



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 05:39 AM UTC

PDB ID : 3R1R / pdb_00003r1r
Title : RIBONUCLEOTIDE REDUCTASE R1 PROTEIN WITH AMPPNP OCCUPYING THE ACTIVITY SITE FROM ESCHERICHIA COLI
Authors : Eriksson, M.; Eklund, H.
Deposited on : 1997-07-21
Resolution : 3.00 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

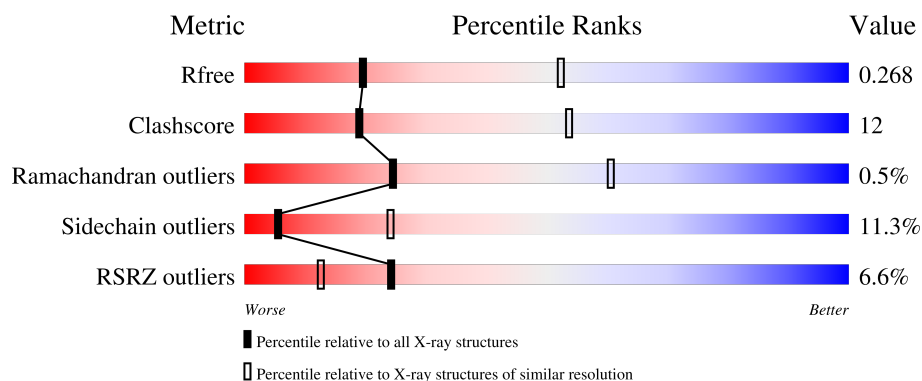
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	761	5% 61% 30% 5%
1	B	761	5% 61% 30% 5%
1	C	761	8% 61% 30% 5%
2	D	20	25% 50% 10% 5% 35%
2	E	20	15% 50% 10% 5% 35%

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Mol	Chain	Length	Quality of chain
2	F	20	 10% 50% 10% 5% 35%
2	P	20	 5% 5% 5% 5% 85%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 18027 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.

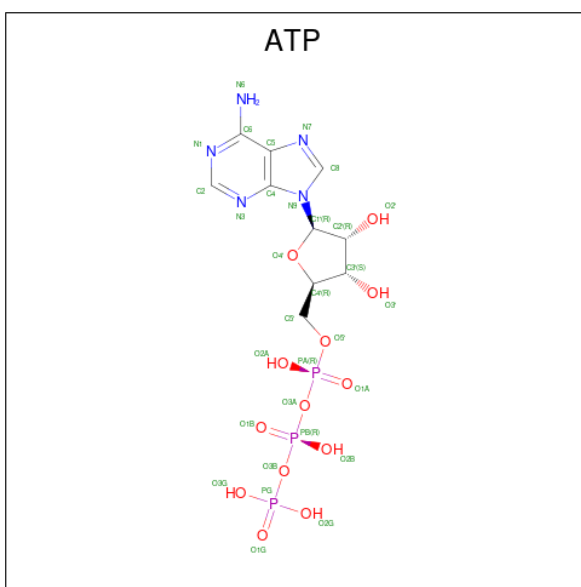
- Molecule 1 is a protein called RIBONUCLEOTIDE REDUCTASE R1 PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	733	Total	C	N	O	S	0	0	0
			5837	3708	1002	1103	24			
1	B	733	Total	C	N	O	S	0	0	0
			5837	3708	1002	1103	24			
1	C	733	Total	C	N	O	S	0	0	0
			5837	3708	1002	1103	24			

- Molecule 2 is a protein called RIBONUCLEOTIDE REDUCTASE R2 PROTEIN.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	D	13	Total	C	N	O	0	0	0
			104	62	15	27			
2	E	13	Total	C	N	O	0	0	0
			104	62	15	27			
2	F	13	Total	C	N	O	0	0	0
			104	62	15	27			
2	P	3	Total	C	N	O	0	0	0
			27	20	3	4			

- Molecule 3 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 31	C 10	N 5	O 13	P 3	0	0
3	B	1	Total 31	C 10	N 5	O 13	P 3	0	0
3	C	1	Total 31	C 10	N 5	O 13	P 3	0	0

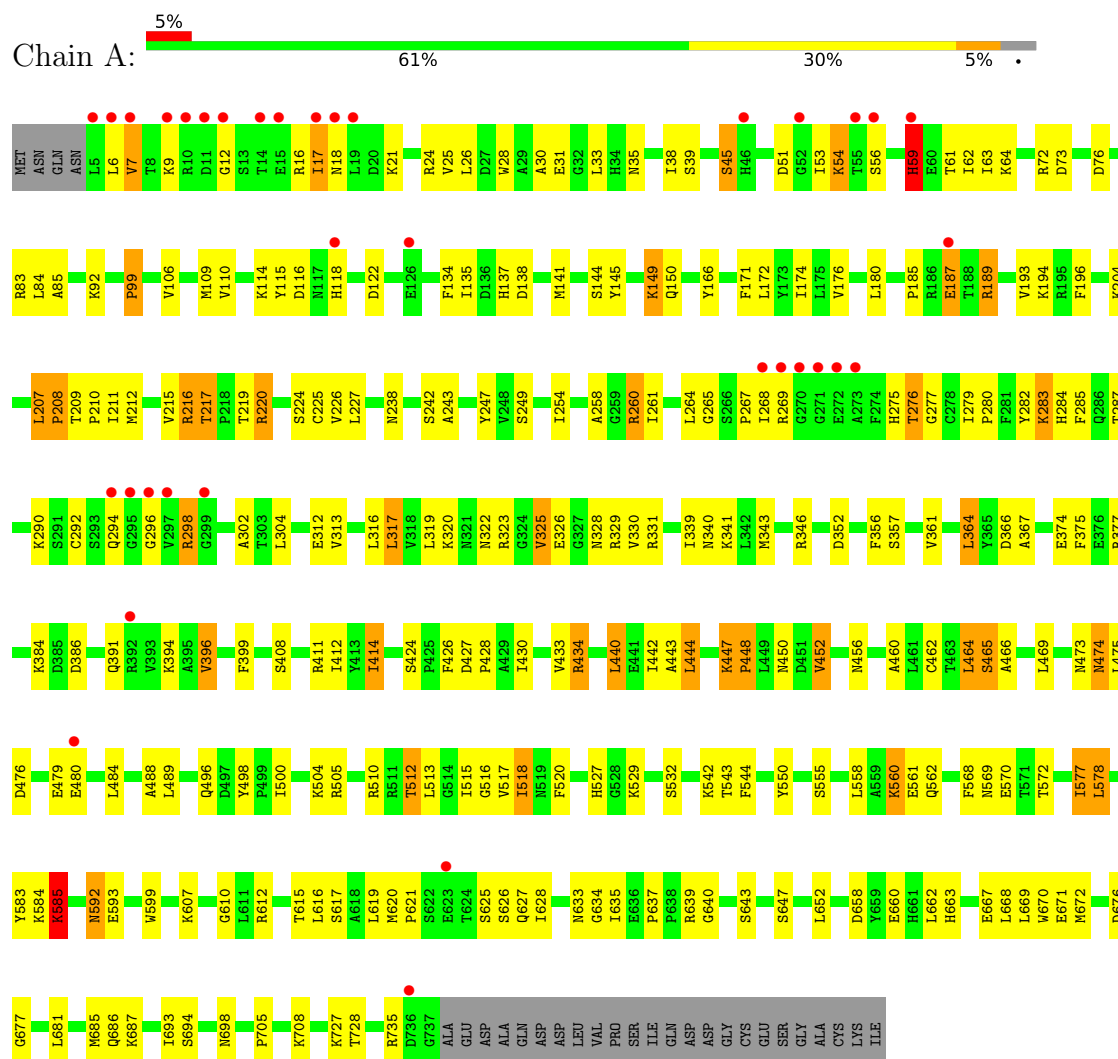
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	27	Total O 27 27	0	0
4	B	28	Total O 28 28	0	0
4	C	29	Total O 29 29	0	0

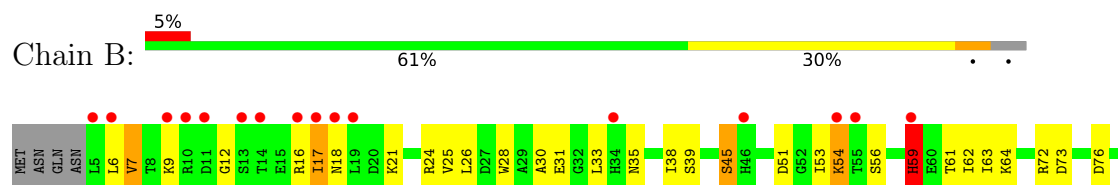
3 Residue-property plots

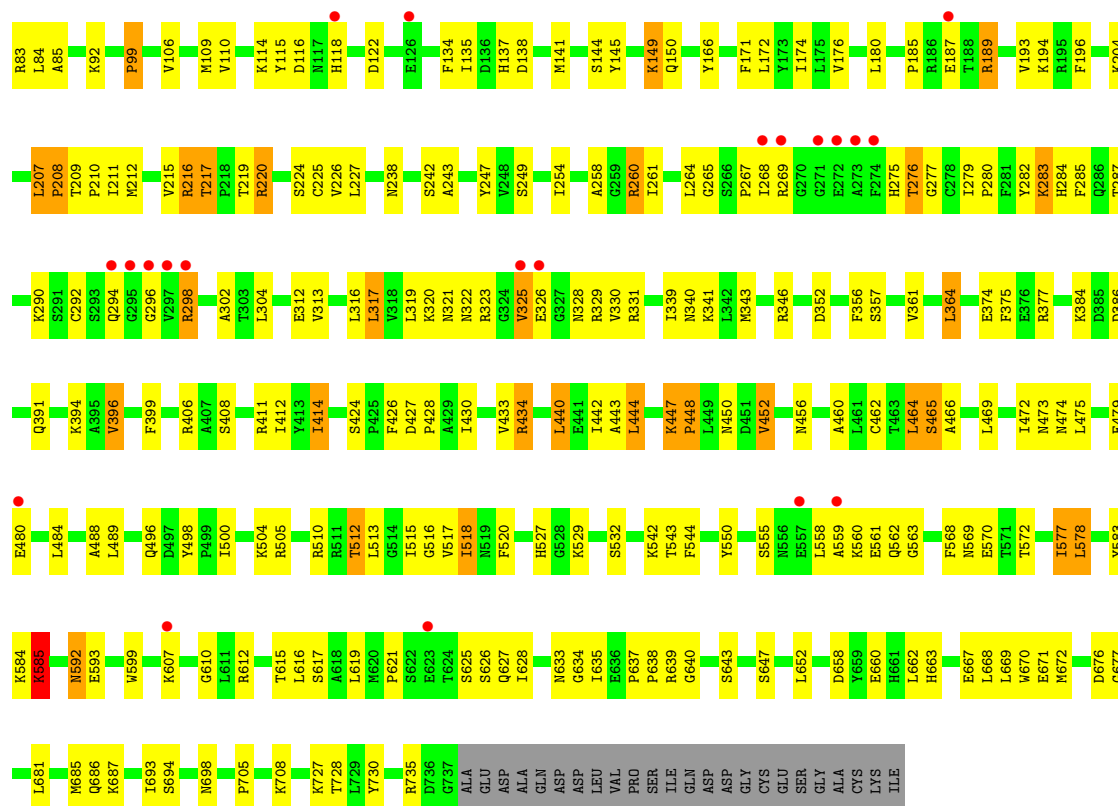
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: RIBONUCLEOTIDE REDUCTASE R1 PROTEIN

