



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 02:07 AM UTC

PDB ID : 2DR3 / pdb_00002dr3
Title : Crystal Structure of RecA superfamily ATPase PH0284 from *Pyrococcus horikoshii* OT3
Authors : Bagautdinov, B.; Kunishima, N.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)
Deposited on : 2006-06-06
Resolution : 2.00 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:

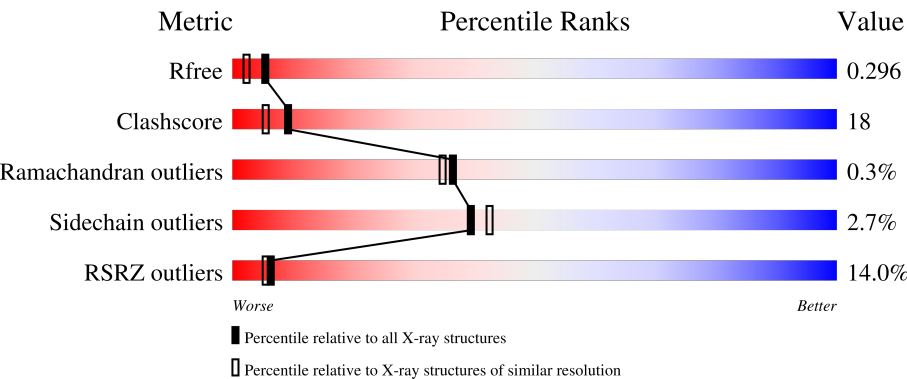
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal 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 i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	247	21% 56% 37% 6%
1	B	247	9% 69% 26% 6%
1	C	247	6% 67% 25% 6%
1	D	247	19% 59% 37% 6%

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Mol	Chain	Length	Quality of chain
1	E	247	13% 64% 29%
1	F	247	13% 63% 29%

2 Entry composition [i](#)

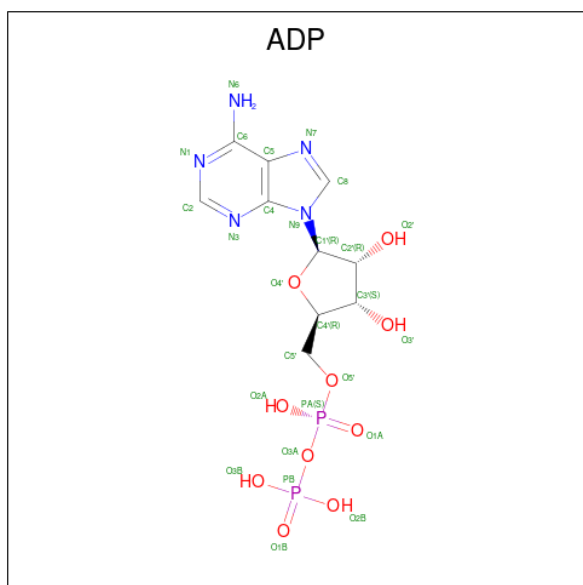
There are 3 unique types of molecules in this entry. The entry contains 12543 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 UPF0273 protein PH0284.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	232	Total	C	N	O	S	0	0	0
			1826	1167	323	328	8			
1	B	240	Total	C	N	O	S	0	0	0
			1875	1195	334	338	8			
1	C	233	Total	C	N	O	S	0	0	0
			1835	1171	324	332	8			
1	D	242	Total	C	N	O	S	0	0	0
			1896	1208	338	342	8			
1	E	236	Total	C	N	O	S	0	0	0
			1853	1184	328	333	8			
1	F	236	Total	C	N	O	S	0	0	0
			1854	1184	329	333	8			

- Molecule 2 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	C	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	D	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	E	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	F	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

