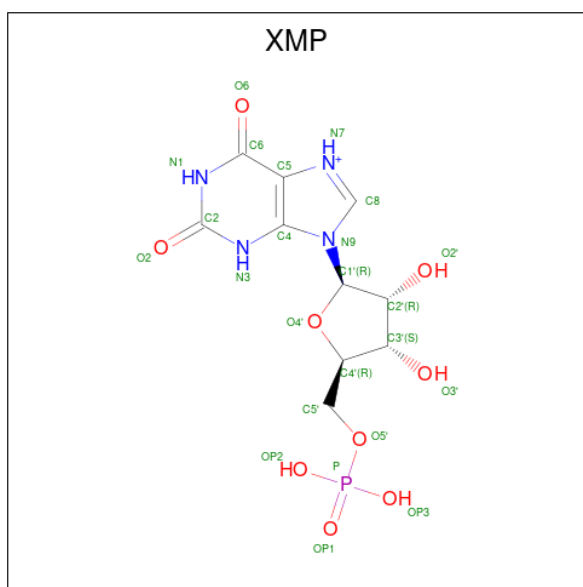
There are 3 unique types of molecules in this entry. The entry contains 15201 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 GMP synthase [glutamine-hydrolyzing].

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	475	Total	C	N	O	S	Se	0	0	0
			3742	2395	665	676	1	5			
1	B	467	Total	C	N	O	S	Se	0	0	0
			3685	2360	657	662	1	5			
1	C	467	Total	C	N	O	S	Se	0	0	0
			3685	2360	657	662	1	5			
1	D	467	Total	C	N	O	S	Se	0	0	0
			3687	2361	660	660	1	5			

- Molecule 2 is XANTHOSINE-5'-MONOPHOSPHATE (CCD ID: XMP) (formula: $C_{10}H_{14}N_4O_9P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			24	10	4	9	1		
2	B	1	Total	C	N	O	P	0	0
			24	10	4	9	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	C	1	Total	C	N	O	P	0	0
			24	10	4	9	1		
2	D	1	Total	C	N	O	P	0	0
			24	10	4	9	1		

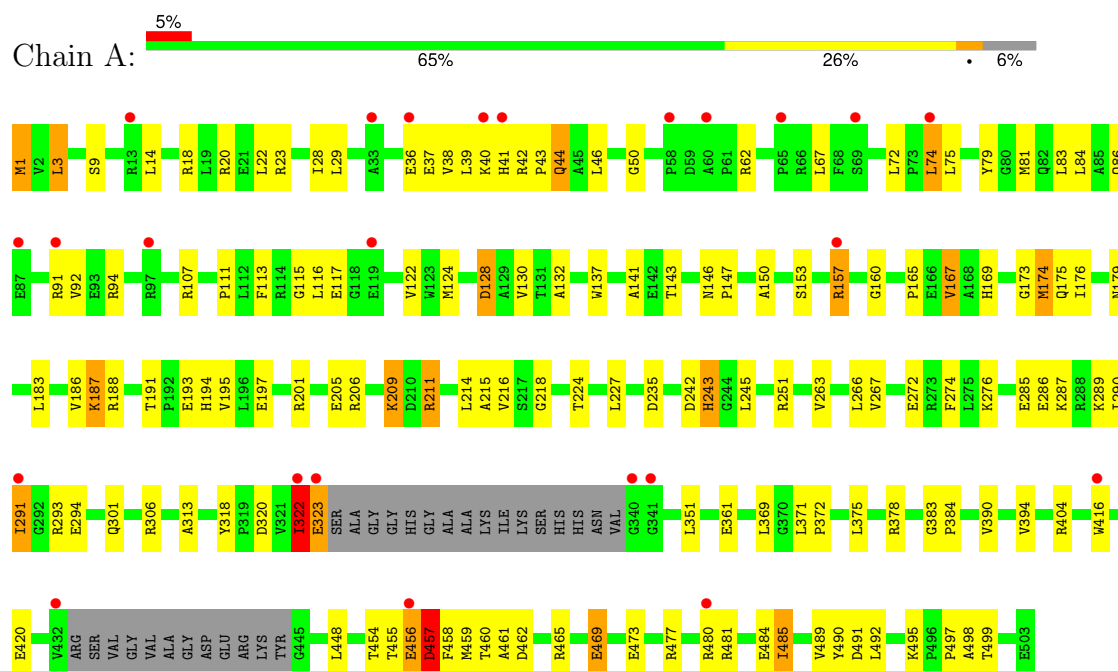
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	110	Total	O	0	0
			110	110		
3	B	66	Total	O	0	0
			66	66		
3	C	86	Total	O	0	0
			86	86		
3	D	44	Total	O	0	0
			44	44		

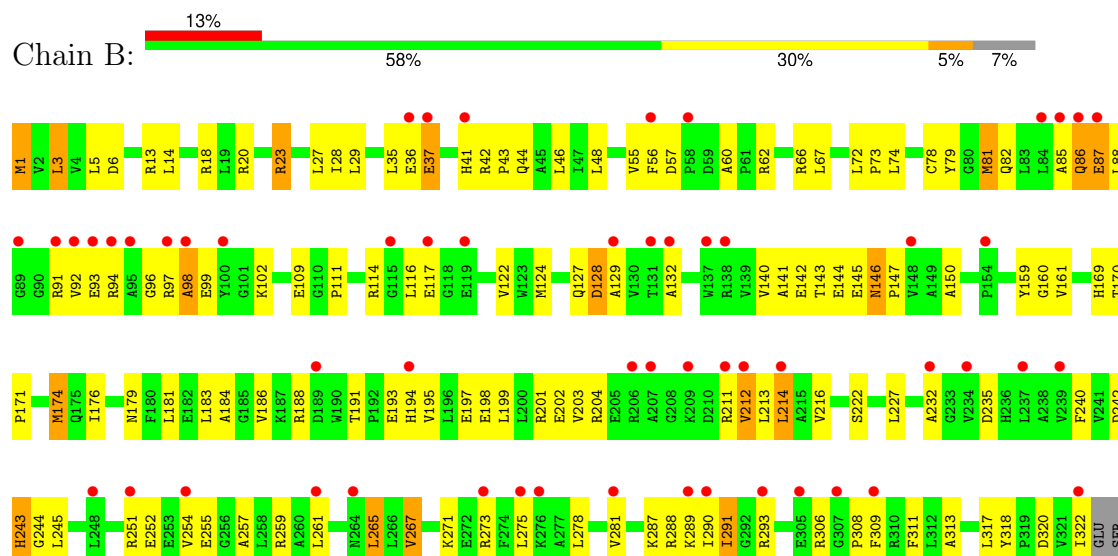
3 Residue-property plots [i](#)

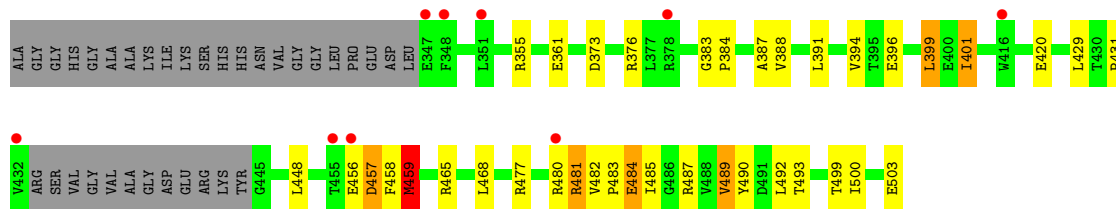
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: GMP synthase [glutamine-hydrolyzing]

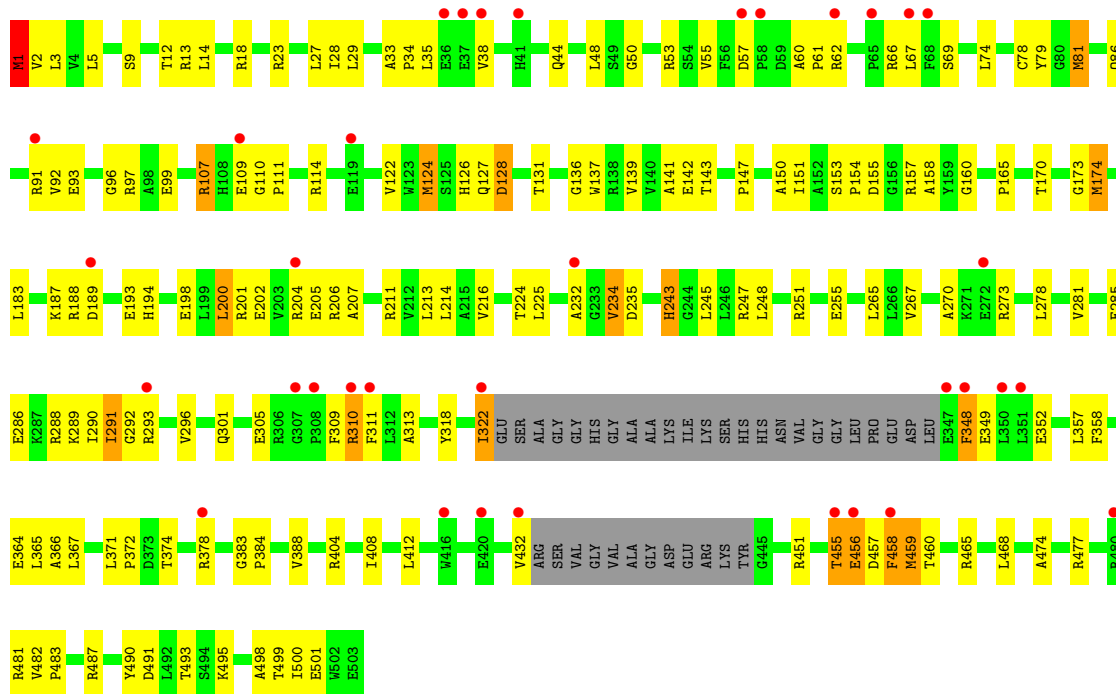


• Molecule 1: GMP synthase [glutamine-hydrolyzing]

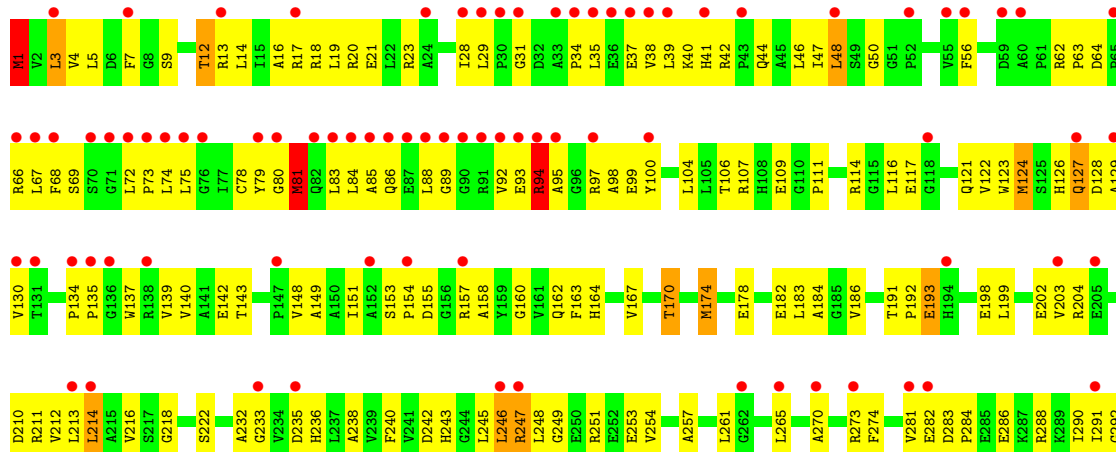


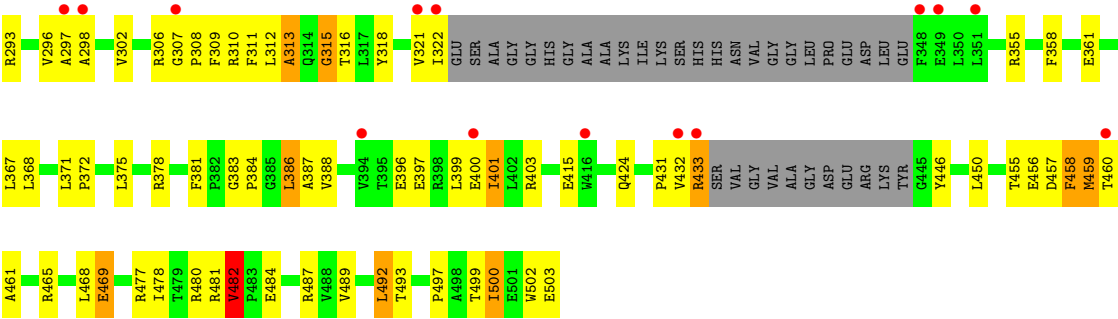


• Molecule 1: GMP synthase [glutamine-hydrolyzing]



• Molecule 1: GMP synthase [glutamine-hydrolyzing]





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	142.58Å 115.21Å 159.35Å 90.00° 93.21° 90.00°	Depositor
Resolution (Å)	31.82 – 2.20 31.82 – 2.21	Depositor EDS
% Data completeness (in resolution range)	87.9 (31.82-2.20) 97.1 (31.82-2.21)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.50 (at 2.20Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.236 , 0.278 0.241 , 0.241	Depositor DCC
R_{free} test set	6319 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å ²)	40.5	Xtriage
Anisotropy	0.142	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 42.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	15201	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.27% 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, 0.333 respectively for untwinned datasets, and 0.375, 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:
XMP

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	0.52	2/3816 (0.1%)	1.02	17/5168 (0.3%)
1	B	0.51	6/3758 (0.2%)	0.96	18/5089 (0.4%)
1	C	0.51	5/3758 (0.1%)	0.97	17/5089 (0.3%)
1	D	0.48	4/3760 (0.1%)	1.03	22/5091 (0.4%)
All	All	0.50	17/15092 (0.1%)	1.00	74/20437 (0.4%)

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	B	0	5
1	C	0	2
1	D	0	5
All	All	0	14