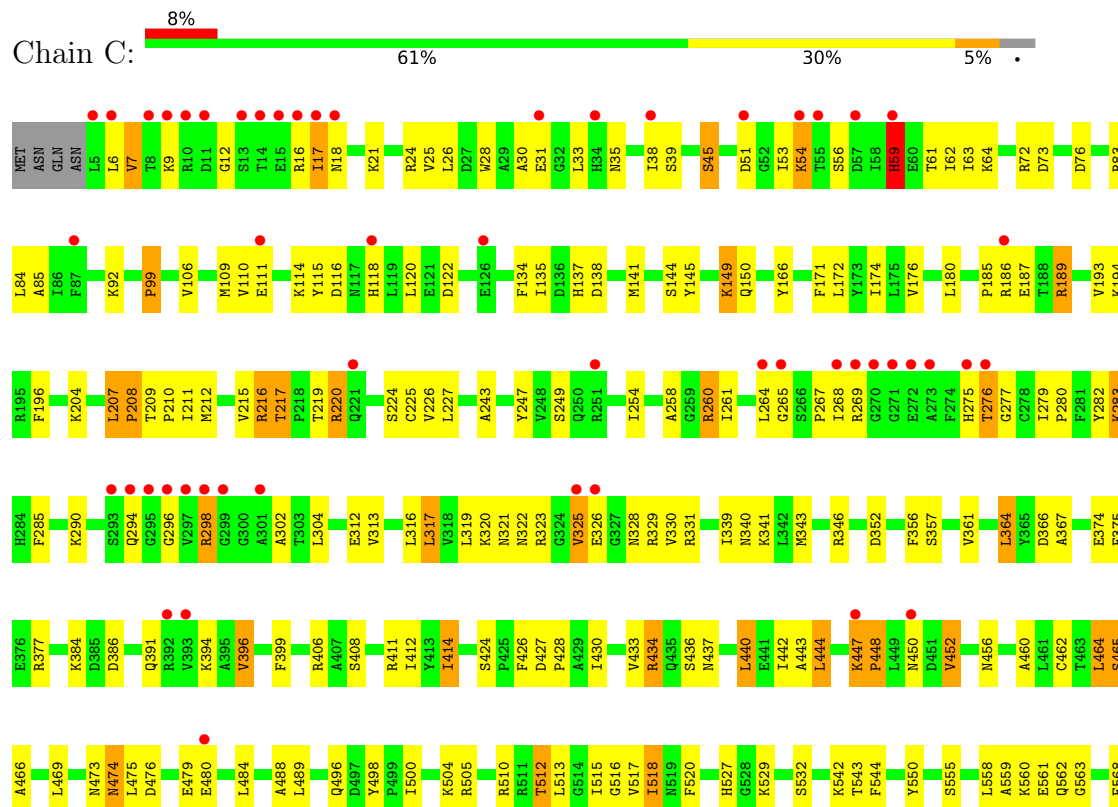


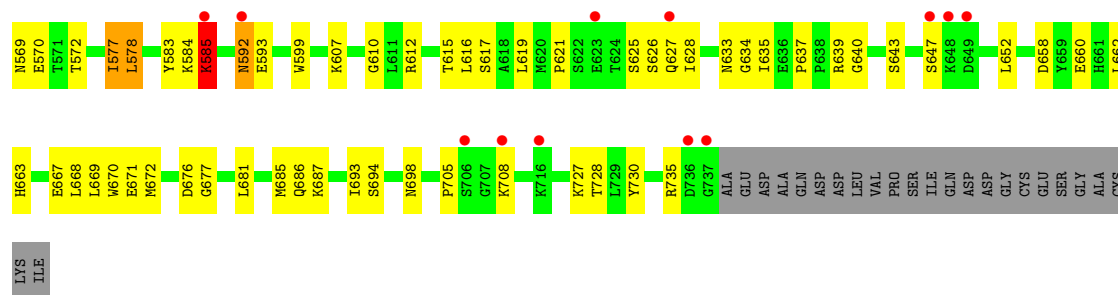
• Molecule 1: RIBONUCLEOTIDE REDUCTASE R1 PROTEIN



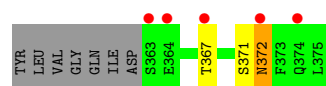


• Molecule 1: RIBONUCLEOTIDE REDUCTASE R1 PROTEIN

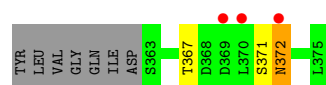




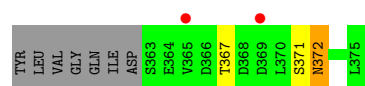
• Molecule 2: RIBONUCLEOTIDE REDUCTASE R2 PROTEIN



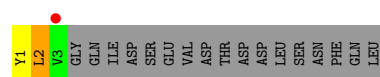
• Molecule 2: RIBONUCLEOTIDE REDUCTASE R2 PROTEIN



• Molecule 2: RIBONUCLEOTIDE REDUCTASE R2 PROTEIN



• Molecule 2: RIBONUCLEOTIDE REDUCTASE R2 PROTEIN



4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	224.61Å 224.61Å 336.63Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 3.00 20.00 – 3.00	Depositor EDS
% Data completeness (in resolution range)	96.1 (20.00-3.00) 95.8 (20.00-3.00)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.07 (at 3.01Å)	Xtriage
Refinement program	TNT, REFMAC	Depositor
R, R_{free}	0.263 , 0.287 (Not available) , 0.268	Depositor DCC
R_{free} test set	1275 reflections (2.02%)	wwPDB-VP
Wilson B-factor (Å ²)	59.6	Xtriage
Anisotropy	0.052	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 39.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.53$, $\langle L^2 \rangle = 0.37$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	18027	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.22% 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: ATP

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	0.43	0/5965	1.35	50/8079 (0.6%)
1	B	0.44	0/5965	1.35	53/8079 (0.7%)
1	C	0.43	0/5965	1.35	51/8079 (0.6%)
2	D	0.38	0/104	1.24	1/139 (0.7%)
2	E	0.39	0/104	1.24	1/139 (0.7%)
2	F	0.38	0/104	1.24	1/139 (0.7%)
2	P	0.57	0/27	1.75	0/36
All	All	0.43	0/18234	1.35	157/24690 (0.6%)

There are no bond length outliers.

All (157) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	544	PHE	CA-CB-CG	-8.38	105.42	113.80
1	A	544	PHE	CA-CB-CG	-8.35	105.45	113.80
1	C	544	PHE	CA-CB-CG	-8.31	105.49	113.80
1	C	452	VAL	N-CA-CB	7.13	118.42	110.51
1	A	452	VAL	N-CA-CB	7.11	118.40	110.51
1	B	452	VAL	N-CA-CB	7.09	118.39	110.51
1	B	35	ASN	CA-CB-CG	-6.55	106.05	112.60
1	B	532	SER	N-CA-C	6.54	120.52	112.54
1	A	35	ASN	CA-CB-CG	-6.53	106.07	112.60
1	C	532	SER	N-CA-C	6.53	120.50	112.54
1	A	532	SER	N-CA-C	6.51	120.48	112.54
1	C	35	ASN	CA-CB-CG	-6.48	106.12	112.60
1	A	430	ILE	CB-CA-C	-6.32	103.97	111.94
1	B	430	ILE	CB-CA-C	-6.32	103.97	111.94
1	C	430	ILE	CB-CA-C	-6.31	103.99	111.94
1	B	217	THR	CA-C-N	6.29	125.98	119.56
1	B	217	THR	C-N-CA	6.29	125.98	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	217	THR	CA-C-N	6.29	125.97	119.56
1	C	217	THR	C-N-CA	6.29	125.97	119.56
1	C	207	LEU	CA-C-N	6.28	126.24	119.78
1	C	207	LEU	C-N-CA	6.28	126.24	119.78
1	B	448	PRO	N-CA-CB	6.26	108.80	103.35
1	A	207	LEU	CA-C-N	6.26	126.23	119.78
1	A	207	LEU	C-N-CA	6.26	126.23	119.78
1	A	217	THR	CA-C-N	6.26	125.94	119.56
1	A	217	THR	C-N-CA	6.26	125.94	119.56
1	B	207	LEU	CA-C-N	6.24	126.21	119.78
1	B	207	LEU	C-N-CA	6.24	126.21	119.78
1	A	448	PRO	N-CA-CB	6.23	108.77	103.35
1	C	448	PRO	N-CA-CB	6.19	108.73	103.35
1	B	450	ASN	CA-CB-CG	-6.15	106.45	112.60
1	A	450	ASN	CA-CB-CG	-6.12	106.48	112.60
1	C	450	ASN	CA-CB-CG	-6.10	106.50	112.60
1	A	444	LEU	CA-C-O	5.97	125.99	120.50
1	B	444	LEU	CA-C-O	5.97	125.99	120.50
1	C	444	LEU	CA-C-O	5.95	125.97	120.50
1	B	464	LEU	N-CA-C	5.94	118.88	110.14
1	C	464	LEU	N-CA-C	5.94	118.87	110.14
1	A	464	LEU	N-CA-C	5.93	118.86	110.14
2	F	371	SER	N-CA-C	5.92	118.50	111.33
2	D	371	SER	N-CA-C	5.92	118.49	111.33
2	E	371	SER	N-CA-C	5.91	118.48	111.33
1	B	498	TYR	CA-C-N	5.90	125.44	119.19
1	B	498	TYR	C-N-CA	5.90	125.44	119.19
1	A	498	TYR	CA-C-N	5.88	125.43	119.19
1	A	498	TYR	C-N-CA	5.88	125.43	119.19
1	C	498	TYR	CA-C-N	5.86	125.40	119.19
1	C	498	TYR	C-N-CA	5.86	125.40	119.19
1	C	208	PRO	N-CA-CB	5.69	108.30	103.35
1	A	208	PRO	N-CA-CB	5.66	108.28	103.35
1	B	578	LEU	CA-C-N	5.65	125.12	119.24
1	B	578	LEU	C-N-CA	5.65	125.12	119.24
1	A	578	LEU	CA-C-N	5.64	125.10	119.24
1	A	578	LEU	C-N-CA	5.64	125.10	119.24
1	B	208	PRO	N-CA-CB	5.62	108.24	103.35
1	A	705	PRO	N-CA-CB	5.62	108.25	103.19
1	B	456	ASN	CA-CB-CG	-5.61	106.99	112.60
1	C	578	LEU	CA-C-N	5.61	125.07	119.24
1	C	578	LEU	C-N-CA	5.61	125.07	119.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	456	ASN	CA-CB-CG	-5.60	107.00	112.60
1	C	705	PRO	N-CA-CB	5.60	108.23	103.19
1	C	412	ILE	N-CA-CB	5.59	118.71	111.83
1	B	705	PRO	N-CA-CB	5.59	108.22	103.19
1	C	456	ASN	CA-CB-CG	-5.58	107.02	112.60
1	A	593	GLU	CA-C-O	5.58	124.39	119.71
1	B	518	ILE	CA-C-O	-5.57	116.11	121.63
1	A	35	ASN	OD1-CG-ND2	5.56	128.16	122.60
1	A	412	ILE	N-CA-CB	5.56	118.67	111.83
1	B	472	ILE	CA-C-O	-5.56	115.71	121.93
1	B	35	ASN	OD1-CG-ND2	5.55	128.15	122.60
1	B	593	GLU	CA-C-O	5.54	124.37	119.71
1	A	518	ILE	CA-C-O	-5.54	116.14	121.63
1	C	593	GLU	CA-C-O	5.53	124.36	119.71
1	C	35	ASN	OD1-CG-ND2	5.51	128.11	122.60
1	C	496	GLN	N-CA-C	5.50	117.63	110.53
1	C	518	ILE	CA-C-O	-5.50	116.18	121.63
1	A	396	VAL	CB-CA-C	-5.50	104.71	112.14
1	B	412	ILE	N-CA-CB	5.50	118.59	111.83
1	A	496	GLN	N-CA-C	5.49	117.62	110.53
1	B	396	VAL	CB-CA-C	-5.49	104.74	112.14
1	B	496	GLN	N-CA-C	5.49	117.61	110.53
1	C	396	VAL	CB-CA-C	-5.47	104.75	112.14
1	C	357	SER	N-CA-C	-5.46	103.17	109.93
1	A	357	SER	N-CA-C	-5.44	103.18	109.93
1	B	357	SER	N-CA-C	-5.44	103.19	109.93
1	A	637	PRO	N-CA-CB	5.43	106.05	103.22
1	A	176	VAL	N-CA-C	-5.43	105.23	110.72
1	B	176	VAL	N-CA-C	-5.43	105.24	110.72
1	C	356	PHE	CA-CB-CG	5.42	119.22	113.80
1	C	99	PRO	CA-C-N	5.41	126.17	120.11
1	C	99	PRO	C-N-CA	5.41	126.17	120.11
1	B	59	HIS	CA-CB-CG	-5.41	108.39	113.80
1	A	356	PHE	CA-CB-CG	5.41	119.21	113.80
1	C	637	PRO	N-CA-CB	5.40	106.03	103.22
1	A	59	HIS	CA-CB-CG	-5.39	108.41	113.80
1	A	99	PRO	CA-C-N	5.39	126.15	120.11
1	A	99	PRO	C-N-CA	5.39	126.15	120.11
1	B	99	PRO	CA-C-N	5.38	126.14	120.11
1	B	99	PRO	C-N-CA	5.38	126.14	120.11
1	C	176	VAL	N-CA-C	-5.38	105.28	110.72
1	C	59	HIS	CA-CB-CG	-5.37	108.43	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	637	PRO	N-CA-CB	5.36	106.01	103.22
1	B	356	PHE	CA-CB-CG	5.35	119.15	113.80
1	A	17	ILE	CB-CA-C	-5.34	104.83	111.08
1	B	17	ILE	CB-CA-C	-5.34	104.84	111.08
1	B	440	LEU	N-CA-C	5.34	118.94	111.90
1	C	17	ILE	CB-CA-C	-5.32	104.85	111.08
1	A	440	LEU	N-CA-C	5.32	118.92	111.90
1	C	440	LEU	N-CA-C	5.31	118.91	111.90
1	A	498	TYR	CA-C-O	5.28	124.59	119.62
1	B	498	TYR	CA-C-O	5.28	124.59	119.62
1	C	285	PHE	CA-CB-CG	5.28	119.08	113.80
1	B	285	PHE	CA-CB-CG	5.27	119.07	113.80
1	A	285	PHE	CA-CB-CG	5.27	119.07	113.80
1	C	498	TYR	CA-C-O	5.25	124.56	119.62
1	B	452	VAL	CB-CA-C	-5.24	105.17	111.88
1	B	267	PRO	N-CA-CB	5.23	107.90	103.35
1	C	452	VAL	CB-CA-C	-5.22	105.20	111.88
1	B	473	ASN	CA-CB-CG	-5.21	107.39	112.60
1	A	452	VAL	CB-CA-C	-5.21	105.21	111.88
1	C	473	ASN	CA-CB-CG	-5.19	107.41	112.60
1	A	399	PHE	CA-CB-CG	-5.18	108.62	113.80
1	A	473	ASN	CA-CB-CG	-5.18	107.42	112.60
1	C	399	PHE	CA-CB-CG	-5.18	108.62	113.80
1	A	267	PRO	N-CA-CB	5.17	107.85	103.35
1	B	399	PHE	CA-CB-CG	-5.17	108.63	113.80
1	C	267	PRO	N-CA-CB	5.16	107.84	103.35
1	C	427	ASP	CA-C-N	5.15	125.19	119.32
1	C	427	ASP	C-N-CA	5.15	125.19	119.32
1	A	672	MET	CA-C-N	5.15	124.76	119.56
1	A	672	MET	C-N-CA	5.15	124.76	119.56
1	B	427	ASP	CA-C-N	5.15	125.19	119.32
1	B	427	ASP	C-N-CA	5.15	125.19	119.32
1	A	427	ASP	CA-C-N	5.13	125.17	119.32
1	A	427	ASP	C-N-CA	5.13	125.17	119.32
1	C	672	MET	CA-C-N	5.12	124.73	119.56
1	C	672	MET	C-N-CA	5.12	124.73	119.56
1	B	672	MET	CA-C-N	5.12	124.73	119.56
1	B	672	MET	C-N-CA	5.12	124.73	119.56
1	C	12	GLY	N-CA-C	-5.10	107.64	116.01
1	A	12	GLY	N-CA-C	-5.09	107.66	116.01
1	B	12	GLY	N-CA-C	-5.09	107.66	116.01
1	B	185	PRO	N-CA-CB	5.09	107.78	103.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	585	LYS	N-CA-C	5.09	117.48	111.33
1	A	585	LYS	N-CA-C	5.08	117.47	111.33
1	C	585	LYS	N-CA-C	5.07	117.47	111.33
1	C	185	PRO	N-CA-CB	5.07	107.76	103.35
1	B	637	PRO	O-C-N	5.07	123.53	121.15
1	A	185	PRO	N-CA-CB	5.06	107.75	103.35
1	B	313	VAL	N-CA-C	5.05	115.67	110.36
1	C	313	VAL	N-CA-C	5.05	115.66	110.36
1	A	313	VAL	N-CA-C	5.04	115.65	110.36
1	C	99	PRO	N-CA-CB	5.02	107.95	103.08
1	C	317	LEU	N-CA-C	5.01	117.47	111.71
1	A	317	LEU	N-CA-C	5.01	117.47	111.71
1	B	638	PRO	N-CA-CB	5.01	108.00	103.34
1	B	317	LEU	N-CA-C	5.00	117.47	111.71