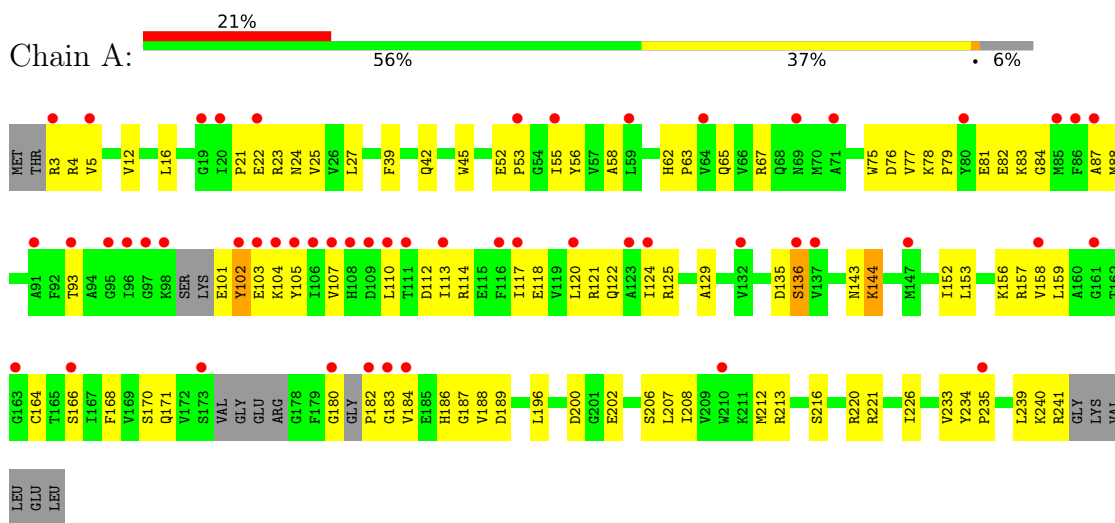
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	190	Total	O	0	0
			190	190		
3	B	220	Total	O	0	0
			220	220		
3	C	213	Total	O	0	0
			213	213		
3	D	228	Total	O	0	0
			228	228		
3	E	196	Total	O	0	0
			196	196		
3	F	195	Total	O	0	0
			195	195		

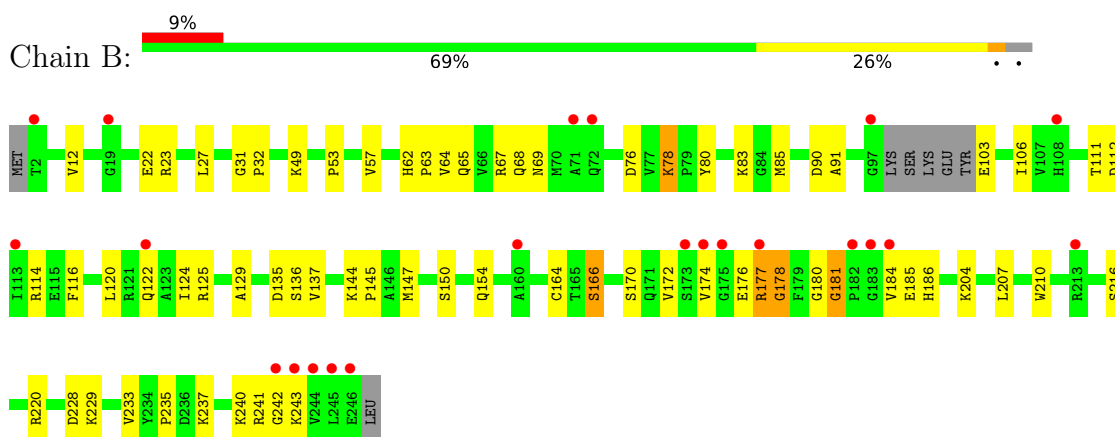
3 Residue-property plots [i](#)

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.