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	174	MSE	SE-CE	-6.20	1.76	1.95
1	A	1	MSE	SE-CE	-5.98	1.77	1.95
1	B	1	MSE	SE-CE	-5.91	1.77	1.95
1	D	1	MSE	SE-CE	-5.81	1.78	1.95
1	B	81	MSE	SE-CE	-5.49	1.78	1.95
1	D	124	MSE	CG-SE	-5.46	1.79	1.95
1	B	459	MSE	CG-SE	-5.42	1.79	1.95
1	C	1	MSE	CG-SE	-5.39	1.79	1.95
1	C	81	MSE	SE-CE	-5.38	1.79	1.95
1	C	174	MSE	SE-CE	-5.32	1.79	1.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	1	MSE	SE-CE	-5.20	1.79	1.95
1	B	459	MSE	SE-CE	-5.14	1.80	1.95
1	C	124	MSE	CG-SE	-5.12	1.80	1.95
1	D	174	MSE	CG-SE	-5.12	1.80	1.95
1	D	124	MSE	SE-CE	-5.11	1.80	1.95
1	B	174	MSE	SE-CE	-5.08	1.80	1.95
1	B	81	MSE	CG-SE	-5.02	1.80	1.95

All (74) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	457	ASP	O-C-N	-13.53	106.58	122.27
1	C	456	GLU	O-C-N	-12.82	108.99	122.19
1	A	457	ASP	CA-C-N	12.58	140.58	122.08
1	A	457	ASP	C-N-CA	12.58	140.58	122.08
1	D	315	GLY	O-C-N	-11.54	107.70	122.70
1	D	456	GLU	O-C-N	-11.20	106.46	122.36
1	D	456	GLU	CA-C-N	10.70	138.46	121.44
1	D	456	GLU	C-N-CA	10.70	138.46	121.44
1	B	457	ASP	CA-C-N	8.49	137.76	121.54
1	B	457	ASP	C-N-CA	8.49	137.76	121.54
1	A	322	ILE	CA-C-N	-8.23	106.88	121.70
1	A	322	ILE	C-N-CA	-8.23	106.88	121.70
1	C	456	GLU	CA-C-N	8.15	137.11	121.54
1	C	456	GLU	C-N-CA	8.15	137.11	121.54
1	C	459	MSE	CA-C-N	8.10	134.00	121.76
1	C	459	MSE	C-N-CA	8.10	134.00	121.76
1	B	457	ASP	O-C-N	-7.95	113.42	122.09
1	D	459	MSE	N-CA-C	-7.88	103.50	113.43
1	B	86	GLN	O-C-N	7.68	130.91	122.15
1	D	313	ALA	O-C-N	7.62	131.96	123.04
1	B	456	GLU	CA-C-N	7.44	133.26	121.44
1	B	456	GLU	C-N-CA	7.44	133.26	121.44
1	D	94	ARG	O-C-N	-7.26	114.00	122.93
1	A	457	ASP	N-CA-C	-7.09	104.26	114.12
1	B	146	ASN	CA-C-N	6.95	126.65	119.56
1	B	146	ASN	C-N-CA	6.95	126.65	119.56
1	B	482	VAL	CA-C-N	6.75	128.28	119.84
1	B	482	VAL	C-N-CA	6.75	128.28	119.84
1	A	456	GLU	N-CA-C	-6.75	104.93	113.43
1	C	265	LEU	N-CA-C	6.58	119.67	109.07
1	D	127	GLN	CA-C-N	6.53	134.01	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	127	GLN	C-N-CA	6.53	134.01	121.54
1	D	482	VAL	CA-C-N	6.43	127.88	119.84
1	D	482	VAL	C-N-CA	6.43	127.88	119.84
1	D	218	GLY	N-CA-C	-6.37	106.90	114.48
1	A	211	ARG	CA-C-N	6.29	131.91	122.91
1	A	211	ARG	C-N-CA	6.29	131.91	122.91
1	C	127	GLN	CA-C-N	6.16	133.31	121.54
1	C	127	GLN	C-N-CA	6.16	133.31	121.54
1	C	352	GLU	CA-C-N	6.13	126.03	119.28
1	C	352	GLU	C-N-CA	6.13	126.03	119.28
1	B	265	LEU	N-CA-C	6.09	119.17	109.24
1	B	459	MSE	N-CA-C	-6.09	105.80	113.72
1	D	313	ALA	CA-C-N	-6.00	113.51	122.74
1	D	313	ALA	C-N-CA	-6.00	113.51	122.74
1	C	358	PHE	N-CA-C	-5.91	101.26	110.42
1	A	143	THR	N-CA-C	-5.85	100.88	109.18
1	A	115	GLY	N-CA-C	-5.82	108.15	115.08
1	D	315	GLY	CA-C-N	5.81	130.50	121.26
1	D	315	GLY	C-N-CA	5.81	130.50	121.26
1	C	482	VAL	CA-C-N	5.75	127.03	119.84
1	C	482	VAL	C-N-CA	5.75	127.03	119.84
1	C	348	PHE	N-CA-C	5.63	117.18	110.19
1	C	143	THR	N-CA-C	-5.63	100.85	109.41
1	D	358	PHE	N-CA-C	-5.63	101.37	110.32
1	D	459	MSE	O-C-N	5.61	129.62	122.10
1	D	126	HIS	O-C-N	5.59	128.75	122.27
1	B	170	THR	CA-C-N	5.52	126.73	119.84
1	B	170	THR	C-N-CA	5.52	126.73	119.84
1	A	128	ASP	CA-C-N	5.44	131.76	121.69
1	A	128	ASP	C-N-CA	5.44	131.76	121.69
1	D	81	MSE	O-C-N	5.41	128.92	122.27
1	D	170	THR	N-CA-C	-5.37	99.48	108.94
1	B	493	THR	N-CA-C	5.34	117.95	109.24
1	B	87	GLU	O-C-N	-5.32	115.36	122.43
1	A	218	GLY	N-CA-C	-5.31	107.68	114.37
1	A	113	PHE	N-CA-C	5.29	119.70	112.88
1	C	170	THR	N-CA-C	-5.20	97.81	108.21
1	B	6	ASP	N-CA-C	5.18	116.70	108.67
1	A	22	LEU	CA-C-N	5.16	129.45	122.07
1	A	22	LEU	C-N-CA	5.16	129.45	122.07
1	B	170	THR	N-CA-C	-5.08	99.72	108.97
1	C	200	LEU	N-CA-C	-5.08	105.66	111.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	254	VAL	N-CA-C	5.01	115.24	110.53

There are no chirality outliers.

All (14) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	322	ILE	Peptide
1	A	457	ASP	Mainchain
1	B	128	ASP	Mainchain
1	B	129	ALA	Mainchain
1	B	23	ARG	Mainchain
1	B	459	MSE	Mainchain
1	B	85	ALA	Mainchain
1	C	128	ASP	Mainchain
1	C	458	PHE	Mainchain
1	D	129	ALA	Mainchain
1	D	23	ARG	Mainchain
1	D	315	GLY	Mainchain
1	D	458	PHE	Mainchain
1	D	94	ARG	Mainchain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3742	0	3812	139	0
1	B	3685	0	3761	145	0
1	C	3685	0	3761	135	0
1	D	3687	0	3768	212	0
2	A	24	0	12	1	0
2	B	24	0	12	3	0
2	C	24	0	12	4	0
2	D	24	0	12	2	0
3	A	110	0	0	3	0
3	B	66	0	0	2	0
3	C	86	0	0	3	0
3	D	44	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	15201	0	15150	615	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 20.