There are no chirality outliers.

There are no planarity outliers.

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	5837	0	5762	142	0
1	B	5837	0	5762	138	0
1	C	5837	0	5762	138	0
2	D	104	0	88	3	0
2	E	104	0	88	2	0
2	F	104	0	88	3	0
2	P	27	0	31	4	0
3	A	31	0	12	1	0
3	B	31	0	12	1	0
3	C	31	0	12	1	0
4	A	27	0	0	0	0
4	B	28	0	0	0	0
4	C	29	0	0	0	0
All	All	18027	0	17617	419	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 12.

All (419) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:658:ASP:HB3	1:B:662:LEU:HD12	1.60	0.83
1:A:658:ASP:HB3	1:A:662:LEU:HD12	1.60	0.82
1:A:292:CYS:HA	1:B:276:THR:HG21	1.60	0.82
1:C:658:ASP:HB3	1:C:662:LEU:HD12	1.60	0.81
1:A:561:GLU:HG2	1:A:562:GLN:HG3	1.65	0.77
1:C:275:HIS:CD2	1:C:277:GLY:H	2.03	0.77
1:B:275:HIS:CD2	1:B:277:GLY:H	2.03	0.77
1:B:561:GLU:HG2	1:B:562:GLN:HG3	1.65	0.77
1:A:207:LEU:HB2	1:A:212:MET:HE3	1.68	0.76
1:C:561:GLU:HG2	1:C:562:GLN:HG3	1.65	0.76
1:C:558:LEU:HD23	1:C:612:ARG:HG2	1.68	0.76
1:A:275:HIS:CD2	1:A:277:GLY:H	2.03	0.76
2:D:372:ASN:H	2:D:372:ASN:ND2	1.84	0.75
1:B:207:LEU:HB2	1:B:212:MET:HE3	1.68	0.75
1:C:207:LEU:HB2	1:C:212:MET:HE3	1.68	0.75
1:B:558:LEU:HD23	1:B:612:ARG:HG2	1.68	0.75
1:A:558:LEU:HD23	1:A:612:ARG:HG2	1.68	0.74
1:A:275:HIS:HD2	1:A:277:GLY:H	1.34	0.73
1:C:283:LYS:HG3	1:C:330:VAL:HG22	1.71	0.73
2:E:372:ASN:H	2:E:372:ASN:ND2	1.84	0.73
1:A:7:VAL:HG23	1:A:17:ILE:HG12	1.71	0.73
1:C:275:HIS:HD2	1:C:277:GLY:H	1.34	0.73
1:A:283:LYS:HG3	1:A:330:VAL:HG22	1.71	0.73
1:B:275:HIS:HD2	1:B:277:GLY:H	1.34	0.73
1:B:283:LYS:HG3	1:B:330:VAL:HG22	1.71	0.73
1:C:444:LEU:HD22	1:C:512:THR:HG21	1.71	0.72
2:F:372:ASN:ND2	2:F:372:ASN:H	1.84	0.72
1:B:7:VAL:HG23	1:B:17:ILE:HG12	1.71	0.72
1:C:120:LEU:HD13	2:P:1:TYR:CG	2.25	0.72
1:A:258:ALA:HB3	1:A:304:LEU:HD21	1.72	0.71
1:A:444:LEU:HD22	1:A:512:THR:HG21	1.71	0.71
1:C:7:VAL:HG23	1:C:17:ILE:HG12	1.71	0.71
1:B:258:ALA:HB3	1:B:304:LEU:HD21	1.72	0.71
1:A:584:LYS:HD2	1:A:585:LYS:HE2	1.72	0.70
1:B:444:LEU:HD22	1:B:512:THR:HG21	1.71	0.70
1:C:258:ALA:HB3	1:C:304:LEU:HD21	1.72	0.70
1:B:584:LYS:HD2	1:B:585:LYS:HE2	1.72	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:465:SER:HB2	1:C:489:LEU:HD11	1.74	0.70
1:B:465:SER:HB2	1:B:489:LEU:HD11	1.74	0.70
1:B:26:LEU:HB3	1:B:38:ILE:HD12	1.74	0.70
1:C:584:LYS:HD2	1:C:585:LYS:HE2	1.72	0.70
1:C:26:LEU:HB3	1:C:38:ILE:HD12	1.74	0.69
1:C:215:VAL:O	1:C:216:ARG:HB3	1.92	0.69
1:A:26:LEU:HB3	1:A:38:ILE:HD12	1.74	0.68
1:A:465:SER:HB2	1:A:489:LEU:HD11	1.74	0.68
1:B:619:LEU:HD12	1:B:693:ILE:HG12	1.75	0.68
1:A:215:VAL:O	1:A:216:ARG:HB3	1.92	0.68
1:B:215:VAL:O	1:B:216:ARG:HB3	1.92	0.68
1:B:208:PRO:HD2	1:B:211:ILE:HD12	1.77	0.67
1:C:208:PRO:HD2	1:C:211:ILE:HD12	1.77	0.67
1:C:619:LEU:HD12	1:C:693:ILE:HG12	1.75	0.66
1:A:619:LEU:HD12	1:A:693:ILE:HG12	1.75	0.66
1:A:208:PRO:HD2	1:A:211:ILE:HD12	1.77	0.65
1:A:149:LYS:HG2	1:A:652:LEU:HD21	1.79	0.65
1:A:440:LEU:HD12	1:A:728:THR:HB	1.79	0.64
1:C:18:ASN:HD22	1:C:21:LYS:HE3	1.63	0.64
1:B:440:LEU:HD12	1:B:728:THR:HB	1.79	0.64
1:B:18:ASN:HD22	1:B:21:LYS:HE3	1.63	0.64
1:B:149:LYS:HG2	1:B:652:LEU:HD21	1.79	0.64
1:C:440:LEU:HD12	1:C:728:THR:HB	1.79	0.64
1:A:18:ASN:HD22	1:A:21:LYS:HE3	1.63	0.63
1:A:33:LEU:HB3	1:A:76:ASP:HB3	1.81	0.63
1:C:33:LEU:HB3	1:C:76:ASP:HB3	1.81	0.63
1:C:149:LYS:HG2	1:C:652:LEU:HD21	1.79	0.63
1:B:33:LEU:HB3	1:B:76:ASP:HB3	1.81	0.63
1:B:279:ILE:HD13	1:B:319:LEU:HD21	1.80	0.62
1:A:279:ILE:HD13	1:A:319:LEU:HD21	1.80	0.62
1:C:111:GLU:OE2	2:P:2:LEU:HB2	2.00	0.62
1:C:279:ILE:HD13	1:C:319:LEU:HD21	1.80	0.61
1:B:30:ALA:HB2	1:B:38:ILE:HD11	1.83	0.61
1:C:30:ALA:HB2	1:C:38:ILE:HD11	1.83	0.61
1:A:30:ALA:HB2	1:A:38:ILE:HD11	1.83	0.60
1:A:276:THR:HG23	1:A:280:PRO:HG2	1.84	0.60
1:A:276:THR:HG21	1:B:292:CYS:HA	1.84	0.59
1:B:227:LEU:HB2	1:B:460:ALA:HB3	1.84	0.59
1:B:226:VAL:HG21	1:B:247:TYR:CG	2.38	0.59
1:B:260:ARG:NH2	1:B:434:ARG:HH22	2.00	0.59
1:C:227:LEU:HB2	1:C:460:ALA:HB3	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:226:VAL:HG21	1:C:247:TYR:CG	2.38	0.59
1:B:196:PHE:HZ	1:B:207:LEU:HD11	1.68	0.59
1:C:196:PHE:HZ	1:C:207:LEU:HD11	1.68	0.59
1:C:276:THR:HG23	1:C:280:PRO:HG2	1.84	0.59
1:B:444:LEU:HD12	1:B:460:ALA:HB1	1.85	0.58
1:C:207:LEU:CB	1:C:212:MET:HE3	2.33	0.58
1:A:207:LEU:CB	1:A:212:MET:HE3	2.33	0.58
1:A:227:LEU:HB2	1:A:460:ALA:HB3	1.84	0.58
1:B:276:THR:HG23	1:B:280:PRO:HG2	1.84	0.58
1:A:260:ARG:NH2	1:A:434:ARG:HH22	2.00	0.58
1:A:226:VAL:HG21	1:A:247:TYR:CG	2.38	0.58
1:B:325:VAL:HG13	1:B:328:ASN:HB2	1.86	0.58
1:C:325:VAL:HG13	1:C:328:ASN:HB2	1.86	0.58
1:A:196:PHE:HZ	1:A:207:LEU:HD11	1.68	0.58
1:C:260:ARG:NH2	1:C:434:ARG:HH22	2.00	0.58
1:B:207:LEU:CB	1:B:212:MET:HE3	2.33	0.58
1:A:444:LEU:HD12	1:A:460:ALA:HB1	1.85	0.58
1:C:444:LEU:HD12	1:C:460:ALA:HB1	1.85	0.57
1:A:325:VAL:HG13	1:A:328:ASN:HB2	1.86	0.57
1:C:180:LEU:HD12	1:C:488:ALA:HB1	1.86	0.57
1:A:180:LEU:HD12	1:A:488:ALA:HB1	1.86	0.57
1:B:585:LYS:H	1:B:585:LYS:HD3	1.69	0.57
1:B:180:LEU:HD12	1:B:488:ALA:HB1	1.86	0.57
1:C:585:LYS:H	1:C:585:LYS:HD3	1.69	0.57
1:A:585:LYS:H	1:A:585:LYS:HD3	1.69	0.57
1:A:122:ASP:O	1:A:189:ARG:NH2	2.38	0.57
1:A:145:TYR:CZ	1:A:149:LYS:HD3	2.40	0.56
1:A:442:ILE:HG13	1:A:462:CYS:SG	2.45	0.56
1:B:442:ILE:HG13	1:B:462:CYS:SG	2.45	0.56
1:C:145:TYR:CZ	1:C:149:LYS:HD3	2.40	0.56
1:C:122:ASP:O	1:C:189:ARG:NH2	2.38	0.56
1:A:83:ARG:HG2	1:A:141:MET:HG3	1.88	0.56
1:B:122:ASP:O	1:B:189:ARG:NH2	2.38	0.56
1:A:339:ILE:HD12	1:A:414:ILE:HG23	1.88	0.56
1:C:442:ILE:HG13	1:C:462:CYS:SG	2.45	0.56
1:B:145:TYR:CZ	1:B:149:LYS:HD3	2.40	0.56
1:C:339:ILE:HD12	1:C:414:ILE:HG23	1.88	0.56
1:B:339:ILE:HD12	1:B:414:ILE:HG23	1.88	0.56
1:C:7:VAL:CG2	1:C:17:ILE:HG12	2.36	0.56
1:C:572:THR:HB	1:C:577:ILE:HB	1.88	0.55
1:B:7:VAL:CG2	1:B:17:ILE:HG12	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:433:VAL:HG11	1:B:443:ALA:HB1	1.89	0.55
1:C:433:VAL:HG11	1:C:443:ALA:HB1	1.89	0.55
1:A:433:VAL:HG11	1:A:443:ALA:HB1	1.89	0.55
1:B:254:ILE:O	1:B:302:ALA:HA	2.07	0.55
1:B:572:THR:HB	1:B:577:ILE:HB	1.88	0.55
1:A:626:SER:CB	1:A:633:ASN:HD22	2.20	0.55
1:C:215:VAL:O	1:C:216:ARG:CB	2.55	0.55
1:C:254:ILE:O	1:C:302:ALA:HA	2.07	0.55
1:A:686:GLN:CD	1:A:727:LYS:HD2	2.32	0.54
1:C:686:GLN:CD	1:C:727:LYS:HD2	2.32	0.54
1:A:215:VAL:O	1:A:216:ARG:CB	2.55	0.54
1:A:572:THR:HB	1:A:577:ILE:HB	1.88	0.54
1:B:215:VAL:O	1:B:216:ARG:CB	2.55	0.54
1:B:626:SER:CB	1:B:633:ASN:HD22	2.20	0.54
1:B:83:ARG:HG2	1:B:141:MET:HG3	1.88	0.54