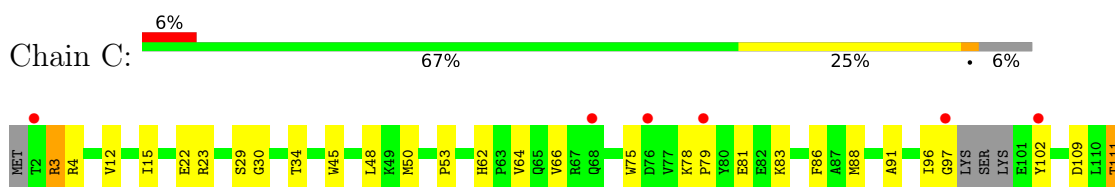
• Molecule 1: UPF0273 protein PH0284

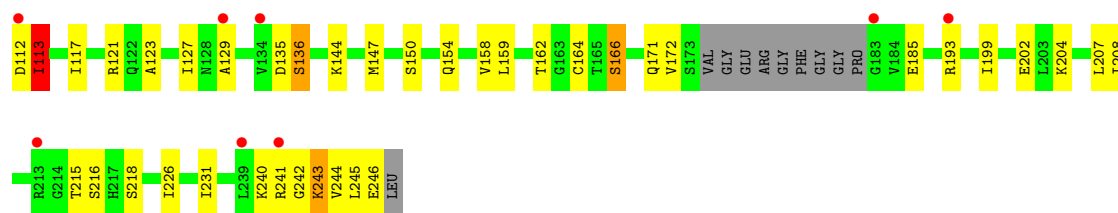


• Molecule 1: UPF0273 protein PH0284

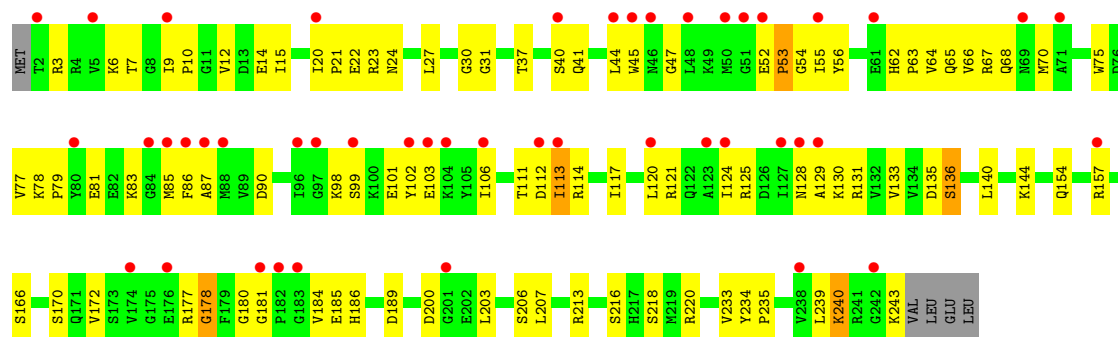


• Molecule 1: UPF0273 protein PH0284

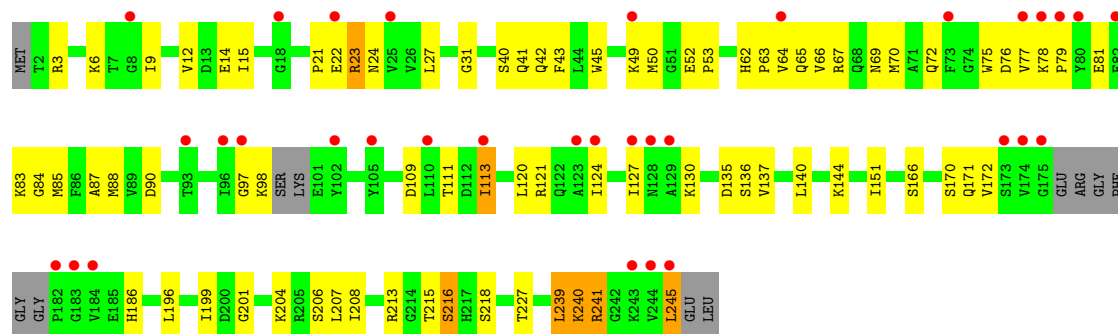




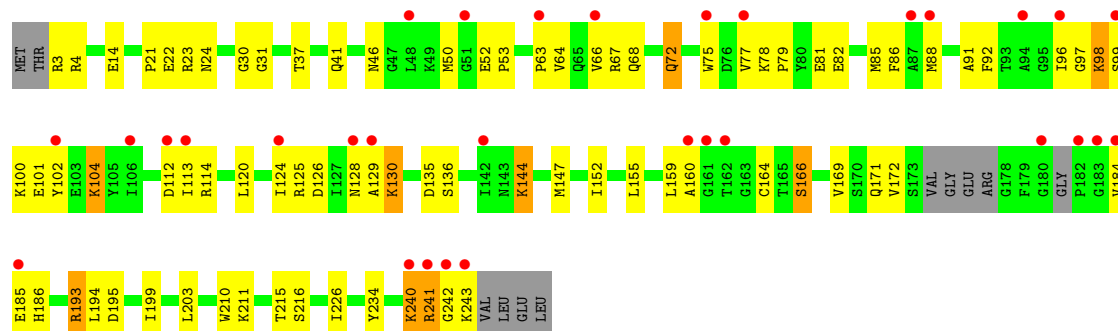
• Molecule 1: UPF0273 protein PH0284



• Molecule 1: UPF0273 protein PH0284



• Molecule 1: UPF0273 protein PH0284



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	96.06Å 96.06Å 298.90Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	38.38 – 2.00 38.38 – 2.00	Depositor EDS
% Data completeness (in resolution range)	91.5 (38.38-2.00) 91.5 (38.38-2.00)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.40 (at 2.00Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.251 , 0.295 0.252 , 0.296	Depositor DCC
R_{free} test set	5013 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	37.7	Xtriage
Anisotropy	0.088	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 47.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.007 for -h,-k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	12543	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 3.45% 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: ADP

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	0.47	0/1859	1.02	13/2502 (0.5%)
1	B	0.51	0/1909	1.01	11/2573 (0.4%)
1	C	0.49	0/1867	0.99	7/2516 (0.3%)
1	D	0.58	0/1932	1.07	13/2603 (0.5%)
1	E	0.50	0/1886	1.01	6/2541 (0.2%)
1	F	0.57	1/1888 (0.1%)	1.01	9/2540 (0.4%)
All	All	0.52	1/11341 (0.0%)	1.02	59/15275 (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	D	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	75	TRP	NE1-CE2	10.21	1.48	1.37