All (615) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:74:LEU:C	1:A:74:LEU:HD23	1.66	1.20
1:A:74:LEU:C	1:A:74:LEU:CD2	2.13	1.17
1:B:401:ILE:CD1	1:B:484:GLU:HG3	1.75	1.15
1:A:74:LEU:HD23	1:A:75:LEU:N	1.64	1.12
1:D:56:PHE:HZ	1:D:92:VAL:O	1.35	1.09
1:B:401:ILE:HD13	1:B:484:GLU:CG	1.82	1.08
1:C:310:ARG:HG3	1:C:310:ARG:HH11	0.99	1.07
1:C:310:ARG:HH11	1:C:310:ARG:CG	1.67	1.06
1:C:1:MSE:HE1	1:C:3:LEU:HD13	1.37	1.03
1:D:457:ASP:OD2	1:D:459:MSE:HE2	1.60	1.01
1:A:157:ARG:HG2	1:A:157:ARG:HH11	1.24	1.01
1:D:281:VAL:HG21	1:D:290:ILE:HD12	1.44	0.98
1:A:318:TYR:CE2	1:A:322:ILE:HD11	2.02	0.94
1:C:3:LEU:HD21	1:C:29:LEU:HD12	1.47	0.93
1:D:281:VAL:HG21	1:D:290:ILE:CD1	1.97	0.93
1:C:1:MSE:CE	1:C:3:LEU:HD13	1.99	0.92
1:C:111:PRO:HB2	1:C:183:LEU:HD21	1.53	0.91
1:A:74:LEU:HD22	1:A:74:LEU:O	1.69	0.91
1:D:243:HIS:HD2	1:D:245:LEU:H	1.18	0.90
1:B:111:PRO:HB2	1:B:183:LEU:HD21	1.54	0.89
1:C:310:ARG:HG3	1:C:310:ARG:NH1	1.79	0.89
1:C:301:GLN:O	1:C:305:GLU:HG2	1.72	0.88
1:D:63:PRO:HB2	1:D:67:LEU:HD22	1.55	0.88
1:A:157:ARG:HG2	1:A:157:ARG:NH1	1.81	0.88
1:D:56:PHE:CZ	1:D:92:VAL:O	2.26	0.87
1:D:153:SER:HB3	1:D:158:ALA:HB3	1.55	0.87
1:B:14:LEU:HD22	1:B:18:ARG:HH12	1.40	0.86
1:A:211:ARG:HG3	1:A:235:ASP:OD2	1.75	0.86
1:D:68:PHE:CD2	1:D:88:LEU:HD21	2.12	0.85
1:A:117:GLU:HB2	1:C:248:LEU:HG	1.59	0.85
1:C:457:ASP:O	1:C:459:MSE:HG3	1.77	0.84
1:C:12:THR:HG22	1:C:28:ILE:HD13	1.58	0.84
1:A:1:MSE:HE1	1:A:3:LEU:HD23	1.59	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:169:HIS:CD2	3:A:797:HOH:O	2.31	0.82
1:A:448:LEU:HB2	1:A:485:ILE:HD13	1.61	0.81
1:D:457:ASP:OD1	1:D:459:MSE:HB3	1.79	0.81
1:D:50:GLY:HA2	1:D:79:TYR:HB3	1.62	0.80
1:A:157:ARG:HH11	1:A:157:ARG:CG	1.94	0.80
1:A:74:LEU:C	1:A:74:LEU:HD22	2.00	0.80
1:A:211:ARG:HG3	1:A:235:ASP:CG	2.07	0.79
1:A:193:GLU:O	1:A:197:GLU:HG2	1.82	0.79
1:B:98:ALA:HB2	1:B:127:GLN:NE2	1.97	0.78
1:C:200:LEU:O	1:C:204:ARG:HG3	1.84	0.78
1:C:1:MSE:N	1:C:44:GLN:HE21	1.81	0.78
1:B:278:LEU:O	1:B:281:VAL:HG12	1.83	0.77
1:A:74:LEU:CD2	1:A:74:LEU:O	2.29	0.77
1:B:401:ILE:HD13	1:B:484:GLU:HG3	0.87	0.75
1:D:214:LEU:HB3	1:D:313:ALA:HB3	1.68	0.75
1:C:35:LEU:HD22	1:C:66:ARG:HB2	1.69	0.75
1:D:318:TYR:CE2	1:D:322:ILE:HD11	2.20	0.75
1:C:318:TYR:CE2	1:C:322:ILE:HD11	2.21	0.75
1:A:480:ARG:HD3	1:A:481:ARG:NH1	2.02	0.75
1:A:272:GLU:HG3	1:A:276:LYS:HE2	1.67	0.74
1:C:14:LEU:HD11	1:C:18:ARG:NH2	2.02	0.74
1:B:55:VAL:HG11	1:B:82:GLN:HB2	1.70	0.74
1:D:4:VAL:HB	1:D:28:ILE:HD13	1.69	0.74
1:A:455:THR:HG23	1:A:460:THR:O	1.87	0.74
1:D:246:LEU:HD12	1:D:246:LEU:H	1.51	0.73
1:A:489:VAL:HB	1:B:489:VAL:HG13	1.71	0.73
1:B:5:LEU:HD11	1:B:67:LEU:HD11	1.69	0.73
1:D:457:ASP:CG	1:D:459:MSE:HB3	2.14	0.73
1:D:88:LEU:O	1:D:135:PRO:HD2	1.89	0.72
1:A:111:PRO:HB2	1:A:183:LEU:HD21	1.70	0.72
1:D:56:PHE:HZ	1:D:92:VAL:C	1.97	0.72
1:A:37:GLU:O	1:A:40:LYS:HG2	1.90	0.72
1:A:62:ARG:HH22	1:A:86:GLN:HE21	1.37	0.71
1:C:96:GLY:C	1:C:97:ARG:HD3	2.15	0.71
1:D:73:PRO:HA	1:D:157:ARG:HG2	1.72	0.71
1:C:310:ARG:HD3	1:C:349:GLU:OE1	1.91	0.70
1:B:204:ARG:HH21	1:B:232:ALA:HA	1.56	0.70
1:B:142:GLU:HG2	1:B:147:PRO:O	1.92	0.70
1:D:375:LEU:HD23	1:D:378:ARG:HD2	1.72	0.70
1:A:74:LEU:HD23	1:A:75:LEU:CA	2.21	0.69
1:C:107:ARG:HB3	1:C:107:ARG:HH11	1.57	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:56:PHE:CZ	1:D:92:VAL:HG23	2.28	0.69
1:B:259:ARG:NH2	3:B:760:HOH:O	2.25	0.69
1:D:122:VAL:HG23	1:D:124:MSE:HG2	1.74	0.69
1:D:247:ARG:HD2	1:D:381:PHE:CE1	2.28	0.69
1:D:242:ASP:OD2	1:D:251:ARG:HD3	1.93	0.68
1:D:243:HIS:CD2	1:D:245:LEU:H	2.08	0.68
1:A:469:GLU:HG3	1:D:469:GLU:HG3	1.75	0.68
1:C:292:GLY:O	1:C:296:VAL:HG23	1.93	0.68
1:B:394:VAL:HG13	1:B:399:LEU:HD13	1.75	0.68
1:D:56:PHE:HE2	1:D:93:GLU:C	2.01	0.67
1:A:216:VAL:HG13	3:A:704:HOH:O	1.93	0.67
1:B:477:ARG:HD2	1:B:481:ARG:CZ	2.24	0.67
1:C:57:ASP:HB3	1:C:60:ALA:HB2	1.77	0.67
1:B:457:ASP:OD2	1:B:459:MSE:HB2	1.94	0.67
1:B:500:ILE:HD12	2:B:702:XMP:H5'1	1.75	0.67
1:C:153:SER:HB3	1:C:158:ALA:HB3	1.77	0.67
1:D:56:PHE:CD2	1:D:94:ARG:HG3	2.29	0.67
1:A:291:ILE:HD12	1:A:384:PRO:CB	2.25	0.67
1:D:247:ARG:HD2	1:D:381:PHE:CD1	2.30	0.67
1:B:477:ARG:HD3	1:B:480:ARG:NH2	2.09	0.66
1:C:111:PRO:HA	1:C:114:ARG:HG3	1.76	0.66
1:D:107:ARG:HH22	1:D:139:VAL:HG23	1.60	0.66
1:C:288:ARG:HH11	1:C:288:ARG:HG2	1.61	0.66
1:D:321:VAL:HG12	1:D:321:VAL:O	1.95	0.66
1:A:285:GLU:O	1:A:289:LYS:HG2	1.95	0.66
1:A:44:GLN:HG3	1:A:187:LYS:HE2	1.77	0.66
1:A:416:TRP:NE1	1:A:473:GLU:OE1	2.29	0.66
1:C:141:ALA:HB3	1:C:150:ALA:HB3	1.78	0.66
1:C:245:LEU:CD1	1:C:291:ILE:CD1	2.74	0.65
1:D:153:SER:HB2	1:D:154:PRO:HD2	1.79	0.65
1:C:1:MSE:H2	1:C:44:GLN:HE21	1.43	0.65
1:D:273:ARG:NH2	1:D:297:ALA:HB3	2.11	0.65
1:B:257:ALA:O	1:B:261:LEU:HD13	1.96	0.65
1:C:198:GLU:HG2	1:C:202:GLU:OE2	1.97	0.65
1:C:310:ARG:CD	1:C:349:GLU:OE1	2.45	0.65
1:D:111:PRO:HA	1:D:114:ARG:HG3	1.77	0.65
1:D:399:LEU:O	1:D:403:ARG:HB2	1.97	0.65
1:B:214:LEU:HB3	1:B:313:ALA:HB3	1.78	0.64
1:C:243:HIS:HD2	1:C:245:LEU:H	1.45	0.64
1:C:499:THR:O	1:D:487:ARG:NH2	2.31	0.64
1:A:18:ARG:HD2	1:A:174:MSE:SE	2.48	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:14:LEU:HD22	1:B:18:ARG:NH1	2.12	0.64
1:A:455:THR:HG22	1:A:456:GLU:N	2.13	0.64
1:B:141:ALA:HB3	1:B:150:ALA:HB3	1.79	0.64
1:D:288:ARG:HE	1:D:388:VAL:HG11	1.63	0.64
1:B:499:THR:HB	2:B:702:XMP:OP3	1.98	0.64
1:C:371:LEU:HD12	1:C:372:PRO:HD2	1.80	0.64
1:D:381:PHE:HZ	1:D:386:LEU:HD13	1.63	0.63
1:A:455:THR:HG21	1:A:458:PHE:HA	1.80	0.63
1:D:34:PRO:HD2	1:D:37:GLU:CD	2.24	0.63
1:B:81:MSE:SE	1:B:160:GLY:C	2.92	0.63
1:D:19:LEU:HD11	1:D:47:ILE:HD12	1.80	0.63
1:B:94:ARG:HA	1:B:128:ASP:OD1	1.99	0.63
1:D:85:ALA:HA	1:D:134:PRO:HG3	1.80	0.63
1:C:310:ARG:CG	1:C:310:ARG:NH1	2.39	0.63
1:D:63:PRO:CB	1:D:67:LEU:HD22	2.28	0.63
1:B:477:ARG:HD3	1:B:480:ARG:HH21	1.63	0.62
1:C:1:MSE:SE	1:C:1:MSE:C	2.92	0.62
1:D:21:GLU:OE2	1:D:174:MSE:HE1	1.99	0.62
1:C:243:HIS:CD2	1:C:245:LEU:H	2.18	0.62
1:B:199:LEU:O	1:B:203:VAL:HG23	1.99	0.62
1:C:500:ILE:HD12	2:C:703:XMP:H5'1	1.81	0.62
1:D:478:ILE:O	1:D:482:VAL:HG13	1.99	0.62
1:B:373:ASP:OD1	1:B:376:ARG:NH1	2.33	0.62
1:A:306:ARG:HH11	1:A:306:ARG:HG3	1.64	0.62
1:B:289:LYS:O	1:B:293:ARG:HG3	2.00	0.62
1:D:62:ARG:HH22	1:D:86:GLN:NE2	1.97	0.62
1:B:275:LEU:HD21	1:B:396:GLU:OE1	2.00	0.62
1:C:211:ARG:HD2	1:C:235:ASP:OD2	2.00	0.61
1:D:214:LEU:O	1:D:214:LEU:HD12	2.01	0.61
1:B:18:ARG:HD3	1:B:174:MSE:SE	2.50	0.61
1:D:212:VAL:HG22	1:D:235:ASP:O	2.01	0.61
1:B:23:ARG:HB2	1:B:188:ARG:HB3	1.82	0.61
1:A:266:LEU:HD23	1:A:266:LEU:C	2.26	0.61
1:A:122:VAL:HG23	1:A:124:MSE:HG2	1.83	0.61
1:D:62:ARG:HH22	1:D:86:GLN:HE21	1.49	0.60
1:D:211:ARG:HG2	1:D:235:ASP:OD1	2.01	0.60
1:B:477:ARG:HD2	1:B:481:ARG:NH1	2.17	0.60
1:D:284:PRO:HB3	1:D:503:GLU:HB2	1.81	0.60
1:A:175:GLN:HE21	1:A:179:ASN:HD21	1.50	0.60
1:D:5:LEU:HA	1:D:29:LEU:O	2.01	0.60
1:D:73:PRO:HG3	1:D:157:ARG:HH11	1.65	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:79:TYR:O	1:D:83:LEU:HG	2.02	0.60
1:A:62:ARG:HH12	1:A:86:GLN:NE2	1.99	0.60
1:A:286:GLU:O	1:A:290:ILE:HG13	2.01	0.60
1:B:97:ARG:O	1:B:99:GLU:HG2	2.01	0.60
1:A:44:GLN:OE1	1:A:187:LYS:HD2	2.02	0.60
1:D:316:THR:O	1:D:355:ARG:HA	2.00	0.60
1:D:288:ARG:HE	1:D:388:VAL:CG1	2.15	0.59
1:C:93:GLU:OE2	1:C:131:THR:HG21	2.02	0.59
1:D:38:VAL:HG23	1:D:39:LEU:N	2.17	0.59
1:D:106:THR:HG22	1:D:142:GLU:O	2.03	0.59
1:C:247:ARG:HD2	3:C:719:HOH:O	2.02	0.59
1:D:40:LYS:HG3	1:D:41:HIS:CD2	2.39	0.58
1:C:136:GLY:O	1:C:154:PRO:HG3	2.03	0.58
1:C:198:GLU:HG3	1:C:201:ARG:HH12	1.67	0.58
1:D:78:CYS:C	1:D:80:GLY:H	2.11	0.58
1:A:243:HIS:CD2	1:A:245:LEU:H	2.21	0.58
1:B:143:THR:HG23	1:B:146:ASN:H	1.69	0.58
1:B:216:VAL:HA	1:B:222:SER:HB3	1.85	0.58
1:D:1:MSE:O	1:D:1:MSE:SE	2.71	0.58
1:D:56:PHE:CZ	1:D:93:GLU:HA	2.38	0.58
1:D:68:PHE:HD2	1:D:88:LEU:HD21	1.68	0.58
1:D:199:LEU:O	1:D:203:VAL:HG12	2.04	0.58
1:D:396:GLU:O	1:D:400:GLU:HG3	2.04	0.58
1:A:293:ARG:HG2	1:A:293:ARG:HH11	1.67	0.57
1:B:3:LEU:HD11	1:B:29:LEU:HD12	1.86	0.57
1:D:482:VAL:O	1:D:482:VAL:HG22	2.03	0.57
1:A:301:GLN:HG3	3:A:778:HOH:O	2.04	0.57
1:B:243:HIS:H	1:B:243:HIS:CD2	2.21	0.57
1:C:122:VAL:HG23	1:C:124:MSE:HG2	1.85	0.57
1:C:224:THR:OG1	1:C:366:ALA:HB2	2.03	0.57
1:D:211:ARG:HH12	1:D:307:GLY:HA3	1.70	0.57
1:B:35:LEU:HD22	1:B:66:ARG:HB2	1.86	0.57
1:D:216:VAL:HA	1:D:222:SER:HB2	1.86	0.57
1:D:257:ALA:O	1:D:261:LEU:HD23	2.04	0.57
1:B:109:GLU:O	1:B:140:VAL:HB	2.05	0.57
1:B:287:LYS:O	1:B:291:ILE:HG12	2.05	0.57
1:D:281:VAL:HG13	1:D:286:GLU:HG2	1.85	0.56
1:B:1:MSE:HE2	1:B:27:LEU:HD12	1.87	0.56
1:C:13:ARG:HD3	3:C:728:HOH:O	2.05	0.56
1:A:378:ARG:HH11	1:A:378:ARG:HB3	1.69	0.56
1:A:457:ASP:OD2	1:A:457:ASP:C	2.49	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1:MSE:HE1	1:C:3:LEU:CD1	2.25	0.56
1:C:432:VAL:HG13	1:C:432:VAL:O	2.05	0.56
1:C:455:THR:HG23	1:C:460:THR:O	2.05	0.56
1:C:457:ASP:C	1:C:457:ASP:OD1	2.47	0.56
1:D:310:ARG:HH11	1:D:310:ARG:HG2	1.70	0.56
1:A:20:ARG:HD3	1:A:361:GLU:OE2	2.05	0.56
1:B:244:GLY:HA3	1:B:271:LYS:HG2	1.87	0.56
1:A:318:TYR:CZ	1:A:322:ILE:HD11	2.40	0.56
1:C:206:ARG:HG2	1:C:206:ARG:HH11	1.71	0.56