1:A:59:HIS:O	1:A:63:ILE:HG13	2.07	0.54
1:A:254:ILE:O	1:A:302:ALA:HA	2.07	0.54
1:C:59:HIS:O	1:C:63:ILE:HG13	2.07	0.54
1:A:30:ALA:HA	1:A:33:LEU:HD12	1.89	0.54
1:C:83:ARG:HG2	1:C:141:MET:HG3	1.88	0.54
1:C:626:SER:CB	1:C:633:ASN:HD22	2.20	0.54
1:A:7:VAL:CG2	1:A:17:ILE:HG12	2.36	0.54
1:B:686:GLN:CD	1:B:727:LYS:HD2	2.32	0.54
1:A:462:CYS:HB3	1:A:464:LEU:HD21	1.90	0.53
1:B:59:HIS:O	1:B:63:ILE:HG13	2.07	0.53
1:C:30:ALA:HA	1:C:33:LEU:HD12	1.89	0.53
1:C:447:LYS:HZ2	1:C:505:ARG:NH2	2.06	0.53
1:C:462:CYS:HB3	1:C:464:LEU:HD21	1.91	0.53
1:B:30:ALA:HA	1:B:33:LEU:HD12	1.89	0.53
1:A:226:VAL:HG21	1:A:247:TYR:CD2	2.44	0.53
1:B:592:ASN:C	1:B:592:ASN:HD22	2.17	0.53
1:C:592:ASN:C	1:C:592:ASN:HD22	2.17	0.53
1:A:592:ASN:C	1:A:592:ASN:HD22	2.17	0.53
1:C:217:THR:OG1	1:C:219:THR:HG22	2.10	0.52
1:A:217:THR:OG1	1:A:219:THR:HG22	2.10	0.52
1:A:626:SER:HB2	1:A:633:ASN:HD22	1.74	0.52
1:B:226:VAL:HG21	1:B:247:TYR:CD2	2.44	0.52
1:B:462:CYS:HB3	1:B:464:LEU:HD21	1.90	0.52
1:B:217:THR:OG1	1:B:219:THR:HG22	2.10	0.52
1:B:322:ASN:HA	1:B:331:ARG:HE	1.74	0.52
1:C:149:LYS:HE2	1:C:149:LYS:HA	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:322:ASN:HA	1:C:331:ARG:HE	1.74	0.52
1:B:569:ASN:H	1:B:569:ASN:ND2	2.08	0.52
1:C:226:VAL:HG21	1:C:247:TYR:CD2	2.44	0.52
1:B:149:LYS:HE2	1:B:149:LYS:HA	1.92	0.52
1:C:518:ILE:HA	1:C:634:GLY:HA2	1.91	0.52
1:C:569:ASN:H	1:C:569:ASN:ND2	2.08	0.52
1:A:149:LYS:HA	1:A:149:LYS:HE2	1.92	0.52
1:C:578:LEU:HD13	1:C:599:TRP:HE3	1.75	0.52
1:B:578:LEU:HD13	1:B:599:TRP:HE3	1.75	0.52
1:A:150:GLN:HE21	1:A:627:GLN:CD	2.18	0.51
1:B:518:ILE:HA	1:B:634:GLY:HA2	1.91	0.51
1:A:322:ASN:HA	1:A:331:ARG:HE	1.74	0.51
1:A:578:LEU:HD13	1:A:599:TRP:HE3	1.75	0.51
1:C:59:HIS:CD2	3:C:762:ATP:H4'	2.46	0.51
1:A:621:PRO:HD3	1:A:694:SER:OG	2.10	0.51
1:C:260:ARG:NH2	1:C:434:ARG:NH2	2.59	0.51
1:B:279:ILE:HB	1:B:280:PRO:HD3	1.93	0.51
1:B:621:PRO:HD3	1:B:694:SER:OG	2.10	0.50
1:C:626:SER:HB2	1:C:633:ASN:HD22	1.74	0.50
1:A:59:HIS:CD2	3:A:762:ATP:H4'	2.46	0.50
1:A:518:ILE:HA	1:A:634:GLY:HA2	1.91	0.50
1:B:626:SER:HB2	1:B:633:ASN:HD22	1.74	0.50
1:C:150:GLN:HE21	1:C:627:GLN:CD	2.18	0.50
1:C:279:ILE:HB	1:C:280:PRO:HD3	1.93	0.50
1:B:150:GLN:HE21	1:B:627:GLN:CD	2.18	0.50
1:A:260:ARG:NH2	1:A:434:ARG:NH2	2.59	0.50
1:B:18:ASN:HB2	1:B:21:LYS:HE3	1.94	0.50
1:B:260:ARG:NH2	1:B:434:ARG:NH2	2.59	0.50
1:C:18:ASN:HB2	1:C:21:LYS:HE3	1.94	0.50
1:C:621:PRO:HD3	1:C:694:SER:OG	2.10	0.50
1:A:569:ASN:ND2	1:A:569:ASN:H	2.08	0.50
1:B:59:HIS:CD2	3:B:762:ATP:H4'	2.46	0.50
1:B:670:TRP:CE2	1:B:735:ARG:HG3	2.48	0.49
1:C:670:TRP:CE2	1:C:735:ARG:HG3	2.48	0.49
1:A:144:SER:O	1:A:145:TYR:C	2.56	0.49
1:A:279:ILE:HB	1:A:280:PRO:HD3	1.93	0.49
1:B:135:ILE:HD11	1:B:174:ILE:HG21	1.94	0.49
1:B:447:LYS:HZ2	1:B:505:ARG:NH2	2.10	0.49
1:A:135:ILE:HD11	1:A:174:ILE:HG21	1.94	0.49
1:A:18:ASN:HB2	1:A:21:LYS:HE3	1.94	0.49
1:C:264:LEU:HD12	1:C:265:GLY:N	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:670:TRP:CE2	1:A:735:ARG:HG3	2.48	0.48
2:F:372:ASN:ND2	2:F:372:ASN:N	2.59	0.48
1:A:264:LEU:HD12	1:A:265:GLY:N	2.28	0.48
1:B:144:SER:O	1:B:145:TYR:C	2.56	0.48
1:B:264:LEU:HD12	1:B:265:GLY:N	2.28	0.48
1:A:284:HIS:HA	1:B:287:THR:OG1	2.13	0.48
1:C:30:ALA:O	1:C:31:GLU:C	2.56	0.48
1:A:30:ALA:O	1:A:31:GLU:C	2.56	0.48
1:A:238:ASN:HB3	1:B:242:SER:OG	2.13	0.48
1:B:116:ASP:OD2	1:B:220:ARG:NH2	2.47	0.48
1:B:583:TYR:CG	1:B:687:LYS:HG3	2.49	0.48
1:C:135:ILE:HD11	1:C:174:ILE:HG21	1.94	0.48
1:A:242:SER:OG	1:B:238:ASN:HB3	2.13	0.48
1:B:30:ALA:O	1:B:31:GLU:C	2.56	0.48
1:B:681:LEU:O	1:B:685:MET:HG3	2.14	0.48
1:A:583:TYR:CG	1:A:687:LYS:HG3	2.49	0.48
1:A:106:VAL:O	1:A:110:VAL:HG23	2.14	0.47
1:A:447:LYS:NZ	1:A:505:ARG:NH2	2.63	0.47
1:C:106:VAL:O	1:C:110:VAL:HG23	2.14	0.47
1:C:322:ASN:O	1:C:331:ARG:NH2	2.47	0.47
1:C:447:LYS:NZ	1:C:505:ARG:NH2	2.63	0.47
1:C:681:LEU:O	1:C:685:MET:HG3	2.14	0.47
1:B:447:LYS:NZ	1:B:505:ARG:NH2	2.63	0.47
1:C:144:SER:O	1:C:145:TYR:C	2.56	0.47
1:A:180:LEU:CD1	1:A:488:ALA:HB1	2.44	0.47
1:A:322:ASN:O	1:A:331:ARG:NH2	2.47	0.47
2:D:372:ASN:H	2:D:372:ASN:HD22	1.61	0.47
1:C:116:ASP:OD2	1:C:220:ARG:NH2	2.47	0.47
1:A:116:ASP:OD2	1:A:220:ARG:NH2	2.47	0.47
1:B:106:VAL:O	1:B:110:VAL:HG23	2.14	0.47
1:B:99:PRO:HG2	1:B:137:HIS:CD2	2.50	0.47
1:B:322:ASN:O	1:B:331:ARG:NH2	2.47	0.47
2:E:372:ASN:H	2:E:372:ASN:HD22	1.61	0.47
1:C:62:ILE:HD11	1:C:84:LEU:HD22	1.97	0.47
1:C:99:PRO:HG2	1:C:137:HIS:CD2	2.50	0.47
1:C:583:TYR:CG	1:C:687:LYS:HG3	2.49	0.47
2:F:372:ASN:H	2:F:372:ASN:HD22	1.61	0.47
1:C:294:GLN:HB2	1:C:298:ARG:HG3	1.97	0.47
1:A:681:LEU:O	1:A:685:MET:HG3	2.14	0.47
1:A:62:ILE:HD11	1:A:84:LEU:HD22	1.96	0.47
1:B:294:GLN:HB2	1:B:298:ARG:HG3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:180:LEU:CD1	1:B:488:ALA:HB1	2.44	0.46
2:D:372:ASN:ND2	2:D:372:ASN:N	2.59	0.46
1:B:258:ALA:HB1	1:B:261:ILE:HD12	1.98	0.46
1:B:558:LEU:CD2	1:B:612:ARG:HG2	2.43	0.46
1:C:180:LEU:CD1	1:C:488:ALA:HB1	2.44	0.46
1:A:558:LEU:CD2	1:A:612:ARG:HG2	2.43	0.46
1:C:258:ALA:HB1	1:C:261:ILE:HD12	1.98	0.46
1:B:260:ARG:NH1	1:B:448:PRO:HG3	2.31	0.46
1:A:640:GLY:HA2	1:A:668:LEU:HD13	1.98	0.46
1:C:558:LEU:CD2	1:C:612:ARG:HG2	2.43	0.46
1:A:260:ARG:NH1	1:A:448:PRO:HG3	2.31	0.46
1:A:512:THR:HG22	1:A:615:THR:HG23	1.97	0.46
1:C:260:ARG:NH1	1:C:448:PRO:HG3	2.31	0.46
1:C:640:GLY:HA2	1:C:668:LEU:HD13	1.98	0.46
1:B:62:ILE:HD11	1:B:84:LEU:HD22	1.97	0.45
1:A:187:GLU:OE2	1:C:186:ARG:HD2	2.16	0.45
1:C:512:THR:HG22	1:C:615:THR:HG23	1.97	0.45
1:A:220:ARG:HD3	1:A:220:ARG:HA	1.74	0.45
1:A:294:GLN:HB2	1:A:298:ARG:HG3	1.97	0.45
1:B:640:GLY:HA2	1:B:668:LEU:HD13	1.98	0.45
1:A:99:PRO:HG2	1:A:137:HIS:CD2	2.50	0.45
1:A:138:ASP:O	1:A:141:MET:HB2	2.17	0.45
1:B:243:ALA:HA	1:B:500:ILE:HD11	1.99	0.45
1:B:268:ILE:HD11	1:B:275:HIS:HA	1.99	0.45
1:A:268:ILE:HD11	1:A:275:HIS:HA	1.99	0.45
1:A:209:THR:N	1:A:210:PRO:HD2	2.32	0.45
1:A:268:ILE:O	1:A:269:ARG:HB3	2.16	0.45
1:B:268:ILE:O	1:B:269:ARG:HB3	2.16	0.45
1:C:243:ALA:HA	1:C:500:ILE:HD11	1.99	0.45
1:B:209:THR:N	1:B:210:PRO:HD2	2.32	0.45
1:C:138:ASP:O	1:C:141:MET:HB2	2.17	0.45
1:C:268:ILE:HD11	1:C:275:HIS:HA	1.99	0.45
1:B:512:THR:HG22	1:B:615:THR:HG23	1.97	0.45
1:C:268:ILE:O	1:C:269:ARG:HB3	2.16	0.44
1:A:447:LYS:HZ3	1:A:505:ARG:HH22	1.64	0.44
1:A:560:LYS:HA	2:P:1:TYR:N	2.31	0.44
1:B:138:ASP:O	1:B:141:MET:HB2	2.17	0.44
1:C:209:THR:N	1:C:210:PRO:HD2	2.32	0.44
1:A:447:LYS:NZ	1:A:505:ARG:HH22	2.15	0.44