All (59) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	178	GLY	O-C-N	-9.14	113.13	122.82
1	D	181	GLY	CA-C-N	8.95	131.02	119.84
1	D	181	GLY	C-N-CA	8.95	131.02	119.84
1	B	178	GLY	O-C-N	-7.92	113.65	122.60
1	B	125	ARG	NE-CZ-NH1	-7.53	113.97	121.50
1	C	166	SER	N-CA-C	7.36	120.93	109.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	125	ARG	NE-CZ-NH2	7.36	125.83	119.20
1	E	166	SER	N-CA-C	7.11	120.54	109.52
1	B	166	SER	N-CA-C	7.04	120.44	109.52
1	D	185	GLU	N-CA-C	6.91	119.65	111.71
1	B	216	SER	N-CA-C	-6.52	101.14	110.59
1	F	216	SER	N-CA-C	-6.42	101.29	110.59
1	A	216	SER	N-CA-C	-6.40	101.05	110.52
1	D	216	SER	N-CA-C	-6.36	101.37	110.59
1	F	234	TYR	CA-C-N	6.33	126.25	119.28
1	F	234	TYR	C-N-CA	6.33	126.25	119.28
1	F	166	SER	N-CA-C	6.31	119.30	109.52
1	B	12	VAL	N-CA-C	6.22	116.39	110.42
1	A	82	GLU	CA-C-N	6.11	129.31	120.38
1	A	82	GLU	C-N-CA	6.11	129.31	120.38
1	F	226	ILE	N-CA-C	-6.06	99.70	108.36
1	E	216	SER	N-CA-C	-6.02	101.86	110.59
1	C	113	ILE	O-C-N	-6.01	115.06	122.57
1	F	185	GLU	O-C-N	-5.99	114.55	122.33
1	C	91	ALA	N-CA-C	-5.97	103.24	110.88
1	C	216	SER	N-CA-C	-5.93	101.75	110.52
1	C	226	ILE	N-CA-C	-5.81	100.04	108.17
1	C	231	ILE	N-CA-C	5.68	116.93	109.21
1	D	53	PRO	N-CA-CB	5.67	107.03	103.23
1	D	234	TYR	CA-C-N	5.62	125.30	119.56
1	D	234	TYR	C-N-CA	5.62	125.30	119.56
1	F	91	ALA	N-CA-C	-5.60	105.13	112.41
1	B	181	GLY	CA-C-N	5.52	125.79	119.83
1	B	181	GLY	C-N-CA	5.52	125.79	119.83
1	C	12	VAL	N-CA-C	5.42	116.20	110.72
1	A	234	TYR	CA-C-N	5.37	125.19	119.28
1	A	234	TYR	C-N-CA	5.37	125.19	119.28
1	D	20	ILE	N-CA-C	5.34	113.16	107.76
1	E	12	VAL	N-CA-C	5.25	115.46	110.42
1	B	91	ALA	N-CA-C	-5.22	104.50	111.87
1	D	12	VAL	N-CA-C	5.21	115.43	110.53
1	B	145	PRO	N-CA-CB	5.19	109.04	103.33
1	A	226	ILE	N-CA-C	-5.16	100.98	108.36
1	A	52	GLU	CA-C-N	5.15	125.16	119.90
1	A	52	GLU	C-N-CA	5.15	125.16	119.90
1	E	113	ILE	O-C-N	-5.14	117.47	122.09
1	F	126	ASP	N-CA-C	5.14	117.28	111.11
1	D	177	ARG	CD-NE-CZ	-5.13	117.22	124.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	177	ARG	CD-NE-CZ	-5.12	117.23	124.40
1	A	144	LYS	CA-C-N	5.12	125.40	119.47
1	A	144	LYS	C-N-CA	5.12	125.40	119.47
1	E	241	ARG	CD-NE-CZ	-5.10	117.26	124.40
1	A	220	ARG	CD-NE-CZ	-5.09	117.27	124.40
1	A	84	GLY	O-C-N	-5.07	116.40	122.33
1	D	125	ARG	CD-NE-CZ	-5.07	117.31	124.40
1	D	111	THR	N-CA-C	-5.05	105.85	111.36
1	E	23	ARG	CD-NE-CZ	-5.05	117.33	124.40
1	A	12	VAL	N-CA-C	5.05	115.27	110.42
1	F	130	LYS	N-CA-C	-5.04	107.79	114.04

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	178	GLY	Mainchain

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	1826	0	1867	83	0
1	B	1875	0	1923	54	0
1	C	1835	0	1881	66	0
1	D	1896	0	1944	76	0
1	E	1853	0	1908	69	0
1	F	1854	0	1902	81	0
2	A	27	0	12	0	0
2	B	27	0	12	0	0
2	C	27	0	12	0	0
2	D	27	0	12	0	0
2	E	27	0	12	0	0
2	F	27	0	12	0	0
3	A	190	0	0	5	0
3	B	220	0	0	11	0
3	C	213	0	0	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	228	0	0	10	0
3	E	196	0	0	10	0
3	F	195	0	0	10	0
All	All	12543	0	11497	414	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 18.