1:B:55:VAL:HG11	1:B:82:GLN:CB	2.36	0.56
1:D:35:LEU:HD22	1:D:66:ARG:HB2	1.88	0.56
1:D:371:LEU:HD12	1:D:372:PRO:HD2	1.87	0.56
1:B:420:GLU:HG2	3:B:703:HOH:O	2.06	0.56
1:D:56:PHE:HD2	1:D:94:ARG:HG3	1.70	0.55
1:D:212:VAL:HG12	1:D:311:PHE:HB2	1.88	0.55
1:D:211:ARG:NH2	1:D:308:PRO:HD2	2.21	0.55
1:B:62:ARG:HH12	1:B:86:GLN:HE22	1.54	0.55
1:C:53:ARG:NH1	1:C:61:PRO:HD3	2.22	0.55
1:A:390:VAL:HG23	1:A:390:VAL:O	2.05	0.55
1:C:1:MSE:H2	1:C:44:GLN:HG3	1.70	0.55
1:D:499:THR:HB	2:D:704:XMP:OP3	2.06	0.55
1:B:56:PHE:HZ	1:B:92:VAL:O	1.90	0.55
1:A:209:LYS:HB3	1:A:209:LYS:NZ	2.21	0.55
1:A:455:THR:HG22	1:A:457:ASP:H	1.72	0.55
1:B:143:THR:CG2	1:B:146:ASN:H	2.19	0.55
1:C:137:TRP:CD1	1:C:154:PRO:HD3	2.42	0.54
1:A:477:ARG:HG3	1:A:481:ARG:NH1	2.22	0.54
1:C:142:GLU:HG2	1:C:147:PRO:O	2.07	0.54
1:C:109:GLU:CD	1:C:110:GLY:H	2.15	0.54
1:D:78:CYS:C	1:D:80:GLY:N	2.64	0.54
1:A:167:VAL:HG13	1:A:169:HIS:H	1.72	0.54
1:D:198:GLU:HG3	1:D:202:GLU:OE2	2.08	0.54
1:D:273:ARG:HH22	1:D:297:ALA:HB3	1.72	0.54
1:A:322:ILE:O	1:A:322:ILE:HG22	2.07	0.54
1:D:3:LEU:HD21	1:D:29:LEU:HB2	1.88	0.54
1:A:499:THR:HB	2:A:701:XMP:OP2	2.07	0.54
1:C:3:LEU:HD12	1:C:27:LEU:O	2.07	0.54
1:D:56:PHE:CE2	1:D:93:GLU:HA	2.43	0.54
1:D:214:LEU:HD12	1:D:238:ALA:HA	1.89	0.54
1:D:401:ILE:HD13	1:D:484:GLU:CB	2.38	0.54
1:D:500:ILE:HG13	2:D:704:XMP:H5'1	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:198:GLU:HA	1:B:201:ARG:HH12	1.73	0.53
1:A:187:LYS:H	1:A:187:LYS:HD3	1.73	0.53
1:C:53:ARG:HH11	1:C:61:PRO:HD3	1.73	0.53
1:D:104:LEU:O	1:D:143:THR:HG22	2.09	0.53
1:B:1:MSE:SE	1:B:1:MSE:C	3.01	0.53
1:D:1:MSE:SE	1:D:1:MSE:C	3.01	0.53
1:D:211:ARG:HG2	1:D:235:ASP:CG	2.32	0.53
1:D:480:ARG:HG3	1:D:480:ARG:HH11	1.73	0.53
1:A:492:LEU:HD11	1:B:490:TYR:HB2	1.90	0.53
1:D:265:LEU:HD12	1:D:265:LEU:C	2.33	0.53
1:C:499:THR:HB	2:C:703:XMP:OP2	2.08	0.53
1:B:144:GLU:HG3	1:B:145:GLU:OE2	2.08	0.53
1:B:193:GLU:OE1	1:B:193:GLU:N	2.38	0.53
1:B:143:THR:HG22	1:B:146:ASN:HB3	1.91	0.53
1:C:1:MSE:SE	1:C:2:VAL:N	2.91	0.53
1:D:1:MSE:N	1:D:44:GLN:HE21	2.07	0.53
1:A:141:ALA:HB3	1:A:150:ALA:HB3	1.92	0.52
1:A:457:ASP:CG	1:A:459:MSE:HB2	2.33	0.52
1:B:114:ARG:HG3	1:B:114:ARG:HH11	1.74	0.52
1:B:211:ARG:HD3	1:B:308:PRO:O	2.08	0.52
1:A:175:GLN:HE21	1:A:179:ASN:ND2	2.07	0.52
1:B:35:LEU:HB3	1:B:66:ARG:HH21	1.75	0.52
1:D:3:LEU:HD11	1:D:29:LEU:HD12	1.91	0.52
1:A:28:ILE:HD12	1:A:322:ILE:HD13	1.90	0.52
1:A:378:ARG:HB3	1:A:378:ARG:NH1	2.24	0.52
1:D:88:LEU:CB	1:D:134:PRO:HB3	2.39	0.52
1:D:122:VAL:CG2	1:D:124:MSE:HG2	2.38	0.52
1:D:245:LEU:HD13	1:D:387:ALA:HB2	1.92	0.52
1:B:198:GLU:HA	1:B:201:ARG:NH1	2.25	0.52
1:D:85:ALA:HA	1:D:134:PRO:CG	2.40	0.52
1:A:14:LEU:HD11	1:A:18:ARG:NH2	2.24	0.52
1:D:3:LEU:HD21	1:D:29:LEU:HD12	1.91	0.52
1:D:211:ARG:HH22	1:D:308:PRO:HD2	1.75	0.52
1:D:214:LEU:HD12	1:D:214:LEU:C	2.34	0.52
1:D:292:GLY:O	1:D:296:VAL:HG23	2.10	0.52
1:C:97:ARG:HD3	1:C:97:ARG:N	2.24	0.51
1:A:495:LYS:HB2	1:A:498:ALA:O	2.09	0.51
1:D:12:THR:HG23	1:D:28:ILE:HD12	1.93	0.51
1:A:211:ARG:CG	1:A:235:ASP:OD2	2.54	0.51
1:A:455:THR:OG1	1:A:461:ALA:CB	2.59	0.51
1:D:270:ALA:O	1:D:274:PHE:HD2	1.94	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:187:LYS:HD3	1:A:187:LYS:N	2.25	0.51
1:D:106:THR:HG22	1:D:142:GLU:C	2.35	0.51
1:A:243:HIS:HE1	1:A:383:GLY:O	1.94	0.51
1:C:288:ARG:HG2	1:C:288:ARG:NH1	2.25	0.51
1:B:193:GLU:O	1:B:197:GLU:HG3	2.10	0.51
1:D:84:LEU:HD21	1:D:137:TRP:CZ3	2.46	0.51
1:D:431:PRO:HG3	1:D:446:TYR:HE1	1.74	0.51
1:B:87:GLU:O	1:B:88:LEU:HD23	2.10	0.51
1:C:1:MSE:H1	1:C:44:GLN:HE21	1.55	0.51
1:D:56:PHE:CE2	1:D:93:GLU:C	2.87	0.50
1:B:5:LEU:CD1	1:B:67:LEU:HD11	2.39	0.50
1:B:42:ARG:N	1:B:43:PRO:HD3	2.26	0.50
1:C:53:ARG:HD2	1:C:61:PRO:HD2	1.94	0.50
1:D:3:LEU:HD23	1:D:4:VAL:N	2.26	0.50
1:B:448:LEU:HB2	1:B:485:ILE:HD12	1.93	0.50
1:D:211:ARG:HB3	1:D:309:PHE:HD1	1.76	0.50
1:B:78:CYS:O	1:B:82:GLN:HG2	2.10	0.50
1:C:81:MSE:HE3	1:C:151:ILE:HG12	1.94	0.50
1:C:107:ARG:HH12	1:C:142:GLU:HG3	1.77	0.50
1:A:448:LEU:CB	1:A:485:ILE:HD13	2.39	0.50
1:B:181:LEU:CD2	1:B:186:VAL:HG21	2.41	0.50
1:B:271:LYS:O	1:B:275:LEU:HD13	2.11	0.50
1:B:181:LEU:HD22	1:B:186:VAL:HG21	1.94	0.50
1:D:7:PHE:CE1	1:D:31:GLY:HA3	2.47	0.50
1:D:89:GLY:C	1:D:135:PRO:HD3	2.37	0.50
1:C:281:VAL:HG21	1:C:290:ILE:CD1	2.42	0.49
1:C:455:THR:HG22	1:C:456:GLU:H	1.77	0.49
1:D:56:PHE:CE2	1:D:93:GLU:CA	2.95	0.49
1:D:67:LEU:C	1:D:69:SER:H	2.19	0.49
1:B:288:ARG:NH1	2:B:702:XMP:O6	2.44	0.49
1:C:408:ILE:O	1:C:412:LEU:HD13	2.13	0.49
1:D:130:VAL:HG23	1:D:130:VAL:O	2.11	0.49
1:D:249:GLY:O	1:D:253:GLU:HG3	2.12	0.49
1:A:44:GLN:CD	1:A:187:LYS:HD2	2.37	0.49
1:B:48:LEU:N	1:B:48:LEU:HD12	2.28	0.49
1:C:281:VAL:HG13	1:C:286:GLU:HG2	1.94	0.49
1:D:56:PHE:CZ	1:D:92:VAL:C	2.84	0.49
1:D:48:LEU:HD22	1:D:74:LEU:HD21	1.94	0.49
1:D:191:THR:HB	1:D:193:GLU:OE1	2.13	0.49
1:D:457:ASP:OD2	1:D:459:MSE:CE	2.48	0.49
1:A:371:LEU:HD12	1:A:372:PRO:HD2	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:245:LEU:HD11	1:C:291:ILE:CD1	2.40	0.49
1:C:245:LEU:CD1	1:C:291:ILE:HD13	2.42	0.49
1:C:288:ARG:NH1	1:C:388:VAL:HG11	2.28	0.49
1:C:495:LYS:HB2	1:C:498:ALA:O	2.13	0.49
1:A:214:LEU:HD12	1:A:215:ALA:N	2.28	0.49
1:A:242:ASP:OD2	1:A:251:ARG:HD3	2.13	0.49
1:A:490:TYR:HB2	1:B:492:LEU:HD11	1.94	0.49
1:C:1:MSE:HE2	1:C:27:LEU:HB2	1.94	0.49
1:D:211:ARG:HH22	1:D:308:PRO:CD	2.25	0.49
1:B:318:TYR:HA	1:B:355:ARG:O	2.13	0.48
1:A:266:LEU:HD23	1:A:267:VAL:N	2.28	0.48
1:B:159:TYR:OH	1:B:183:LEU:HD13	2.13	0.48
1:C:107:ARG:HB3	1:C:107:ARG:NH1	2.27	0.48
1:D:62:ARG:HH12	1:D:86:GLN:HE22	1.61	0.48
1:A:1:MSE:SE	1:A:1:MSE:C	3.07	0.48
1:B:91:ARG:HH11	1:B:91:ARG:HB3	1.78	0.48
1:C:141:ALA:HB3	1:C:150:ALA:CB	2.41	0.48
1:B:179:ASN:O	1:B:183:LEU:HG	2.13	0.48
1:C:404:ARG:HD3	3:C:733:HOH:O	2.12	0.48
1:A:187:LYS:H	1:A:187:LYS:CD	2.25	0.48
1:A:480:ARG:HD3	1:A:481:ARG:HH11	1.77	0.48
1:A:91:ARG:NH1	1:A:132:ALA:HB2	2.28	0.48
1:C:107:ARG:HH11	1:C:107:ARG:CB	2.25	0.48
1:C:451:ARG:HG2	1:C:491:ASP:HB3	1.95	0.48
1:C:198:GLU:HG3	1:C:201:ARG:NH1	2.27	0.48
1:D:16:ALA:HB2	1:D:28:ILE:HD11	1.95	0.48
1:D:318:TYR:CD2	1:D:322:ILE:HD11	2.49	0.48
1:B:44:GLN:O	1:B:73:PRO:HD2	2.13	0.48
1:D:281:VAL:CG2	1:D:290:ILE:CD1	2.82	0.48
1:D:293:ARG:HG3	1:D:293:ARG:HH11	1.77	0.48
1:B:62:ARG:HH12	1:B:86:GLN:NE2	2.12	0.48
1:C:251:ARG:HD3	1:C:267:VAL:HG11	1.96	0.48
1:B:243:HIS:HE1	1:B:383:GLY:O	1.97	0.47
1:C:9:SER:HB2	1:C:50:GLY:C	2.39	0.47
1:A:266:LEU:C	1:A:266:LEU:CD2	2.87	0.47
1:B:1:MSE:HE3	1:B:41:HIS:HB3	1.96	0.47
1:B:169:HIS:C	1:B:171:PRO:HD3	2.38	0.47
1:C:155:ASP:OD1	1:C:157:ARG:HB2	2.14	0.47
1:D:424:GLN:HE21	1:D:458:PHE:HE1	1.60	0.47
1:A:40:LYS:HG3	1:A:41:HIS:ND1	2.30	0.47
1:C:288:ARG:CZ	1:C:388:VAL:HG11	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:491:ASP:HA	1:D:489:VAL:HG12	1.95	0.47
1:C:288:ARG:NH1	1:C:384:PRO:HG3	2.29	0.47
1:D:35:LEU:O	1:D:38:VAL:HG22	2.14	0.47
1:A:91:ARG:HH12	1:A:132:ALA:HB2	1.79	0.47
1:B:481:ARG:C	1:B:483:PRO:HD3	2.39	0.47
1:D:213:LEU:O	1:D:312:LEU:HD12	2.14	0.47
1:B:102:LYS:HE2	1:D:415:GLU:OE2	2.15	0.47
1:C:107:ARG:NH2	1:C:139:VAL:O	2.48	0.47
1:C:278:LEU:HD11	1:C:291:ILE:HD11	1.97	0.47
1:A:46:LEU:HD13	1:A:67:LEU:HD11	1.97	0.47
1:A:320:ASP:O	1:A:323:GLU:C	2.58	0.47
1:A:390:VAL:HG21	1:A:394:VAL:HG22	1.96	0.47
1:C:285:GLU:O	1:C:289:LYS:HG3	2.14	0.47
1:D:265:LEU:HD12	1:D:265:LEU:O	2.13	0.47
1:D:273:ARG:NH1	1:D:298:ALA:HB2	2.30	0.47
1:B:244:GLY:CA	1:B:271:LYS:HG2	2.44	0.47
1:D:68:PHE:CD2	1:D:88:LEU:CD2	2.93	0.47
1:B:457:ASP:CG	1:B:459:MSE:HB2	2.39	0.47
1:D:81:MSE:SE	1:D:151:ILE:HG12	2.65	0.47
1:B:288:ARG:HH21	1:B:503:GLU:C	2.22	0.47
1:B:484:GLU:CD	1:B:484:GLU:H	2.23	0.47
1:C:270:ALA:HB1	1:C:273:ARG:HD3	1.96	0.47
1:B:227:LEU:HD21	1:B:261:LEU:HD23	1.98	0.46
1:D:41:HIS:O	1:D:42:ARG:C	2.59	0.46
1:D:92:VAL:HG12	1:D:130:VAL:HG12	1.97	0.46
1:D:397:GLU:O	1:D:401:ILE:HG13	2.14	0.46
1:B:243:HIS:CD2	1:B:245:LEU:H	2.33	0.46
1:D:84:LEU:HD21	1:D:137:TRP:CH2	2.50	0.46
1:B:93:GLU:HG2	1:B:94:ARG:N	2.30	0.46
1:C:91:ARG:HG3	1:C:91:ARG:HH11	1.80	0.46
1:B:117:GLU:OE2	1:D:249:GLY:HA2	2.14	0.46
1:A:94:ARG:HA	1:A:128:ASP:OD1	2.16	0.46
1:B:116:LEU:HD21	1:B:176:ILE:HG13	1.98	0.46
1:D:74:LEU:HD23	1:D:75:LEU:N	2.30	0.46
1:D:238:ALA:O	1:D:265:LEU:HA	2.15	0.46
1:A:465:ARG:HB3	1:B:468:LEU:HD13	1.96	0.46
1:B:213:LEU:HB2	1:B:309:PHE:CG	2.51	0.46
1:D:14:LEU:O	1:D:18:ARG:HB2	2.15	0.46
1:A:214:LEU:HD12	1:A:215:ALA:H	1.81	0.46
1:B:67:LEU:C	1:B:67:LEU:HD23	2.40	0.46
1:D:184:ALA:HB3	1:D:186:VAL:HG23	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:317:LEU:O	1:B:320:ASP:HB2	2.16	0.46
1:C:255:GLU:OE1	1:C:267:VAL:HG21	2.16	0.46
1:B:81:MSE:SE	1:B:161:VAL:N	2.99	0.46
1:C:322:ILE:O	1:C:322:ILE:HG22	2.16	0.46
1:D:111:PRO:HB2	1:D:183:LEU:HD21	1.98	0.46
1:A:404:ARG:NH2	1:A:484:GLU:OE2	2.43	0.45
1:D:17:ARG:NH2	3:D:736:HOH:O	2.49	0.45
1:A:390:VAL:O	1:A:390:VAL:CG2	2.63	0.45
1:D:3:LEU:HB3	1:D:46:LEU:HD23	1.97	0.45
1:B:141:ALA:HB3	1:B:150:ALA:CB	2.47	0.45
1:C:141:ALA:CB	1:C:150:ALA:HB3	2.45	0.45
1:C:457:ASP:OD1	1:C:459:MSE:N	2.46	0.45