1:B:475:LEU:HD21	1:B:543:THR:HG23	2.00	0.44
1:C:447:LYS:NZ	1:C:505:ARG:HH22	2.15	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:258:ALA:HB1	1:A:261:ILE:HD12	1.98	0.44
1:B:479:GLU:HB2	1:B:550:TYR:CE1	2.53	0.44
1:C:312:GLU:O	1:C:316:LEU:HG	2.18	0.44
1:C:520:PHE:HB3	1:C:635:ILE:HA	2.00	0.44
1:A:469:LEU:HD11	1:A:517:VAL:HG11	2.00	0.44
1:B:676:ASP:O	1:B:677:GLY:C	2.61	0.44
1:C:45:SER:HB3	1:C:61:THR:HG22	1.99	0.44
1:C:475:LEU:HD21	1:C:543:THR:HG23	2.00	0.44
1:B:312:GLU:O	1:B:316:LEU:HG	2.18	0.44
1:B:275:HIS:HD2	1:B:277:GLY:N	2.10	0.44
1:B:527:HIS:O	1:B:529:LYS:HE2	2.18	0.44
1:C:527:HIS:O	1:C:529:LYS:HE2	2.18	0.44
1:A:527:HIS:O	1:A:529:LYS:HE2	2.18	0.43
1:A:171:PHE:O	1:A:174:ILE:HG22	2.18	0.43
1:A:243:ALA:HA	1:A:500:ILE:HD11	1.99	0.43
1:A:475:LEU:HD21	1:A:543:THR:HG23	2.00	0.43
1:A:479:GLU:HB2	1:A:550:TYR:CE1	2.53	0.43
1:B:321:ASN:O	1:B:329:ARG:NE	2.51	0.43
1:B:447:LYS:NZ	1:B:505:ARG:HH22	2.15	0.43
1:C:479:GLU:HB2	1:C:550:TYR:CE1	2.53	0.43
1:A:45:SER:HB3	1:A:61:THR:HG22	1.99	0.43
1:A:287:THR:OG1	1:B:284:HIS:HA	2.18	0.43
1:A:520:PHE:HB3	1:A:635:ILE:HA	1.99	0.43
1:A:312:GLU:O	1:A:316:LEU:HG	2.18	0.43
1:A:320:LYS:HE2	1:A:411:ARG:HB2	2.01	0.43
1:A:329:ARG:HG3	1:A:331:ARG:NH2	2.34	0.43
1:A:619:LEU:HB2	1:A:693:ILE:HG12	2.00	0.43
1:B:171:PHE:O	1:B:174:ILE:HG22	2.18	0.43
1:A:63:ILE:HD13	1:A:85:ALA:HA	2.01	0.43
1:A:447:LYS:HZ2	1:A:505:ARG:NH2	2.16	0.43
1:B:134:PHE:CE2	1:B:194:LYS:HB2	2.54	0.43
1:B:320:LYS:HE2	1:B:411:ARG:HB2	2.01	0.43
1:B:619:LEU:HB2	1:B:693:ILE:HG12	2.00	0.43
1:C:53:ILE:O	1:C:54:LYS:C	2.62	0.43
1:C:321:ASN:O	1:C:329:ARG:NE	2.51	0.43
1:B:63:ILE:HD13	1:B:85:ALA:HA	2.01	0.43
1:B:520:PHE:HB3	1:B:635:ILE:HA	1.99	0.43
1:C:489:LEU:HB3	1:C:513:LEU:HD22	2.01	0.43
1:B:172:LEU:C	1:B:172:LEU:HD23	2.44	0.42
1:C:220:ARG:HA	1:C:220:ARG:HD3	1.74	0.42
1:C:320:LYS:HE2	1:C:411:ARG:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:469:LEU:HD11	1:C:517:VAL:HG11	2.00	0.42
1:C:619:LEU:HB2	1:C:693:ILE:HG12	2.00	0.42
1:B:45:SER:HB3	1:B:61:THR:HG22	1.99	0.42
1:C:172:LEU:HD23	1:C:172:LEU:C	2.44	0.42
1:C:282:TYR:CE2	1:C:316:LEU:HD22	2.55	0.42
1:A:134:PHE:CE2	1:A:194:LYS:HB2	2.54	0.42
1:A:676:ASP:O	1:A:677:GLY:C	2.61	0.42
1:B:109:MET:HB2	1:B:115:TYR:CD2	2.54	0.42
1:B:469:LEU:HD11	1:B:517:VAL:HG11	2.00	0.42
1:C:515:ILE:O	1:C:617:SER:HA	2.20	0.42
1:C:662:LEU:O	1:C:663:HIS:C	2.61	0.42
1:C:676:ASP:O	1:C:677:GLY:C	2.61	0.42
1:A:109:MET:HB2	1:A:115:TYR:CD2	2.54	0.42
1:A:172:LEU:C	1:A:172:LEU:HD23	2.44	0.42
1:A:364:LEU:HD22	1:A:375:PHE:CD1	2.55	0.42
1:C:134:PHE:CE2	1:C:194:LYS:HB2	2.54	0.42
1:C:171:PHE:O	1:C:174:ILE:HG22	2.19	0.42
1:A:662:LEU:O	1:A:663:HIS:C	2.61	0.42
1:C:109:MET:HB2	1:C:115:TYR:CD2	2.54	0.42
1:C:329:ARG:HG3	1:C:331:ARG:NH2	2.34	0.42
1:C:364:LEU:HD22	1:C:375:PHE:CD1	2.55	0.42
1:A:114:LYS:HE2	1:A:166:TYR:CE2	2.55	0.42
1:A:282:TYR:CE2	1:A:316:LEU:HD22	2.55	0.42
1:A:346:ARG:HD2	1:A:352:ASP:O	2.20	0.42
1:A:366:ASP:O	1:A:367:ALA:C	2.63	0.42
1:C:99:PRO:HG2	1:C:137:HIS:CG	2.55	0.42
1:A:489:LEU:HB3	1:A:513:LEU:HD22	2.01	0.42
1:B:53:ILE:O	1:B:54:LYS:C	2.62	0.42
1:B:282:TYR:CE2	1:B:316:LEU:HD22	2.55	0.42
1:A:53:ILE:O	1:A:54:LYS:C	2.62	0.42
1:B:329:ARG:HG3	1:B:331:ARG:NH2	2.34	0.42
1:B:339:ILE:HG23	1:B:343:MET:HB2	2.02	0.42
1:C:63:ILE:HD13	1:C:85:ALA:HA	2.01	0.42
1:C:339:ILE:HG23	1:C:343:MET:HB2	2.02	0.42
1:C:366:ASP:O	1:C:367:ALA:C	2.63	0.42
1:A:99:PRO:HG2	1:A:137:HIS:CG	2.55	0.41
1:A:426:PHE:O	1:A:428:PRO:HD3	2.21	0.41
1:B:220:ARG:HA	1:B:220:ARG:HD3	1.73	0.41
1:A:339:ILE:HG23	1:A:343:MET:HB2	2.02	0.41
1:A:668:LEU:HB2	1:A:671:GLU:HG3	2.01	0.41
1:B:99:PRO:HG2	1:B:137:HIS:CG	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:464:LEU:HB3	1:A:620:MET:HE2	2.03	0.41
1:A:466:ALA:HA	1:A:516:GLY:O	2.21	0.41
1:B:28:TRP:O	1:B:31:GLU:HB2	2.20	0.41
1:B:114:LYS:HE2	1:B:166:TYR:CE2	2.55	0.41
1:B:364:LEU:HD22	1:B:375:PHE:CD1	2.55	0.41
1:B:489:LEU:HB3	1:B:513:LEU:HD22	2.01	0.41
1:C:426:PHE:O	1:C:428:PRO:HD3	2.21	0.41
1:A:21:LYS:O	1:A:25:VAL:HG23	2.21	0.41
1:B:374:GLU:OE2	1:B:377:ARG:NH2	2.53	0.41
1:C:21:LYS:O	1:C:25:VAL:HG23	2.21	0.41
1:C:406:ARG:NH2	1:C:730:TYR:O	2.52	0.41
1:A:374:GLU:OE2	1:A:377:ARG:NH2	2.53	0.41
1:A:515:ILE:O	1:A:617:SER:HA	2.20	0.41
1:B:26:LEU:HD21	1:B:62:ILE:HD12	2.02	0.41
1:B:466:ALA:HA	1:B:516:GLY:O	2.21	0.41
1:C:114:LYS:HE2	1:C:166:TYR:CE2	2.55	0.41
1:C:172:LEU:HD12	1:C:216:ARG:NH2	2.35	0.41
1:B:669:LEU:HD11	1:B:698:ASN:CG	2.46	0.41
1:C:28:TRP:O	1:C:31:GLU:HB2	2.20	0.41
1:C:669:LEU:HD11	1:C:698:ASN:CG	2.46	0.41
1:B:339:ILE:HG22	1:B:340:ASN:N	2.36	0.41
1:B:515:ILE:O	1:B:617:SER:HA	2.20	0.41
1:B:668:LEU:HB2	1:B:671:GLU:HG3	2.01	0.41
1:A:172:LEU:HD12	1:A:216:ARG:NH2	2.35	0.41
1:A:633:ASN:O	1:A:634:GLY:C	2.64	0.41
1:A:669:LEU:HD11	1:A:698:ASN:CG	2.46	0.41
1:B:559:ALA:O	1:B:563:GLY:N	2.43	0.41
1:C:275:HIS:HD2	1:C:277:GLY:N	2.10	0.41
1:C:374:GLU:OE2	1:C:377:ARG:NH2	2.53	0.41
1:A:18:ASN:HB2	1:A:21:LYS:HD2	2.03	0.41
1:C:26:LEU:HD21	1:C:62:ILE:HD12	2.03	0.41
1:C:346:ARG:HD2	1:C:352:ASP:O	2.20	0.41
1:C:466:ALA:HA	1:C:516:GLY:O	2.21	0.41
1:C:474:ASN:OD1	1:C:476:ASP:HB2	2.21	0.41
1:C:668:LEU:HB2	1:C:671:GLU:HG3	2.01	0.41
1:B:172:LEU:HD12	1:B:216:ARG:NH2	2.35	0.41
1:A:28:TRP:O	1:A:31:GLU:HB2	2.20	0.40
1:B:21:LYS:O	1:B:25:VAL:HG23	2.21	0.40
1:B:426:PHE:O	1:B:428:PRO:HD3	2.21	0.40
1:C:559:ALA:O	1:C:563:GLY:N	2.43	0.40
1:A:474:ASN:OD1	1:A:476:ASP:HB2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:568:PHE:CZ	1:A:610:GLY:HA2	2.56	0.40
1:B:406:ARG:NH2	1:B:730:TYR:O	2.52	0.40
1:B:346:ARG:HD2	1:B:352:ASP:O	2.20	0.40
1:A:26:LEU:HD21	1:A:62:ILE:HD12	2.02	0.40
1:A:339:ILE:HG22	1:A:340:ASN:N	2.36	0.40
1:B:568:PHE:CZ	1:B:610:GLY:HA2	2.56	0.40
1:B:662:LEU:O	1:B:663:HIS:C	2.61	0.40
1:C:339:ILE:HG22	1:C:340:ASN:N	2.36	0.40
1:C:436:SER:OG	1:C:437:ASN:N	2.53	0.40
1:C:568:PHE:CZ	1:C:610:GLY:HA2	2.56	0.40
1:A:18:ASN:HB2	1:A:21:LYS:CD	2.52	0.40
1:B:18:ASN:HB2	1:B:21:LYS:CD	2.52	0.40
1:C:120:LEU:HD13	2:P:1:TYR:CB	2.51	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	731/761 (96%)	668 (91%)	59 (8%)	4 (0%)	24	60
1	B	731/761 (96%)	668 (91%)	59 (8%)	4 (0%)	24	60
1	C	731/761 (96%)	668 (91%)	59 (8%)	4 (0%)	24	60
2	D	11/20 (55%)	11 (100%)	0	0	100	100
2	E	11/20 (55%)	11 (100%)	0	0	100	100
2	F	11/20 (55%)	11 (100%)	0	0	100	100
2	P	1/20 (5%)	0	1 (100%)	0	100	100
All	All	2227/2363 (94%)	2037 (92%)	178 (8%)	12 (0%)	24	60

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	298	ARG
1	B	298	ARG
1	C	298	ARG
1	A	6	LEU
1	A	216	ARG
1	B	6	LEU
1	B	216	ARG
1	C	6	LEU
1	C	216	ARG
1	A	296	GLY
1	B	296	GLY
1	C	296	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	628/651 (96%)	558 (89%)	70 (11%)	6	25
1	B	628/651 (96%)	558 (89%)	70 (11%)	6	25
1	C	628/651 (96%)	558 (89%)	70 (11%)	6	25
2	D	13/19 (68%)	11 (85%)	2 (15%)	2	13
2	E	13/19 (68%)	11 (85%)	2 (15%)	2	13
2	F	13/19 (68%)	11 (85%)	2 (15%)	2	13
2	P	3/19 (16%)	2 (67%)	1 (33%)	0	1
All	All	1926/2029 (95%)	1709 (89%)	217 (11%)	5	24

All (217) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	VAL
1	A	9	LYS
1	A	16	ARG
1	A	24	ARG
1	A	39	SER
1	A	45	SER

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Mol	Chain	Res	Type
1	A	51	ASP
1	A	54	LYS
1	A	56	SER
1	A	59	HIS
1	A	64	LYS
1	A	72	ARG
1	A	73	ASP
1	A	92	LYS
1	A	118	HIS
1	A	149	LYS
1	A	187	GLU
1	A	189	ARG
1	A	193	VAL
1	A	204	LYS
1	A	220	ARG
1	A	224	SER
1	A	225	CYS
1	A	249	SER
1	A	260	ARG
1	A	276	THR
1	A	283	LYS
1	A	290	LYS
1	A	317	LEU
1	A	323	ARG
1	A	325	VAL
1	A	326	GLU
1	A	341	LYS
1	A	361	VAL
1	A	364	LEU
1	A	384	LYS
1	A	386	ASP
1	A	391	GLN
1	A	394	LYS
1	A	396	VAL
1	A	408	SER
1	A	414	ILE
1	A	424	SER
1	A	434	ARG
1	A	447	LYS
1	A	452	VAL
1	A	465	SER
1	A	474	ASN

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Mol	Chain	Res	Type
1	A	480	GLU
1	A	484	LEU
1	A	504	LYS
1	A	510	ARG
1	A	512	THR
1	A	542	LYS
1	A	555	SER
1	A	560	LYS
1	A	570	GLU
1	A	577	ILE
1	A	585	LYS
1	A	592	ASN
1	A	607	LYS
1	A	616	LEU
1	A	625	SER
1	A	628	ILE
1	A	639	ARG
1	A	643	SER
1	A	647	SER
1	A	660	GLU
1	A	667	GLU
1	A	708	LYS
2	D	367	THR
2	D	372	ASN
1	B	7	VAL
1	B	9	LYS
1	B	16	ARG
1	B	24	ARG
1	B	39	SER
1	B	45	SER
1	B	51	ASP
1	B	54	LYS
1	B	56	SER
1	B	59	HIS
1	B	64	LYS
1	B	72	ARG
1	B	73	ASP
1	B	92	LYS
1	B	118	HIS
1	B	149	LYS
1	B	187	GLU
1	B	189	ARG

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Mol	Chain	Res	Type
1	B	193	VAL
1	B	204	LYS
1	B	220	ARG
1	B	224	SER
1	B	225	CYS
1	B	249	SER
1	B	260	ARG
1	B	276	THR
1	B	283	LYS
1	B	290	LYS
1	B	317	LEU
1	B	323	ARG
1	B	325	VAL
1	B	326	GLU
1	B	341	LYS
1	B	361	VAL
1	B	364	LEU
1	B	384	LYS
1	B	386	ASP
1	B	391	GLN
1	B	394	LYS
1	B	396	VAL
1	B	408	SER
1	B	414	ILE
1	B	424	SER
1	B	434	ARG
1	B	447	LYS
1	B	452	VAL
1	B	465	SER
1	B	474	ASN
1	B	480	GLU
1	B	484	LEU
1	B	504	LYS
1	B	510	ARG
1	B	512	THR
1	B	542	LYS
1	B	555	SER
1	B	560	LYS
1	B	570	GLU
1	B	577	ILE
1	B	585	LYS
1	B	592	ASN

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Mol	Chain	Res	Type
1	B	607	LYS
1	B	616	LEU
1	B	625	SER
1	B	628	ILE
1	B	639	ARG
1	B	643	SER
1	B	647	SER
1	B	660	GLU
1	B	667	GLU
1	B	708	LYS
2	E	367	THR
2	E	372	ASN
1	C	7	VAL
1	C	9	LYS
1	C	16	ARG
1	C	24	ARG
1	C	39	SER
1	C	45	SER
1	C	51	ASP
1	C	54	LYS
1	C	56	SER
1	C	59	HIS
1	C	64	LYS
1	C	72	ARG
1	C	73	ASP
1	C	92	LYS
1	C	118	HIS
1	C	149	LYS
1	C	187	GLU
1	C	189	ARG
1	C	193	VAL
1	C	204	LYS
1	C	220	ARG
1	C	224	SER
1	C	225	CYS
1	C	249	SER
1	C	260	ARG
1	C	276	THR
1	C	283	LYS
1	C	290	LYS
1	C	317	LEU
1	C	323	ARG

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Mol	Chain	Res	Type
1	C	325	VAL
1	C	326	GLU
1	C	341	LYS
1	C	361	VAL
1	C	364	LEU
1	C	384	LYS
1	C	386	ASP
1	C	391	GLN
1	C	394	LYS
1	C	396	VAL
1	C	408	SER
1	C	414	ILE
1	C	424	SER
1	C	434	ARG
1	C	447	LYS
1	C	452	VAL
1	C	465	SER
1	C	474	ASN
1	C	480	GLU
1	C	484	LEU
1	C	504	LYS
1	C	510	ARG
1	C	512	THR
1	C	542	LYS
1	C	555	SER
1	C	560	LYS
1	C	570	GLU
1	C	577	ILE
1	C	585	LYS
1	C	592	ASN
1	C	607	LYS
1	C	616	LEU
1	C	625	SER
1	C	628	ILE
1	C	639	ARG
1	C	643	SER
1	C	647	SER
1	C	660	GLU
1	C	667	GLU
1	C	708	LYS
2	F	367	THR
2	F	372	ASN

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Mol	Chain	Res	Type
2	P	2	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (40) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	18	ASN
1	A	88	HIS
1	A	96	GLN
1	A	275	HIS
1	A	328	ASN
1	A	416	ASN
1	A	569	ASN
1	A	592	ASN
1	A	613	ASN
1	A	630	ASN
1	A	633	ASN
1	A	733	ASN
2	D	372	ASN
1	B	18	ASN
1	B	46	HIS
1	B	88	HIS
1	B	96	GLN
1	B	221	GLN
1	B	275	HIS
1	B	328	ASN
1	B	569	ASN
1	B	592	ASN
1	B	613	ASN
1	B	630	ASN
1	B	633	ASN
1	B	733	ASN
2	E	372	ASN
1	C	18	ASN
1	C	88	HIS
1	C	96	GLN
1	C	275	HIS
1	C	284	HIS
1	C	328	ASN
1	C	569	ASN
1	C	592	ASN
1	C	613	ASN
1	C	630	ASN

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Mol	Chain	Res	Type
1	C	633	ASN
1	C	733	ASN
2	F	372	ASN

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 ⓘ

3 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	$\# Z > 2$
3	ATP	C	762	-	32,33,33	1.24	2 (6%)	48,52,52	1.22	6 (12%)
3	ATP	A	762	-	32,33,33	1.24	2 (6%)	48,52,52	1.21	5 (10%)
3	ATP	B	762	-	32,33,33	1.24	2 (6%)	48,52,52	1.21	4 (8%)

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
3	ATP	C	762	-	-	6/22/38/38	0/3/3/3
3	ATP	A	762	-	-	6/22/38/38	0/3/3/3
3	ATP	B	762	-	-	6/22/38/38	0/3/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	762	ATP	C5-N7	-3.91	1.31	1.39
3	C	762	ATP	C5-N7	-3.90	1.32	1.39
3	B	762	ATP	C5-N7	-3.89	1.32	1.39
3	B	762	ATP	C2-N1	2.32	1.38	1.33
3	A	762	ATP	C2-N1	2.31	1.38	1.33
3	C	762	ATP	C2-N1	2.31	1.38	1.33

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	762	ATP	C4-N9-C8	-4.36	101.16	105.74
3	B	762	ATP	C4-N9-C8	-4.32	101.20	105.74
3	A	762	ATP	C4-N9-C8	-4.32	101.20	105.74
3	C	762	ATP	N9-C8-N7	3.03	118.24	113.94
3	B	762	ATP	N9-C8-N7	3.00	118.19	113.94
3	A	762	ATP	N9-C8-N7	3.00	118.19	113.94
3	C	762	ATP	O2B-PB-O3B	2.36	113.65	107.27
3	B	762	ATP	O2B-PB-O3B	2.36	113.64	107.27
3	A	762	ATP	O2B-PB-O3B	2.35	113.64	107.27
3	C	762	ATP	C6-C5-N7	-2.04	128.16	132.09
3	A	762	ATP	O4'-C1'-N9	2.03	111.99	108.09
3	B	762	ATP	O4'-C1'-N9	2.02	111.96	108.09
3	C	762	ATP	O4'-C1'-N9	2.01	111.96	108.09
3	A	762	ATP	O2A-PA-O3A	2.01	112.69	107.27
3	C	762	ATP	O2A-PA-O3A	2.00	112.68	107.27

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	762	ATP	C5'-O5'-PA-O1A
3	A	762	ATP	C5'-O5'-PA-O2A
3	A	762	ATP	C5'-O5'-PA-O3A
3	B	762	ATP	C5'-O5'-PA-O1A

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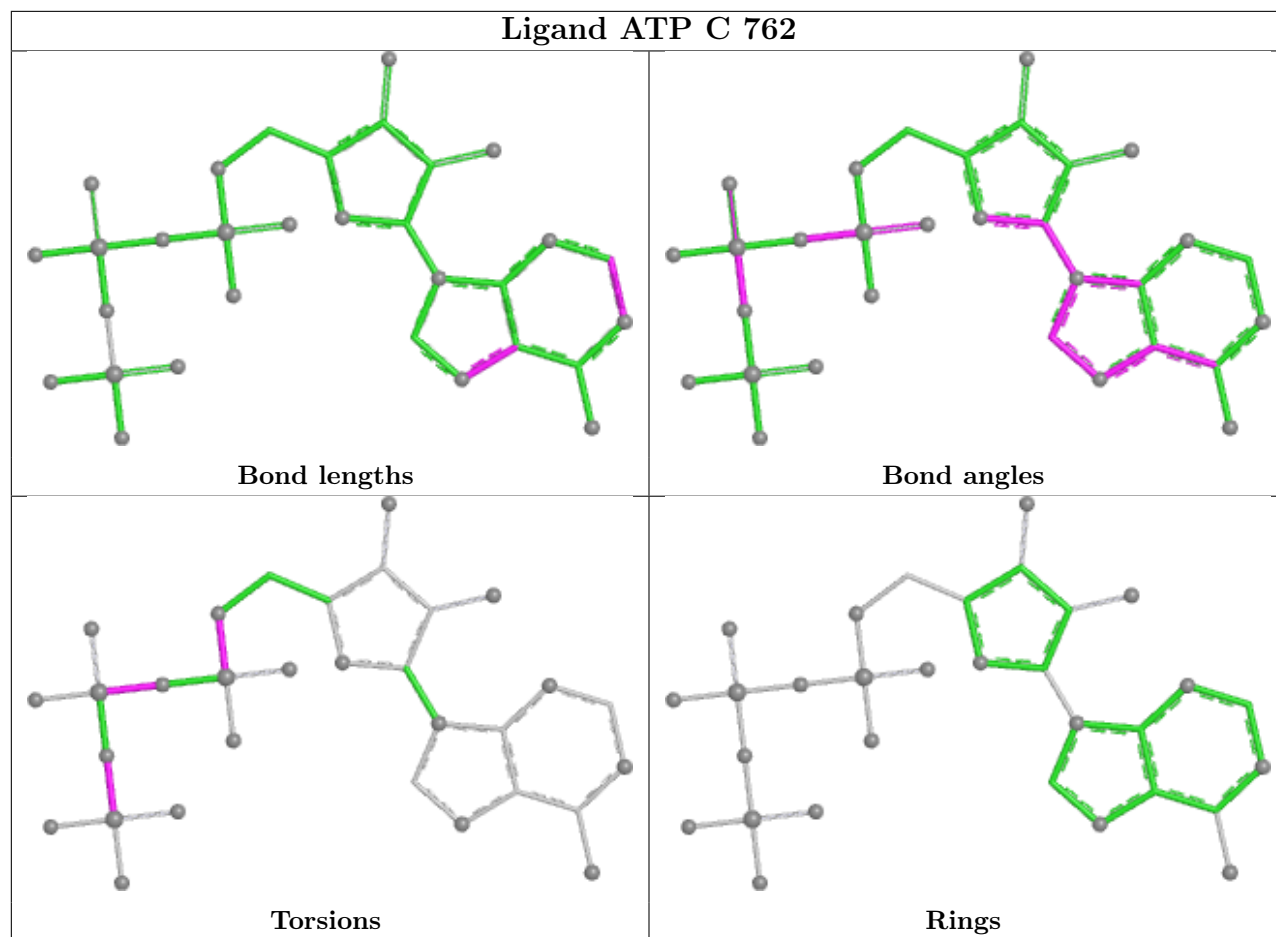
Mol	Chain	Res	Type	Atoms
3	B	762	ATP	C5'-O5'-PA-O2A
3	B	762	ATP	C5'-O5'-PA-O3A
3	C	762	ATP	C5'-O5'-PA-O1A
3	C	762	ATP	C5'-O5'-PA-O2A
3	C	762	ATP	C5'-O5'-PA-O3A
3	A	762	ATP	PB-O3B-PG-O1G
3	B	762	ATP	PB-O3B-PG-O1G
3	C	762	ATP	PB-O3B-PG-O1G
3	A	762	ATP	PA-O3A-PB-O2B
3	B	762	ATP	PA-O3A-PB-O2B
3	C	762	ATP	PA-O3A-PB-O2B
3	A	762	ATP	PA-O3A-PB-O1B
3	B	762	ATP	PA-O3A-PB-O1B
3	C	762	ATP	PA-O3A-PB-O1B

There are no ring outliers.