1:C:487:ARG:HD3	1:D:502:TRP:CE2	2.51	0.45
1:D:212:VAL:O	1:D:236:HIS:HA	2.16	0.45
1:A:448:LEU:HD13	1:A:485:ILE:HD11	1.97	0.45
1:A:454:THR:C	1:A:455:THR:HG1	2.24	0.45
1:C:93:GLU:O	1:C:128:ASP:HB3	2.16	0.45
1:B:117:GLU:HB2	1:D:248:LEU:HG	1.98	0.45
1:B:122:VAL:HG23	1:B:124:MSE:HG2	1.99	0.45
1:D:13:ARG:HH12	1:D:17:ARG:NH1	2.14	0.45
1:D:116:LEU:HD12	1:D:116:LEU:N	2.32	0.45
1:B:62:ARG:HH22	1:B:86:GLN:HE21	1.64	0.45
1:C:14:LEU:HD11	1:C:18:ARG:CZ	2.47	0.45
1:D:88:LEU:HB3	1:D:134:PRO:HB3	1.99	0.45
1:D:455:THR:HB	1:D:461:ALA:CB	2.47	0.45
1:A:191:THR:O	1:A:195:VAL:HG23	2.17	0.45
1:A:455:THR:HG22	1:A:456:GLU:H	1.80	0.45
1:D:211:ARG:HB3	1:D:309:PHE:CD1	2.52	0.45
1:C:232:ALA:HB3	1:C:234:VAL:HG13	1.98	0.45
1:D:139:VAL:HG23	1:D:139:VAL:O	2.17	0.45
1:B:82:GLN:NE2	1:B:128:ASP:HB2	2.32	0.44
1:B:240:PHE:HE2	1:B:254:VAL:HG11	1.82	0.44
1:C:490:TYR:HB2	1:D:492:LEU:HD21	1.98	0.44
1:D:95:ALA:H	1:D:128:ASP:HA	1.82	0.44
1:D:162:GLN:O	1:D:162:GLN:HG3	2.17	0.44
1:D:88:LEU:HB2	1:D:134:PRO:HB3	1.99	0.44
1:D:213:LEU:HB2	1:D:309:PHE:CG	2.52	0.44
1:A:191:THR:HB	1:A:193:GLU:OE1	2.17	0.44
1:B:255:GLU:HA	1:B:265:LEU:CD2	2.47	0.44
1:C:455:THR:HG21	1:C:458:PHE:HA	1.98	0.44
1:D:35:LEU:HB2	1:D:64:ASP:CG	2.41	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:432:VAL:HG22	1:D:433:ARG:HD3	1.99	0.44
1:A:107:ARG:O	1:A:141:ALA:HA	2.17	0.44
1:B:477:ARG:CD	1:B:481:ARG:NH1	2.80	0.44
1:D:121:GLN:O	1:D:170:THR:HA	2.17	0.44
1:D:153:SER:CB	1:D:158:ALA:HB3	2.37	0.44
1:D:433:ARG:HD3	1:D:433:ARG:O	2.17	0.44
1:B:184:ALA:HB3	1:B:186:VAL:HG23	1.99	0.44
1:D:210:ASP:HB3	1:D:310:ARG:HB3	1.99	0.44
1:D:283:ASP:HB3	1:D:286:GLU:HB2	2.00	0.44
1:A:39:LEU:CD2	1:A:72:LEU:HD11	2.48	0.44
1:A:193:GLU:HG2	1:A:194:HIS:N	2.32	0.44
1:B:306:ARG:HG3	1:B:306:ARG:HH11	1.83	0.44
1:C:1:MSE:SE	1:C:2:VAL:C	3.10	0.44
1:C:53:ARG:HD2	1:C:61:PRO:CD	2.47	0.44
1:A:306:ARG:HH11	1:A:306:ARG:CG	2.30	0.44
1:A:455:THR:OG1	1:A:461:ALA:HB2	2.18	0.44
1:C:23:ARG:HB2	1:C:188:ARG:HB3	2.00	0.44
1:C:187:LYS:HE2	1:C:189:ASP:OD1	2.18	0.44
1:C:201:ARG:HG2	1:C:205:GLU:OE2	2.17	0.44
1:D:13:ARG:HB3	1:D:13:ARG:NH2	2.33	0.44
1:D:74:LEU:HD23	1:D:74:LEU:C	2.43	0.44
1:A:92:VAL:HG22	1:A:130:VAL:HG12	1.99	0.44
1:B:141:ALA:CB	1:B:150:ALA:HB3	2.46	0.44
1:A:293:ARG:HG2	1:A:293:ARG:NH1	2.33	0.44
1:B:28:ILE:HD12	1:B:322:ILE:CD1	2.48	0.44
1:B:212:VAL:HB	1:B:311:PHE:HB2	1.99	0.44
1:B:227:LEU:CD2	1:B:261:LEU:HD23	2.47	0.44
1:B:384:PRO:HB2	1:B:388:VAL:HG13	1.99	0.44
1:D:124:MSE:HE1	1:D:149:ALA:HB1	2.00	0.44
1:A:165:PRO:O	1:A:173:GLY:HA3	2.18	0.43
1:B:20:ARG:HD3	1:B:361:GLU:OE2	2.18	0.43
1:B:191:THR:O	1:B:195:VAL:HG23	2.18	0.43
1:B:240:PHE:CE2	1:B:254:VAL:HG11	2.53	0.43
1:B:465:ARG:HG3	1:B:465:ARG:HH11	1.83	0.43
1:C:245:LEU:HD11	1:C:291:ILE:HD13	2.00	0.43
1:A:74:LEU:HD11	1:A:84:LEU:HD13	2.00	0.43
1:B:202:GLU:O	1:B:203:VAL:C	2.60	0.43
1:B:214:LEU:HD13	1:B:214:LEU:O	2.18	0.43
1:C:67:LEU:C	1:C:69:SER:H	2.26	0.43
1:C:412:LEU:HD11	1:C:477:ARG:HD2	1.99	0.43
1:A:14:LEU:HD11	1:A:18:ARG:CZ	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:44:GLN:OE1	1:A:187:LYS:CD	2.64	0.43
1:B:72:LEU:HD23	1:B:72:LEU:HA	1.87	0.43
1:D:107:ARG:NH2	1:D:139:VAL:O	2.51	0.43
1:A:81:MSE:SE	1:A:160:GLY:C	3.12	0.43
1:C:465:ARG:HB3	1:D:468:LEU:HD13	2.01	0.43
1:A:116:LEU:HD21	1:A:176:ILE:HG13	2.00	0.43
1:B:91:ARG:NH1	1:B:132:ALA:CB	2.82	0.43
1:C:481:ARG:C	1:C:483:PRO:HD3	2.43	0.43
1:A:322:ILE:O	1:A:322:ILE:CG2	2.66	0.43
1:B:114:ARG:HG3	1:B:114:ARG:NH1	2.33	0.43
1:D:3:LEU:HD23	1:D:4:VAL:H	1.83	0.43
1:D:81:MSE:SE	1:D:160:GLY:C	3.12	0.43
1:D:123:TRP:CD1	1:D:167:VAL:HG21	2.54	0.43
1:D:302:VAL:HG13	1:D:306:ARG:HG3	2.00	0.43
1:A:36:GLU:H	1:A:36:GLU:CD	2.26	0.43
1:B:57:ASP:HB3	1:B:60:ALA:HB2	2.00	0.43
1:A:455:THR:CG2	1:A:456:GLU:N	2.82	0.43
1:C:62:ARG:NH2	1:C:86:GLN:OE1	2.45	0.43
1:A:206:ARG:HH11	1:A:206:ARG:HG2	1.84	0.43
1:A:291:ILE:HD12	1:A:384:PRO:CA	2.48	0.43
1:A:491:ASP:OD2	1:B:487:ARG:HD3	2.19	0.43
1:B:169:HIS:O	1:B:171:PRO:HD3	2.18	0.43
1:C:193:GLU:HG2	1:C:194:HIS:N	2.34	0.43
1:C:207:ALA:HA	1:C:311:PHE:CE2	2.54	0.43
1:C:214:LEU:HD11	1:C:225:LEU:HD23	2.00	0.43
1:C:468:LEU:HD13	1:D:465:ARG:HB3	2.00	0.43
1:D:19:LEU:HD11	1:D:47:ILE:CD1	2.47	0.43
1:D:39:LEU:HD23	1:D:72:LEU:HD11	2.01	0.43
1:D:139:VAL:HG12	1:D:148:VAL:HG13	2.01	0.43
1:D:211:ARG:NH2	1:D:308:PRO:CD	2.81	0.43
1:D:211:ARG:NH2	1:D:308:PRO:N	2.67	0.43
1:A:46:LEU:CD1	1:A:67:LEU:HD11	2.49	0.43
1:A:383:GLY:N	1:A:384:PRO:HD2	2.34	0.43
1:C:165:PRO:O	1:C:173:GLY:HA3	2.18	0.43
1:D:477:ARG:HG3	1:D:481:ARG:NH1	2.34	0.43
1:A:224:THR:HG23	1:A:369:LEU:HD12	2.00	0.42
1:B:193:GLU:HG2	1:B:194:HIS:N	2.34	0.42
1:C:383:GLY:N	1:C:384:PRO:HD2	2.34	0.42
1:D:114:ARG:O	1:D:116:LEU:HD12	2.19	0.42
1:D:122:VAL:HB	1:D:163:PHE:CG	2.54	0.42
1:A:137:TRP:CE2	1:A:153:SER:HB3	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:245:LEU:HD13	1:B:387:ALA:HB2	2.01	0.42
1:C:99:GLU:HG3	1:C:126:HIS:HB2	2.01	0.42
1:A:455:THR:CG2	1:A:458:PHE:H	2.33	0.42
1:C:109:GLU:CG	1:C:110:GLY:N	2.82	0.42
1:D:34:PRO:O	1:D:37:GLU:HB3	2.19	0.42
1:D:155:ASP:OD1	1:D:157:ARG:N	2.48	0.42
1:D:212:VAL:O	1:D:212:VAL:HG23	2.19	0.42
1:D:310:ARG:HG2	1:D:310:ARG:NH1	2.35	0.42
1:B:211:ARG:NH1	1:B:235:ASP:OD2	2.52	0.42
1:B:288:ARG:NH2	1:B:503:GLU:O	2.52	0.42
1:D:97:ARG:HG3	1:D:99:GLU:HG2	2.01	0.42
1:A:116:LEU:HD21	1:A:176:ILE:CG1	2.49	0.42
1:A:266:LEU:HD12	1:A:306:ARG:HD2	2.01	0.42
1:A:287:LYS:HE2	1:A:394:VAL:HG23	2.02	0.42
1:B:242:ASP:OD2	1:B:251:ARG:HD2	2.20	0.42
1:B:273:ARG:HG2	1:B:273:ARG:HH11	1.83	0.42
1:C:81:MSE:HG3	1:C:160:GLY:HA3	2.00	0.42
1:D:14:LEU:HD12	1:D:14:LEU:N	2.34	0.42
1:D:38:VAL:HG23	1:D:39:LEU:H	1.84	0.42
1:B:278:LEU:C	1:B:281:VAL:HG12	2.43	0.42
1:D:81:MSE:HE3	1:D:130:VAL:HG21	2.01	0.42
1:D:480:ARG:HG3	1:D:480:ARG:NH1	2.35	0.42
1:D:192:PRO:HB2	1:D:368:LEU:CD2	2.49	0.42
1:D:288:ARG:O	1:D:292:GLY:N	2.48	0.42
1:A:313:ALA:HA	1:A:351:LEU:O	2.19	0.42
1:A:390:VAL:CG2	1:A:394:VAL:HG22	2.50	0.42
1:B:391:LEU:O	1:B:431:PRO:HD2	2.19	0.42
1:D:46:LEU:HD11	1:D:72:LEU:HD12	2.02	0.42
1:D:455:THR:HB	1:D:461:ALA:HB2	2.01	0.42
1:A:79:TYR:CE2	1:A:83:LEU:HD11	2.54	0.42
1:C:285:GLU:HG2	1:C:289:LYS:HE3	2.01	0.42
1:D:127:GLN:O	1:D:127:GLN:HG3	2.20	0.42
1:D:204:ARG:HD3	1:D:232:ALA:HB1	2.02	0.42
1:A:23:ARG:HB2	1:A:188:ARG:HB3	2.02	0.41
1:A:318:TYR:CE2	1:A:322:ILE:CD1	2.90	0.41
1:B:36:GLU:OE2	1:B:37:GLU:HB2	2.20	0.41
1:B:251:ARG:HH21	1:B:267:VAL:HG21	1.85	0.41
1:B:3:LEU:HD21	1:B:29:LEU:HD12	2.01	0.41
1:B:251:ARG:HG3	1:B:252:GLU:N	2.36	0.41
1:C:365:LEU:HD23	1:C:365:LEU:HA	1.93	0.41
1:D:288:ARG:NE	1:D:388:VAL:HG11	2.31	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:383:GLY:N	1:D:384:PRO:CD	2.83	0.41
1:A:201:ARG:HG2	1:A:205:GLU:OE2	2.21	0.41
1:C:55:VAL:HG21	1:C:92:VAL:HG11	2.02	0.41
1:C:74:LEU:HD23	1:C:74:LEU:C	2.45	0.41
1:D:20:ARG:HD3	1:D:361:GLU:OE2	2.20	0.41
1:B:78:CYS:O	1:B:79:TYR:C	2.64	0.41
1:D:134:PRO:HA	1:D:135:PRO:HD3	1.95	0.41
1:A:146:ASN:HA	1:A:147:PRO:HD2	1.96	0.41
1:C:288:ARG:NH1	2:C:703:XMP:O6	2.53	0.41
1:B:46:LEU:O	1:B:74:LEU:HA	2.20	0.41
1:B:67:LEU:HD23	1:B:67:LEU:O	2.20	0.41
1:B:98:ALA:HB2	1:B:127:GLN:HE21	1.79	0.41
1:C:33:ALA:HA	1:C:34:PRO:HD3	1.92	0.41
1:C:78:CYS:O	1:C:79:TYR:C	2.64	0.41
1:A:3:LEU:HD11	1:A:29:LEU:HB3	2.02	0.41
1:A:457:ASP:OD2	1:A:459:MSE:N	2.51	0.41
1:B:48:LEU:N	1:B:48:LEU:CD1	2.84	0.41
1:C:18:ARG:HD2	1:C:174:MSE:SE	2.70	0.41
1:C:451:ARG:HG2	1:C:491:ASP:CB	2.50	0.41
1:D:100:TYR:HE1	1:D:164:HIS:CE1	2.38	0.41
1:A:457:ASP:OD1	1:A:459:MSE:HB2	2.20	0.41
1:B:259:ARG:HG2	1:B:259:ARG:HH11	1.85	0.41
1:B:287:LYS:O	1:B:291:ILE:CG1	2.69	0.41
1:B:322:ILE:O	1:B:322:ILE:HG22	2.21	0.41
1:B:429:LEU:O	1:B:431:PRO:HD3	2.21	0.41
1:C:214:LEU:HD13	1:C:313:ALA:HB3	2.02	0.41
1:C:374:THR:O	1:C:378:ARG:HG3	2.21	0.41
1:D:216:VAL:O	1:D:240:PHE:HD1	2.04	0.41
1:D:457:ASP:CG	1:D:459:MSE:HE2	2.39	0.41
1:A:243:HIS:CD2	1:A:243:HIS:H	2.38	0.41
1:A:42:ARG:N	1:A:43:PRO:HD3	2.36	0.40
1:C:412:LEU:CD2	1:C:474:ALA:HA	2.51	0.40
1:D:9:SER:HB2	1:D:50:GLY:C	2.46	0.40
1:A:274:PHE:CE1	1:A:294:GLU:HB2	2.57	0.40
1:C:213:LEU:HB2	1:C:309:PHE:CG	2.56	0.40
1:C:293:ARG:HH11	1:C:293:ARG:HG2	1.86	0.40
1:D:100:TYR:HB2	1:D:123:TRP:CZ2	2.57	0.40
1:D:178:GLU:OE2	1:D:182:GLU:OE2	2.39	0.40
1:A:62:ARG:HH12	1:A:86:GLN:HE22	1.67	0.40
1:B:240:PHE:CD1	1:B:240:PHE:C	2.99	0.40
1:D:66:ARG:HB3	1:D:69:SER:HB3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:9:SER:HB2	1:A:50:GLY:C	2.47	0.40
1:A:44:GLN:OE1	1:A:186:VAL:HA	2.21	0.40
1:A:272:GLU:CG	1:A:276:LYS:HE2	2.42	0.40
1:B:94:ARG:HD3	1:B:128:ASP:OD1	2.21	0.40
1:C:501:GLU:HG2	2:C:703:XMP:H2'	2.03	0.40
1:D:38:VAL:CG2	1:D:39:LEU:N	2.82	0.40
1:D:109:GLU:O	1:D:140:VAL:HB	2.22	0.40
1:D:281:VAL:CG2	1:D:290:ILE:HD12	2.32	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	469/503 (93%)	454 (97%)	15 (3%)	0	100	100
1	B	461/503 (92%)	437 (95%)	21 (5%)	3 (1%)	18	19
1	C	461/503 (92%)	447 (97%)	14 (3%)	0	100	100
1	D	461/503 (92%)	426 (92%)	33 (7%)	2 (0%)	30	34
All	All	1852/2012 (92%)	1764 (95%)	83 (4%)	5 (0%)	36	42