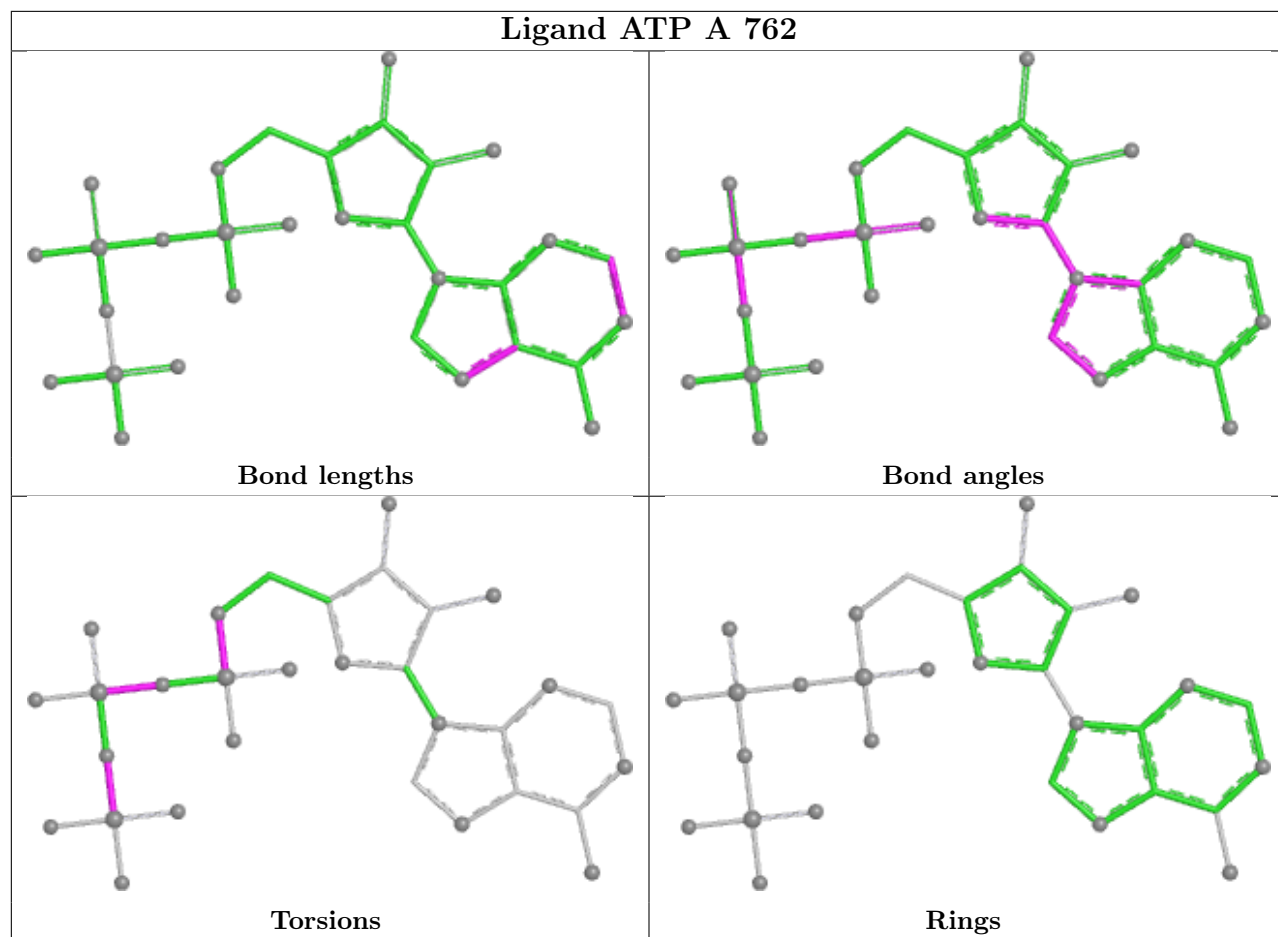
3 monomers are involved in 3 short contacts:

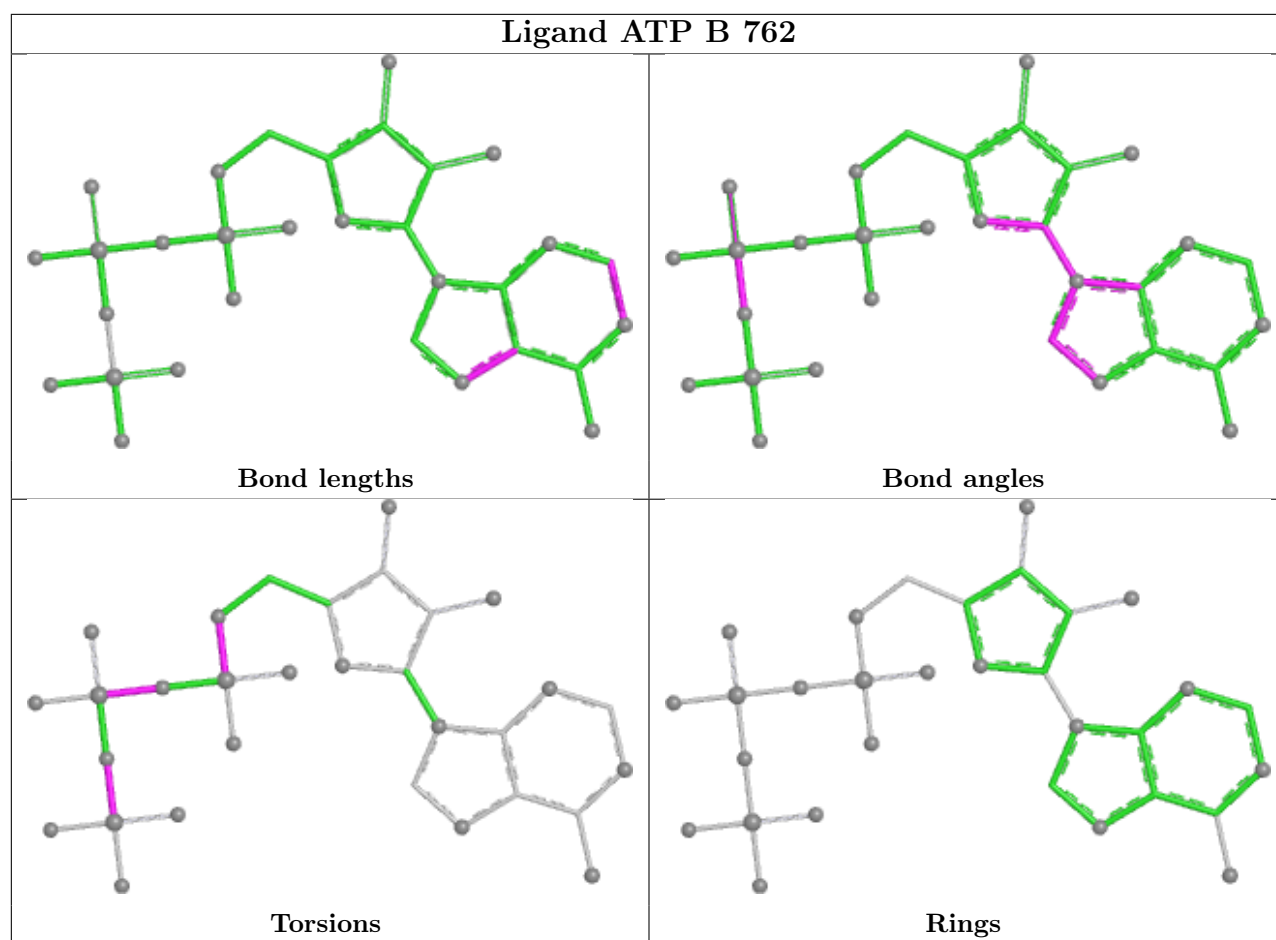
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	762	ATP	1	0
3	A	762	ATP	1	0
3	B	762	ATP	1	0

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.



Ligand ATP A 762





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	733/761 (96%)	0.19	35 (4%)	35	19	27, 42, 81, 114	0
1	B	733/761 (96%)	0.32	37 (5%)	34	18	27, 42, 81, 114	0
1	C	733/761 (96%)	0.58	64 (8%)	16	8	27, 42, 81, 114	0
2	D	13/20 (65%)	1.58	5 (38%)	1	1	65, 87, 101, 101	0
2	E	13/20 (65%)	1.54	3 (23%)	2	1	65, 87, 101, 101	0
2	F	13/20 (65%)	1.36	2 (15%)	5	3	65, 87, 101, 101	0
2	P	3/20 (15%)	1.38	1 (33%)	1	1	49, 49, 55, 63	0
All	All	2241/2363 (94%)	0.39	147 (6%)	24	12	27, 42, 87, 114	0

All (147) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	297	VAL	7.5
1	B	295	GLY	7.4
1	C	295	GLY	6.3
1	B	272	GLU	6.1
2	E	372	ASN	5.7
1	C	272	GLU	5.6
1	C	296	GLY	5.6
1	B	273	ALA	5.5
1	C	271	GLY	5.5
1	B	296	GLY	5.4
1	C	57	ASP	5.3
1	C	270	GLY	4.8
1	B	297	VAL	4.7
1	A	297	VAL	4.4
1	C	298	ARG	4.3
1	A	270	GLY	4.2
1	B	607	LYS	4.1

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Mol	Chain	Res	Type	RSRZ
1	C	14	THR	4.1
1	C	5	LEU	4.0
1	A	273	ALA	4.0
1	C	275	HIS	3.8
1	C	17	ILE	3.8
1	A	17	ILE	3.8
1	A	269	ARG	3.7
1	C	648	LYS	3.7
1	A	11	ASP	3.7
1	A	295	GLY	3.7
1	C	265	GLY	3.7
1	B	118	HIS	3.7
1	A	9	LYS	3.6
1	C	294	GLN	3.5
1	B	6	LEU	3.5
1	C	16	ARG	3.4
1	C	13	SER	3.4
1	B	294	GLN	3.4
1	A	271	GLY	3.4
1	C	649	ASP	3.3
1	A	52	GLY	3.3
1	C	251	ARG	3.3
1	A	268	ILE	3.3
1	A	272	GLU	3.3
1	B	268	ILE	3.3
2	D	363	SER	3.3
1	C	34	HIS	3.2
1	C	392	ARG	3.2
1	A	56	SER	3.1
1	C	15	GLU	3.1
1	C	480	GLU	3.1
1	C	736	ASP	3.1
1	A	296	GLY	3.1
2	P	3	VAL	3.1
1	C	31	GLU	3.1
1	A	10	ARG	3.0
1	C	111	GLU	3.0
1	C	11	ASP	3.0
1	B	13	SER	3.0
1	C	268	ILE	3.0
1	B	559	ALA	3.0
2	D	367	THR	3.0

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Mol	Chain	Res	Type	RSRZ
1	C	450	ASN	2.9
1	B	187	GLU	2.9
1	C	585	LYS	2.9
1	A	736	ASP	2.9
1	A	19	LEU	2.9
1	B	17	ILE	2.8
1	C	126	GLU	2.8
1	A	12	GLY	2.8
1	C	647	SER	2.8
1	B	623	GLU	2.8
2	D	374	GLN	2.7
1	A	15	GLU	2.7
1	B	480	GLU	2.7
1	A	14	THR	2.7
1	A	6	LEU	2.7
1	A	299	GLY	2.7
1	C	10	ARG	2.7
1	C	293	SER	2.7
1	C	54	LYS	2.7
1	C	623	GLU	2.7
1	C	708	LYS	2.6
1	A	294	GLN	2.6
1	C	118	HIS	2.6
1	C	59	HIS	2.6
1	A	46	HIS	2.5
1	B	18	ASN	2.5
1	A	480	GLU	2.5
1	C	276	THR	2.5
1	B	19	LEU	2.5
1	B	59	HIS	2.5
1	C	87	PHE	2.5
2	F	369	ASP	2.5
1	A	5	LEU	2.5
1	C	6	LEU	2.5
1	B	126	GLU	2.4
1	B	326	GLU	2.4
1	C	269	ARG	2.4
1	A	126	GLU	2.4
1	B	54	LYS	2.4
1	B	46	HIS	2.4
1	B	271	GLY	2.4
1	C	706	SER	2.4

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Mol	Chain	Res	Type	RSRZ
1	C	737	GLY	2.4
1	B	5	LEU	2.4
1	C	592	ASN	2.4
1	C	51	ASP	2.4
1	C	716	LYS	2.4
1	C	55	THR	2.3
1	A	18	ASN	2.3
1	C	325	VAL	2.3
1	A	59	HIS	2.3
1	A	118	HIS	2.3
2	D	372	ASN	2.3
1	B	325	VAL	2.3
1	B	16	ARG	2.3
1	B	14	THR	2.2
1	C	8	THR	2.2
1	C	221	GLN	2.2
1	C	264	LEU	2.2
1	B	9	LYS	2.2
1	B	11	ASP	2.2
1	C	447	LYS	2.2
1	A	623	GLU	2.2
1	C	9	LYS	2.2
1	A	7	VAL	2.2
2	E	370	LEU	2.2
2	D	364	GLU	2.2
1	A	392	ARG	2.2
1	B	269	ARG	2.2
1	B	34	HIS	2.2
1	B	55	THR	2.1
1	C	299	GLY	2.1
1	C	18	ASN	2.1
1	B	274	PHE	2.1
2	E	369	ASP	2.1
2	F	365	VAL	2.1
1	B	10	ARG	2.1
1	C	273	ALA	2.1
1	C	301	ALA	2.1
1	A	55	THR	2.1
1	C	326	GLU	2.1
1	C	38	ILE	2.0
1	C	627	GLN	2.0
1	B	298	ARG	2.0

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Mol	Chain	Res	Type	RSRZ
1	C	186	ARG	2.0
1	A	187	GLU	2.0
1	B	557	GLU	2.0
1	C	393	VAL	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

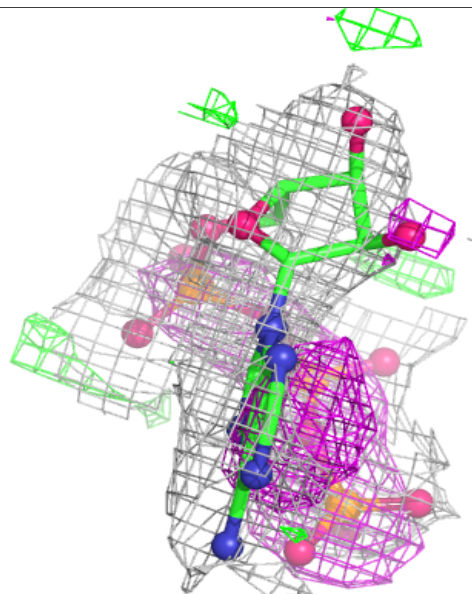
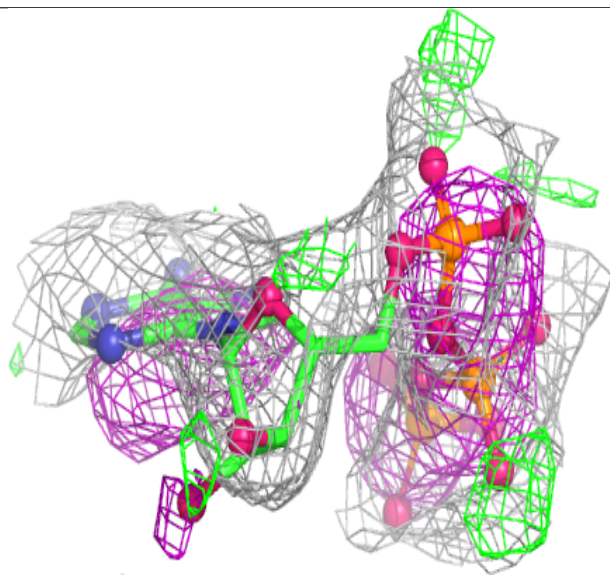
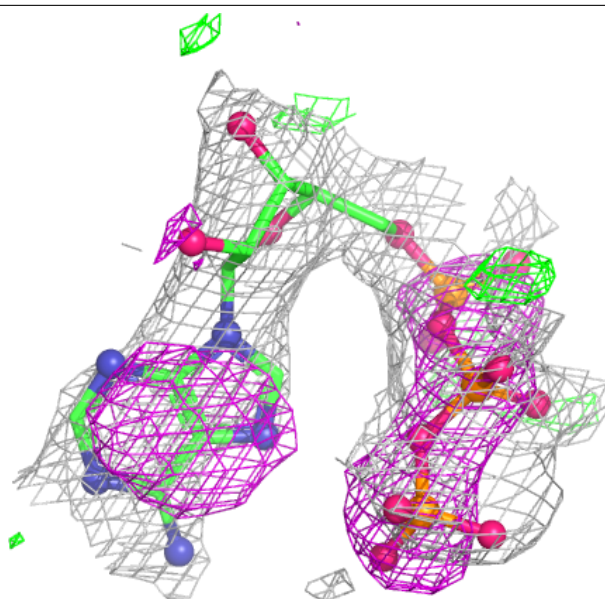
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
3	ATP	C	762	31/31	0.45	0.20	65,66,78,78	0
3	ATP	B	762	31/31	0.58	0.18	65,66,78,78	0
3	ATP	A	762	31/31	0.58	0.17	65,66,78,78	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.

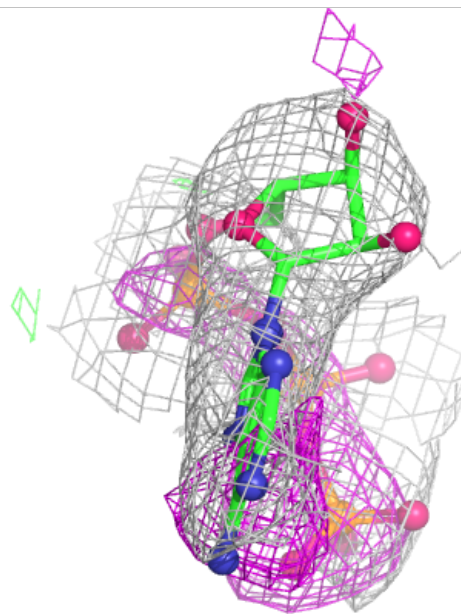
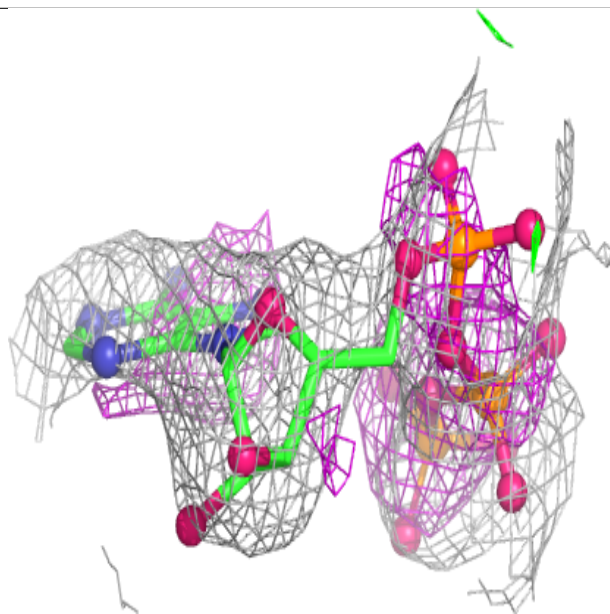
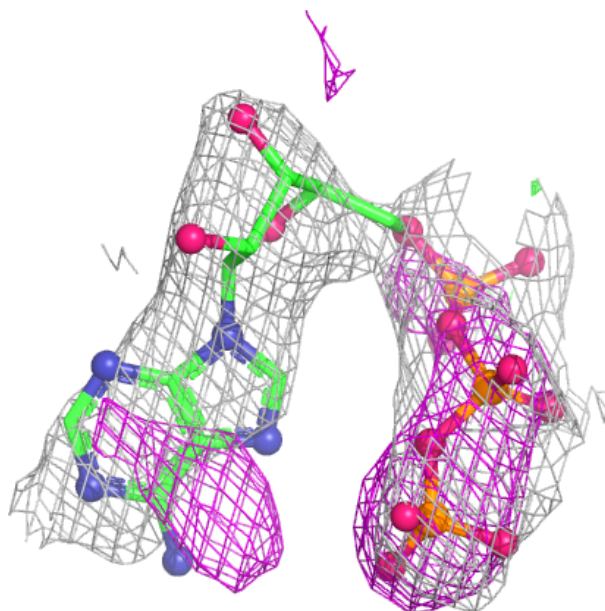
Electron density around ATP C 762:

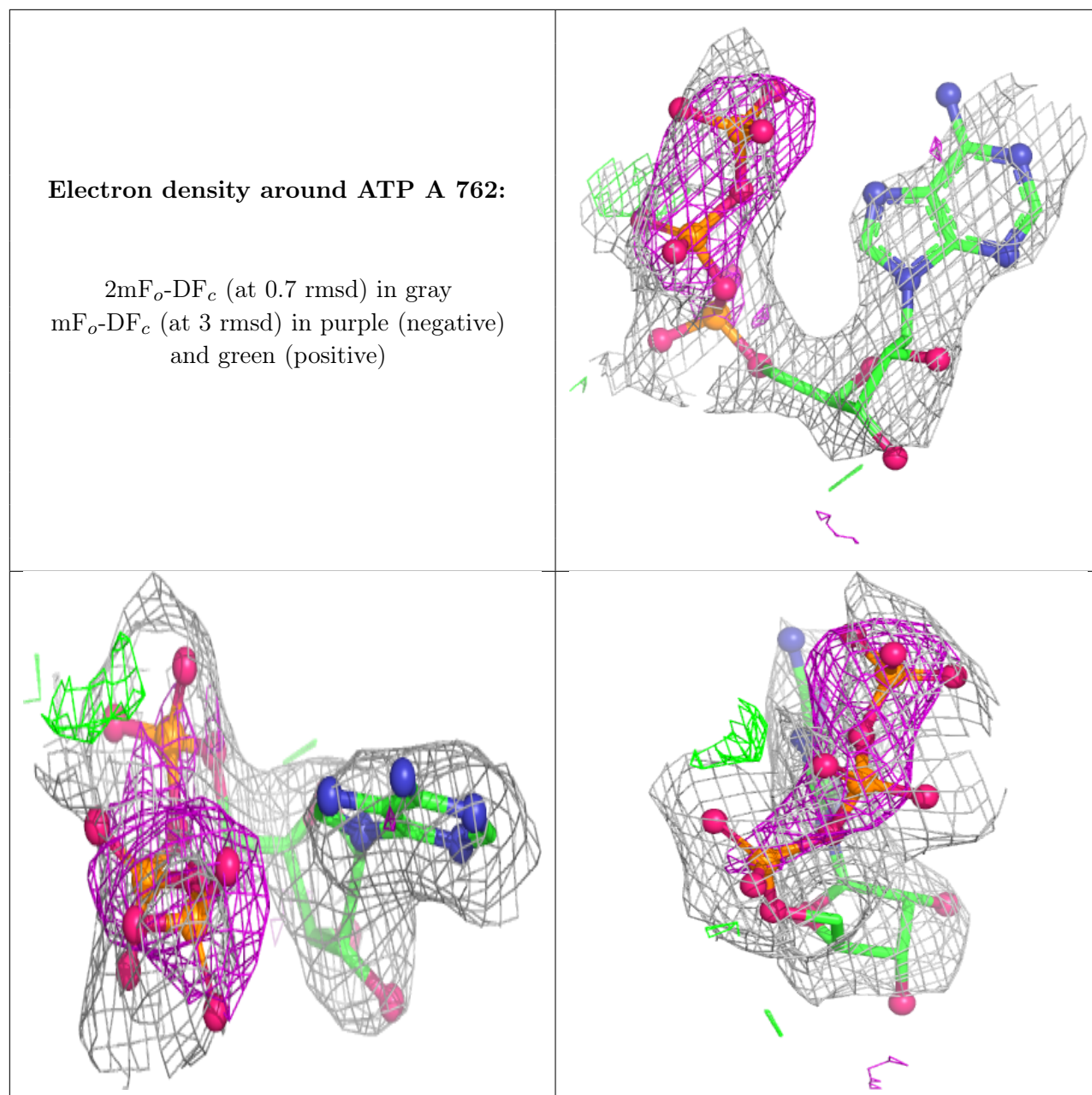
2mF_o-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around ATP B 762:

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





6.5 Other polymers ⓘ

There are no such residues in this entry.