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	98	ALA
1	B	458	PHE
1	B	96	GLY
1	D	98	ALA
1	D	233	GLY

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	390/404 (96%)	371 (95%)	19 (5%)	22	29
1	B	384/404 (95%)	370 (96%)	14 (4%)	31	42
1	C	384/404 (95%)	367 (96%)	17 (4%)	25	34
1	D	384/404 (95%)	360 (94%)	24 (6%)	16	19
All	All	1542/1616 (95%)	1468 (95%)	74 (5%)	23	30

All (74) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LEU
1	A	38	VAL
1	A	44	GLN
1	A	74	LEU
1	A	157	ARG
1	A	167	VAL
1	A	187	LYS
1	A	209	LYS
1	A	227	LEU
1	A	243	HIS
1	A	263	VAL
1	A	291	ILE
1	A	323	GLU
1	A	375	LEU
1	A	420	GLU
1	A	462	ASP
1	A	469	GLU
1	A	485	ILE
1	A	497	PRO
1	B	3	LEU
1	B	13	ARG
1	B	37	GLU
1	B	212	VAL
1	B	214	LEU

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Mol	Chain	Res	Type
1	B	243	HIS
1	B	267	VAL
1	B	290	ILE
1	B	291	ILE
1	B	399	LEU
1	B	401	ILE
1	B	481	ARG
1	B	484	GLU
1	B	489	VAL
1	C	1	MSE
1	C	5	LEU
1	C	38	VAL
1	C	48	LEU
1	C	107	ARG
1	C	216	VAL
1	C	234	VAL
1	C	243	HIS
1	C	291	ILE
1	C	310	ARG
1	C	322	ILE
1	C	348	PHE
1	C	357	LEU
1	C	364	GLU
1	C	367	LEU
1	C	455	THR
1	C	493	THR
1	D	1	MSE
1	D	3	LEU
1	D	12	THR
1	D	48	LEU
1	D	81	MSE
1	D	117	GLU
1	D	193	GLU
1	D	214	LEU
1	D	246	LEU
1	D	247	ARG
1	D	282	GLU
1	D	291	ILE
1	D	367	LEU
1	D	386	LEU
1	D	401	ILE
1	D	433	ARG

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Mol	Chain	Res	Type
1	D	450	LEU
1	D	460	THR
1	D	469	GLU
1	D	482	VAL
1	D	492	LEU
1	D	493	THR
1	D	497	PRO
1	D	500	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	82	GLN
1	A	86	GLN
1	A	127	GLN
1	A	162	GLN
1	A	175	GLN
1	A	179	ASN
1	A	243	HIS
1	A	301	GLN
1	A	314	GLN
1	B	86	GLN
1	B	127	GLN
1	B	175	GLN
1	B	243	HIS
1	C	44	GLN
1	C	164	HIS
1	C	169	HIS
1	C	243	HIS
1	C	314	GLN
1	D	10	GLN
1	D	41	HIS
1	D	44	GLN
1	D	86	GLN
1	D	164	HIS
1	D	175	GLN
1	D	243	HIS
1	D	424	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

4 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	XMP	B	702	-	26,26,26	1.11	3 (11%)	34,40,40	1.45	7 (20%)
2	XMP	C	703	-	26,26,26	1.06	2 (7%)	34,40,40	1.44	6 (17%)
2	XMP	D	704	-	26,26,26	1.07	1 (3%)	34,40,40	1.42	6 (17%)
2	XMP	A	701	-	26,26,26	1.08	1 (3%)	34,40,40	1.44	7 (20%)

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	XMP	B	702	-	-	1/10/26/26	0/3/3/3
2	XMP	C	703	-	-	1/10/26/26	0/3/3/3
2	XMP	D	704	-	-	0/10/26/26	0/3/3/3
2	XMP	A	701	-	-	0/10/26/26	0/3/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	702	XMP	P-OP2	2.25	1.63	1.54
2	D	704	XMP	C4-N9	-2.13	1.35	1.37
2	C	703	XMP	C4-N3	2.08	1.40	1.37
2	C	703	XMP	P-OP3	2.05	1.62	1.54
2	B	702	XMP	O4'-C1'	2.02	1.46	1.42
2	A	701	XMP	C4-N3	2.01	1.40	1.37
2	B	702	XMP	C4-N9	-2.00	1.35	1.37

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	704	XMP	C6-N1-C2	-3.69	121.28	126.37
2	C	703	XMP	C6-N1-C2	-3.67	121.31	126.37
2	B	702	XMP	N1-C2-N3	3.60	121.40	115.74
2	D	704	XMP	N1-C2-N3	3.59	121.39	115.74
2	B	702	XMP	C6-N1-C2	-3.56	121.46	126.37
2	A	701	XMP	C6-N1-C2	-3.47	121.59	126.37
2	C	703	XMP	N1-C2-N3	3.47	121.19	115.74
2	A	701	XMP	N1-C2-N3	3.34	121.00	115.74
2	A	701	XMP	C6-C5-N7	2.66	135.14	130.29
2	C	703	XMP	C8-N7-C5	2.62	108.93	104.26
2	A	701	XMP	C8-N7-C5	2.62	108.93	104.26
2	B	702	XMP	C6-C5-N7	2.62	135.05	130.29
2	D	704	XMP	C8-N7-C5	2.57	108.83	104.26
2	B	702	XMP	C8-N7-C5	2.55	108.81	104.26
2	D	704	XMP	C6-C5-N7	2.44	134.74	130.29
2	C	703	XMP	O6-C6-C5	-2.39	120.22	126.53
2	C	703	XMP	C6-C5-N7	2.36	134.59	130.29
2	A	701	XMP	O6-C6-C5	-2.35	120.34	126.53
2	C	703	XMP	C5-C6-N1	2.30	119.11	113.25
2	A	701	XMP	C5-C6-N1	2.29	119.09	113.25
2	D	704	XMP	O6-C6-C5	-2.29	120.50	126.53
2	A	701	XMP	N9-C8-N7	-2.26	109.20	113.40
2	B	702	XMP	C5-C6-N1	2.23	118.94	113.25
2	B	702	XMP	O6-C6-C5	-2.23	120.65	126.53
2	D	704	XMP	C5-C6-N1	2.14	118.71	113.25
2	B	702	XMP	N9-C8-N7	-2.07	109.56	113.40

There are no chirality outliers.

All (2) torsion outliers are listed below:

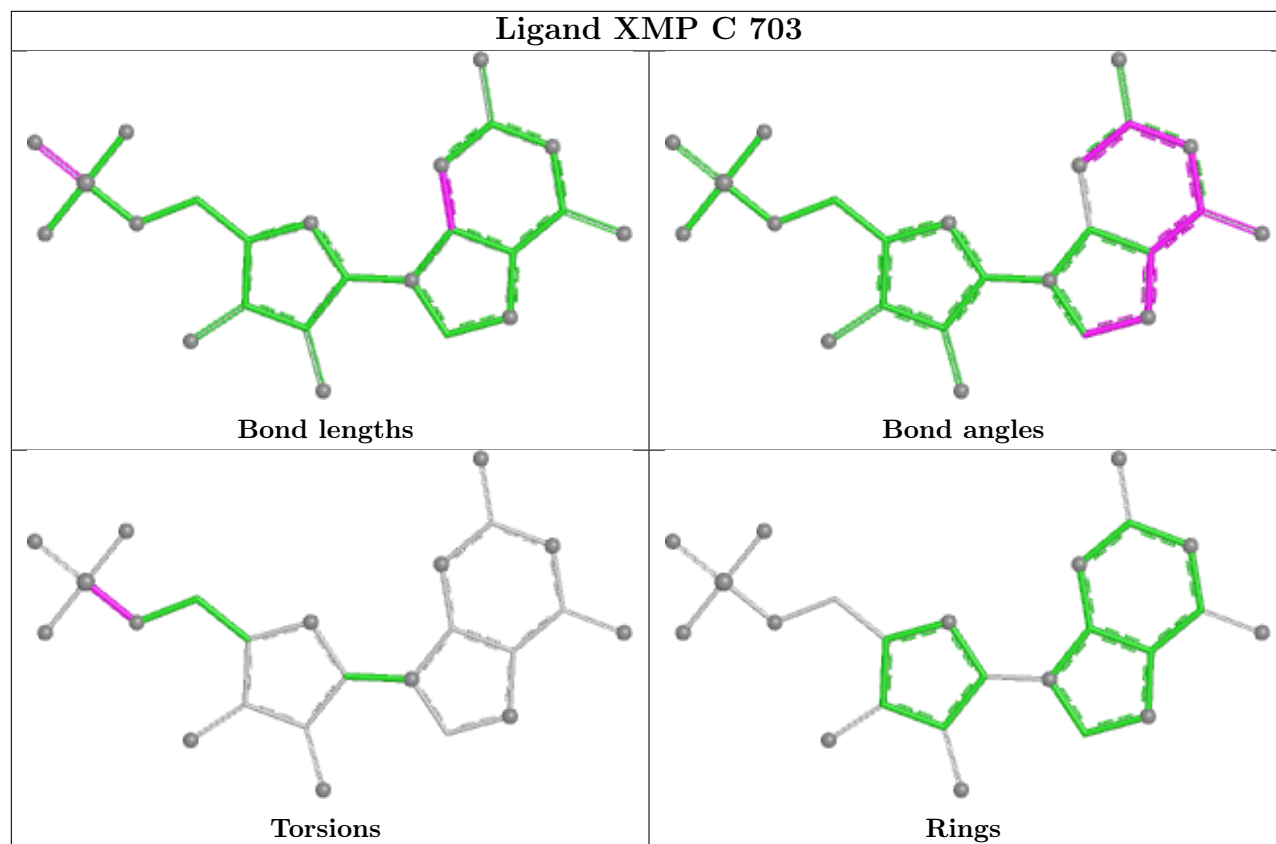
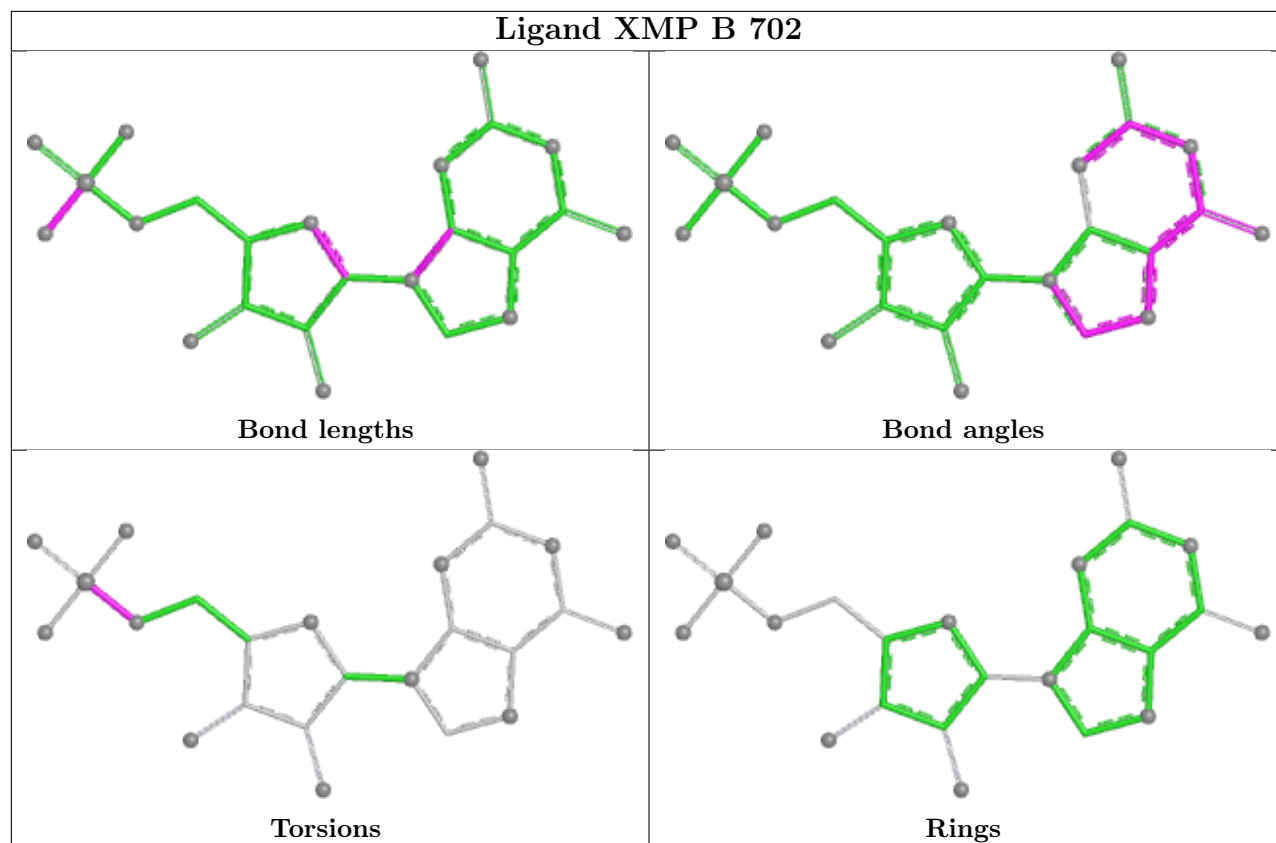
Mol	Chain	Res	Type	Atoms
2	B	702	XMP	C5'-O5'-P-OP1
2	C	703	XMP	C5'-O5'-P-OP2

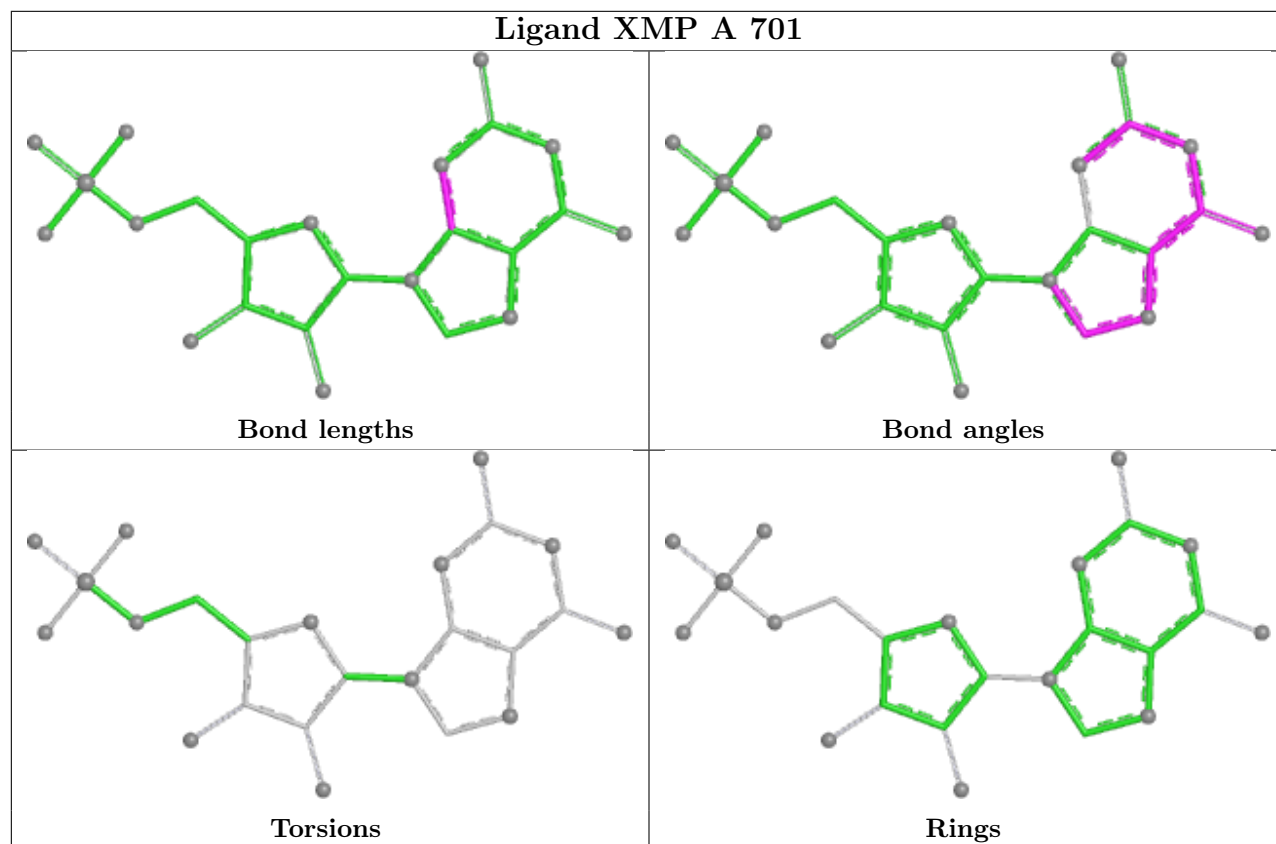
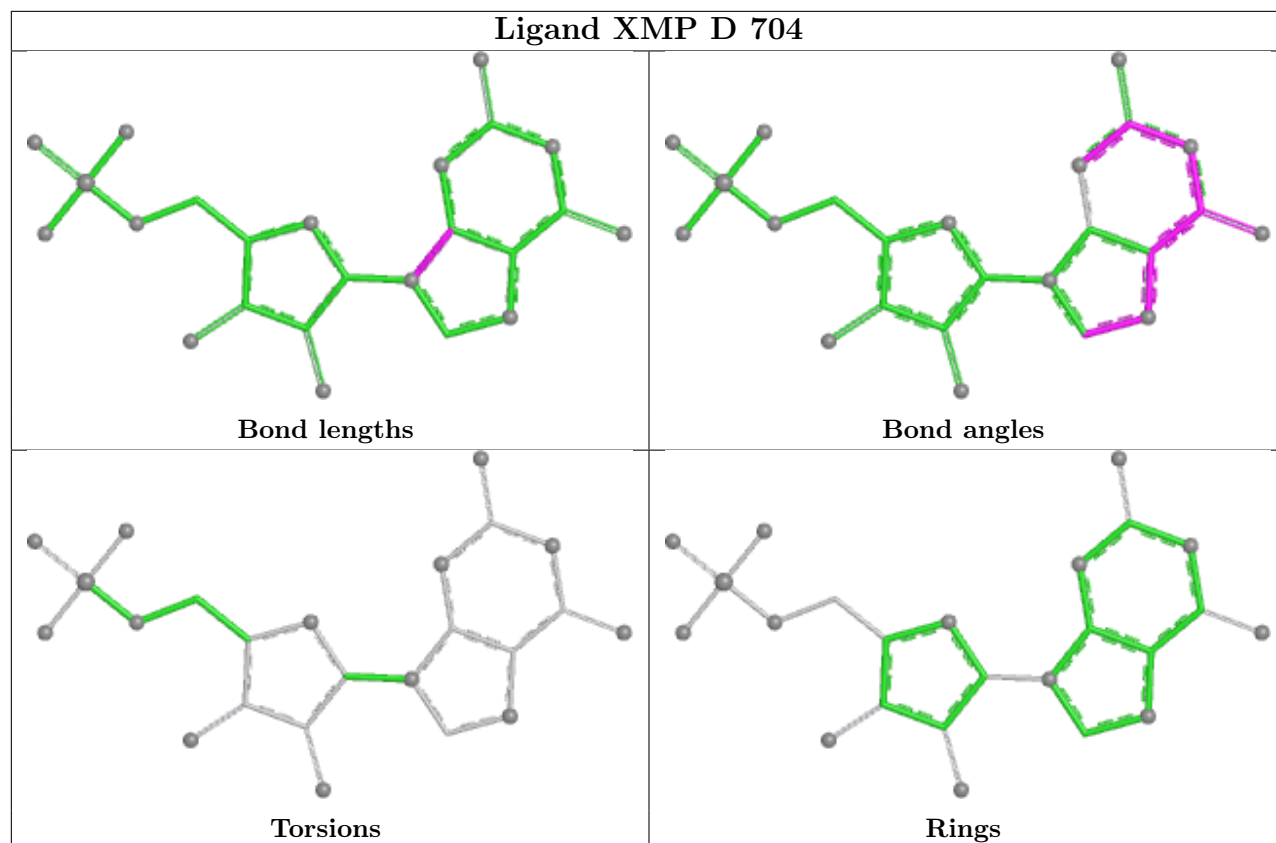
There are no ring outliers.

4 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	702	XMP	3	0
2	C	703	XMP	4	0
2	D	704	XMP	2	0
2	A	701	XMP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	470/503 (93%)	0.27	24 (5%) 33 30	20, 38, 78, 103	0
1	B	462/503 (91%)	0.73	65 (14%) 6 4	20, 50, 85, 117	0
1	C	462/503 (91%)	0.47	35 (7%) 20 17	21, 43, 79, 108	0
1	D	462/503 (91%)	1.19	96 (20%) 2 2	22, 55, 98, 130	0
All	All	1856/2012 (92%)	0.66	220 (11%) 9 7	20, 46, 86, 130	0

All (220) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	85	ALA	8.1
1	D	87	GLU	7.5
1	D	84	LEU	6.9
1	D	136	GLY	6.0
1	D	68	PHE	5.9
1	C	455	THR	5.3
1	D	37	GLU	5.3
1	D	83	LEU	5.2
1	D	135	PRO	5.1
1	D	33	ALA	4.6
1	D	433	ARG	4.5
1	D	31	GLY	4.4
1	D	322	ILE	4.4
1	A	340	GLY	4.0
1	B	91	ARG	4.0
1	B	416	TRP	3.9
1	D	67	LEU	3.9
1	B	89	GLY	3.9
1	B	92	VAL	3.8
1	B	307	GLY	3.8
1	D	88	LEU	3.8

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Mol	Chain	Res	Type	RSRZ
1	D	351	LEU	3.8
1	D	38	VAL	3.8
1	D	86	GLN	3.8
1	C	347	GLU	3.7
1	D	89	GLY	3.6
1	D	56	PHE	3.6
1	D	273	ARG	3.6
1	D	39	LEU	3.6
1	D	93	GLU	3.5
1	A	416	TRP	3.5
1	B	93	GLU	3.4
1	D	28	ILE	3.3
1	D	7	PHE	3.3
1	D	152	ALA	3.3
1	C	432	VAL	3.3
1	D	71	GLY	3.3
1	D	416	TRP	3.3
1	A	157	ARG	3.3
1	C	272	GLU	3.3
1	D	127	GLN	3.2
1	D	94	ARG	3.2
1	D	90	GLY	3.2
1	D	134	PRO	3.2
1	C	348	PHE	3.2
1	D	213	LEU	3.1
1	D	41	HIS	3.1
1	B	432	VAL	3.1
1	D	13	ARG	3.1
1	C	322	ILE	3.0
1	C	416	TRP	3.0
1	D	321	VAL	3.0
1	B	36	GLU	3.0
1	B	293	ARG	3.0
1	D	92	VAL	3.0
1	D	138	ARG	3.0
1	C	456	GLU	3.0
1	D	29	LEU	3.0
1	B	94	ARG	3.0
1	D	3	LEU	2.9
1	D	194	HIS	2.9
1	B	322	ILE	2.9
1	D	348	PHE	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	87	GLU	2.8
1	A	322	ILE	2.8
1	D	36	GLU	2.8
1	B	148	VAL	2.8
1	D	91	ARG	2.8
1	C	308	PRO	2.8
1	A	74	LEU	2.8
1	D	265	LEU	2.8
1	B	347	GLU	2.8
1	B	207	ALA	2.8
1	D	55	VAL	2.8
1	B	189	ASP	2.7
1	A	323	GLU	2.7
1	B	97	ARG	2.7
1	D	35	LEU	2.7
1	A	432	VAL	2.7
1	B	234	VAL	2.7
1	D	432	VAL	2.7
1	D	262	GLY	2.7
1	B	58	PRO	2.7
1	D	72	LEU	2.7
1	A	60	ALA	2.7
1	B	281	VAL	2.7
1	D	34	PRO	2.7
1	B	275	LEU	2.7
1	D	298	ALA	2.6
1	B	348	PHE	2.6
1	D	400	GLU	2.6
1	B	98	ALA	2.6
1	D	95	ALA	2.6
1	B	264	ASN	2.6
1	D	394	VAL	2.6
1	A	58	PRO	2.6
1	D	307	GLY	2.6
1	B	456	GLU	2.6
1	B	378	ARG	2.6
1	B	115	GLY	2.5
1	D	131	THR	2.5
1	D	214	LEU	2.5
1	D	129	ALA	2.5
1	D	80	GLY	2.5
1	D	118	GLY	2.5

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Mol	Chain	Res	Type	RSRZ
1	C	36	GLU	2.5
1	D	65	PRO	2.5
1	D	73	PRO	2.5
1	D	66	ARG	2.5
1	D	205	GLU	2.5
1	D	281	VAL	2.5
1	C	351	LEU	2.5
1	D	82	GLN	2.5
1	D	97	ARG	2.4
1	B	237	LEU	2.4
1	C	41	HIS	2.4
1	C	91	ARG	2.4
1	D	460	THR	2.4
1	C	67	LEU	2.4
1	C	350	LEU	2.4
1	A	480	ARG	2.4
1	A	119	GLU	2.4
1	A	456	GLU	2.4
1	C	109	GLU	2.4
1	B	95	ALA	2.4
1	A	13	ARG	2.4
1	C	480	ARG	2.4
1	A	341	GLY	2.4
1	D	24	ALA	2.4
1	C	311	PHE	2.4
1	D	203	VAL	2.4
1	C	204	ARG	2.4
1	C	232	ALA	2.3
1	D	60	ALA	2.3
1	B	211	ARG	2.3
1	C	378	ARG	2.3
1	B	251	ARG	2.3
1	B	194	HIS	2.3
1	A	87	GLU	2.3
1	D	282	GLU	2.3
1	C	189	ASP	2.3
1	B	154	PRO	2.3
1	D	154	PRO	2.3
1	B	132	ALA	2.3
1	B	273	ARG	2.3
1	B	41	HIS	2.3
1	C	37	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
1	D	30	PRO	2.3
1	C	293	ARG	2.3
1	B	351	LEU	2.2
1	A	36	GLU	2.2
1	D	270	ALA	2.2
1	B	131	THR	2.2
1	B	455	THR	2.2
1	A	40	LYS	2.2
1	D	291	ILE	2.2
1	B	212	VAL	2.2
1	C	38	VAL	2.2
1	D	246	LEU	2.2
1	D	233	GLY	2.2
1	C	420	GLU	2.2
1	D	349	GLU	2.2
1	B	214	LEU	2.2
1	B	248	LEU	2.2
1	D	130	VAL	2.2
1	B	309	PHE	2.2
1	A	97	ARG	2.2
1	D	43	PRO	2.2
1	A	41	HIS	2.2
1	D	17	ARG	2.2
1	D	157	ARG	2.2
1	B	239	VAL	2.2
1	C	68	PHE	2.2
1	D	59	ASP	2.2
1	D	52	PRO	2.2
1	B	117	GLU	2.2
1	B	119	GLU	2.2
1	D	297	ALA	2.2
1	B	305	GLU	2.1
1	C	119	GLU	2.1
1	C	307	GLY	2.1
1	D	70	SER	2.1
1	B	480	ARG	2.1
1	D	100	TYR	2.1
1	D	235	ASP	2.1
1	A	65	PRO	2.1
1	B	137	TRP	2.1
1	B	56	PHE	2.1
1	C	58	PRO	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	65	PRO	2.1
1	D	76	GLY	2.1
1	B	85	ALA	2.1
1	D	74	LEU	2.1
1	B	254	VAL	2.1
1	A	91	ARG	2.1
1	B	138	ARG	2.1
1	A	33	ALA	2.1
1	B	86	GLN	2.1
1	B	261	LEU	2.1
1	C	57	ASP	2.1
1	D	79	TYR	2.1
1	C	62	ARG	2.1
1	B	276	LYS	2.0
1	A	69	SER	2.0
1	B	37	GLU	2.0
1	B	290	ILE	2.0
1	B	100	TYR	2.0
1	D	247	ARG	2.0
1	C	458	PHE	2.0
1	B	209	LYS	2.0
1	B	289	LYS	2.0
1	B	129	ALA	2.0
1	B	232	ALA	2.0
1	B	84	LEU	2.0
1	D	48	LEU	2.0
1	D	75	LEU	2.0
1	A	291	ILE	2.0
1	B	206	ARG	2.0
1	C	310	ARG	2.0
1	D	147	PRO	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 ⓘ

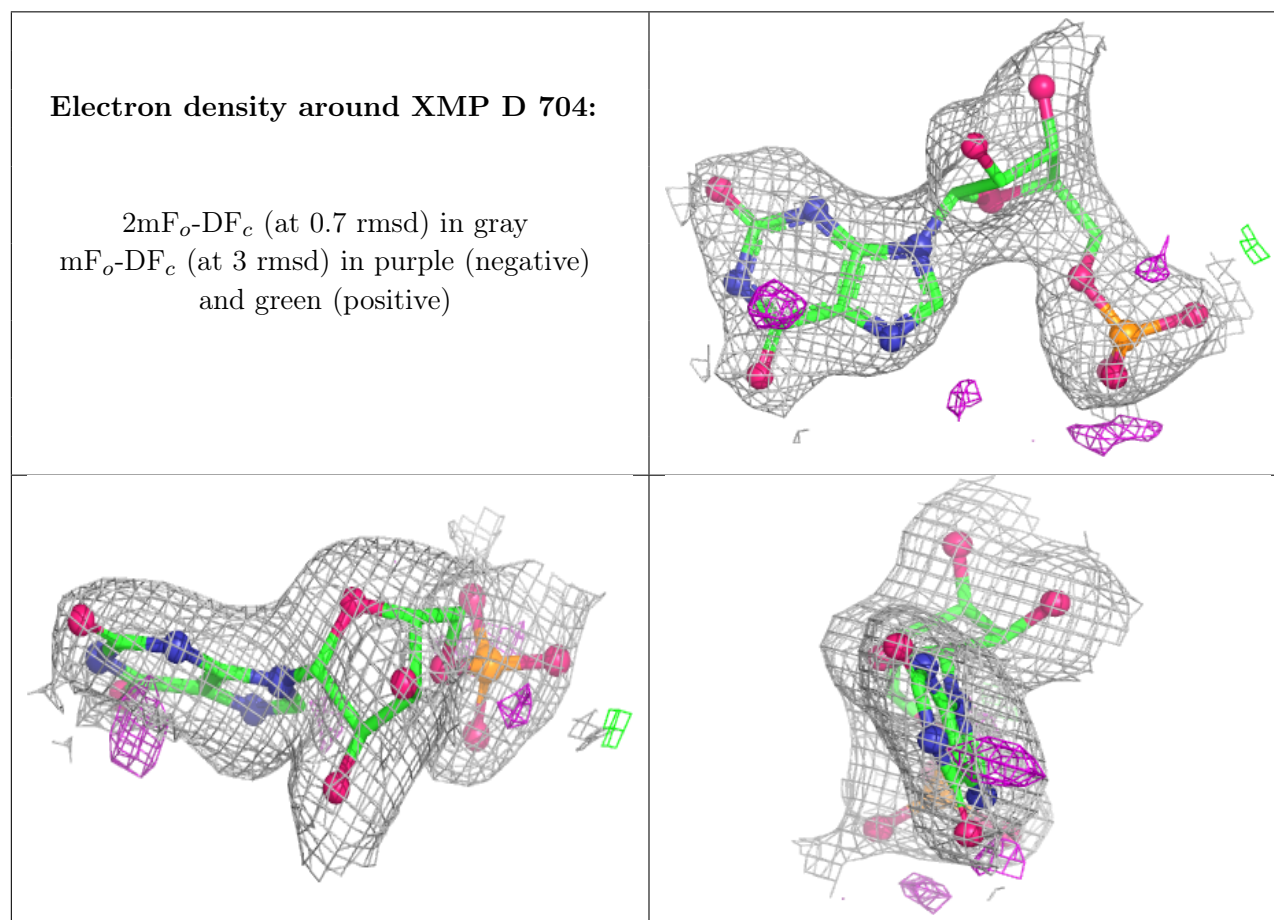
There are no oligosaccharides in this entry.

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. 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.

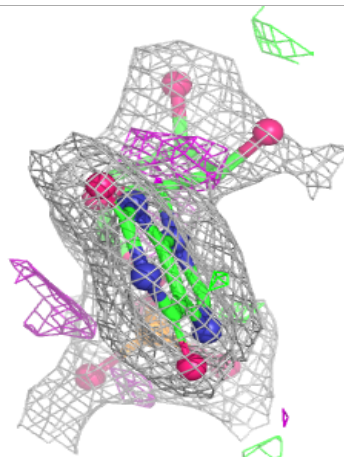
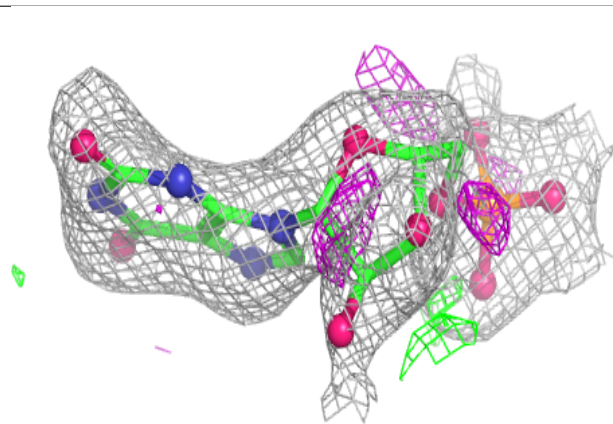
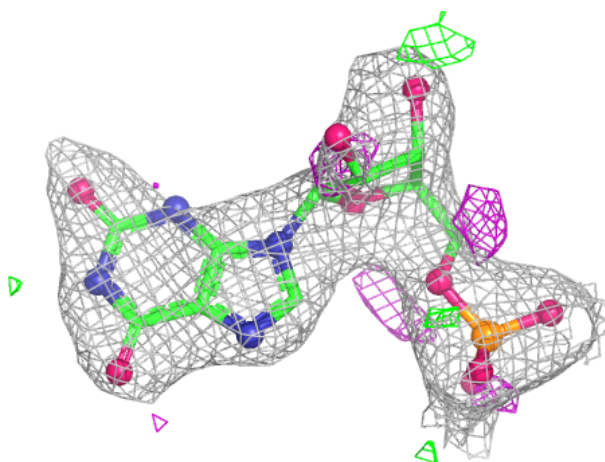
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	XMP	D	704	24/24	0.85	0.13	63,66,71,72	0
2	XMP	C	703	24/24	0.88	0.12	55,58,60,61	0
2	XMP	B	702	24/24	0.91	0.09	49,52,57,57	0
2	XMP	A	701	24/24	0.95	0.07	35,41,45,46	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



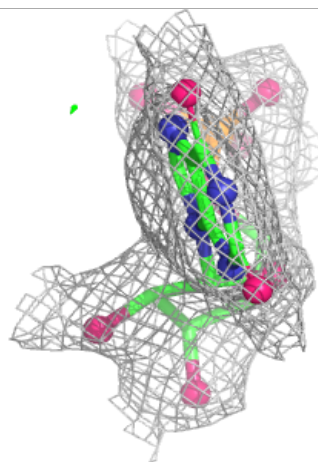
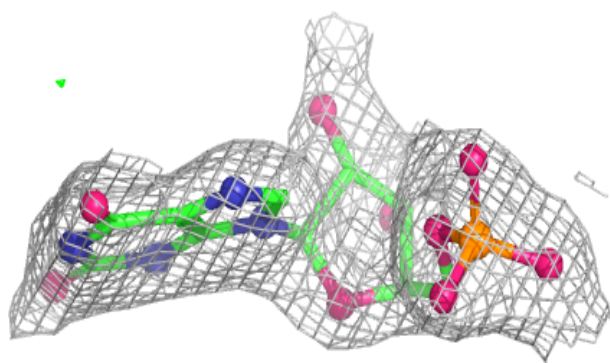
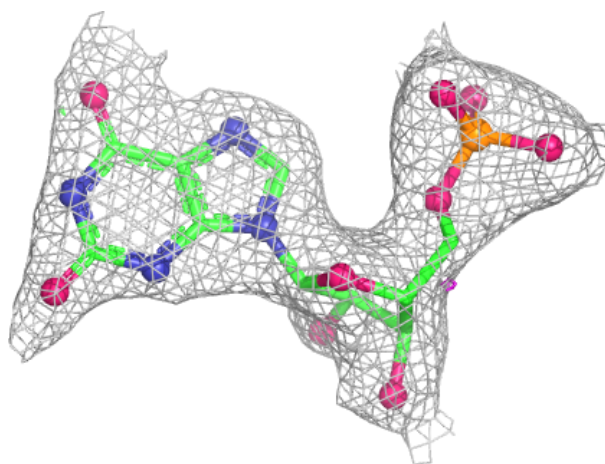
Electron density around XMP C 703:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



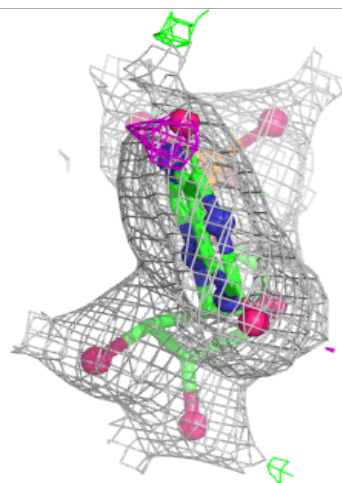
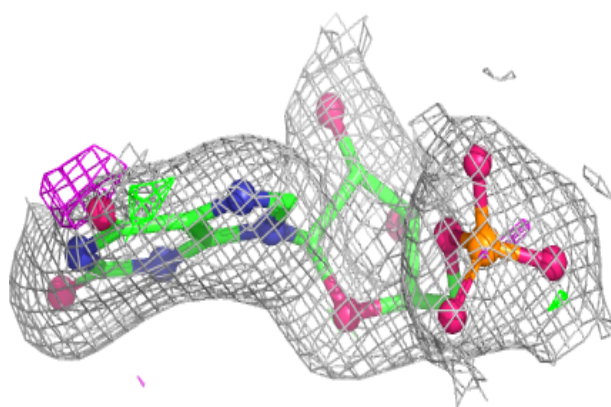
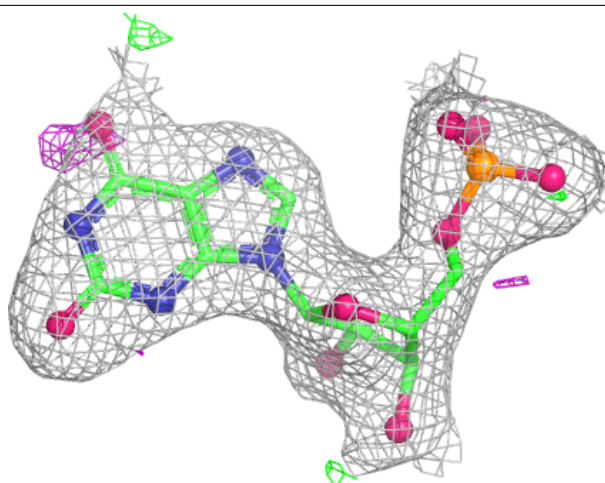
Electron density around XMP B 702:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around XMP A 701:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.