All (414) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:154:GLN:HA	1:D:157:ARG:HH12	1.08	1.11
1:C:240:LYS:HD3	1:C:245:LEU:HD12	1.31	1.07
1:F:104:LYS:H	1:F:104:LYS:HD2	1.21	1.03
1:D:124:ILE:HG23	1:D:129:ALA:HB3	1.49	0.94
1:C:243:LYS:HA	1:C:243:LYS:HE3	1.50	0.93
1:D:53:PRO:HG2	1:D:128:ASN:HB2	1.51	0.92
1:F:199:ILE:HG21	1:F:242:GLY:HA2	1.49	0.91
1:C:240:LYS:CD	1:C:245:LEU:HD12	2.03	0.86
1:D:101:GLU:HG3	1:D:102:TYR:H	1.40	0.85
1:D:117:ILE:O	1:D:121:ARG:HG3	1.74	0.85
1:A:63:PRO:HB3	1:A:88:MET:HG2	1.57	0.83
1:C:193:ARG:HD3	3:C:3863:HOH:O	1.77	0.83
1:D:154:GLN:HA	1:D:157:ARG:NH1	1.93	0.83
1:C:113:ILE:HD13	1:C:113:ILE:H	1.42	0.82
1:E:66:VAL:HB	1:E:88:MET:HE1	1.61	0.82
3:E:3891:HOH:O	1:F:211:LYS:HD2	1.81	0.81
1:C:78:LYS:HB3	1:C:79:PRO:HD3	1.63	0.80
1:C:3:ARG:H	1:C:3:ARG:HE	1.28	0.80
1:A:53:PRO:HB2	1:A:129:ALA:HA	1.64	0.79
1:D:53:PRO:HG2	1:D:128:ASN:O	1.81	0.79
1:E:45:TRP:HE1	1:E:49:LYS:HE3	1.48	0.78
1:A:102:TYR:O	1:A:103:GLU:HG2	1.84	0.77
1:E:3:ARG:HE	1:E:22:GLU:CD	1.92	0.77
1:A:143:ASN:O	1:A:144:LYS:HD2	1.85	0.77
1:E:204:LYS:HE2	3:E:3852:HOH:O	1.83	0.76
1:C:4:ARG:HH21	1:C:215:THR:HB	1.50	0.75
1:A:104:LYS:HG2	1:A:105:TYR:CZ	2.20	0.75
1:D:53:PRO:CG	1:D:128:ASN:HB2	2.16	0.75
1:B:178:GLY:HA3	3:B:3815:HOH:O	1.87	0.75
1:A:117:ILE:HD11	1:A:158:VAL:HG11	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:78:LYS:HB3	1:F:79:PRO:HD3	1.68	0.74
1:E:241:ARG:HB2	3:E:4001:HOH:O	1.87	0.73
1:B:64:VAL:HG12	1:B:68:GLN:HE21	1.53	0.73
1:A:65:GLN:HG3	3:A:3831:HOH:O	1.86	0.72
1:C:53:PRO:HG2	1:C:129:ALA:HA	1.71	0.72
1:C:113:ILE:HD13	1:C:113:ILE:N	2.05	0.72
1:C:113:ILE:H	1:C:113:ILE:CD1	2.02	0.72
1:C:241:ARG:HG2	1:C:241:ARG:HH11	1.55	0.71
1:D:79:PRO:HG2	3:D:3957:HOH:O	1.89	0.71
1:C:30:GLY:C	1:C:172:VAL:HG22	2.15	0.71
1:C:199:ILE:HG21	1:C:242:GLY:HA3	1.73	0.71
1:A:180:GLY:O	1:A:182:PRO:HD2	1.91	0.70
1:A:117:ILE:CD1	1:A:158:VAL:HG11	2.21	0.70
1:B:49:LYS:NZ	3:B:4013:HOH:O	2.24	0.70
1:B:220:ARG:HG3	1:B:220:ARG:HH11	1.57	0.69
1:E:45:TRP:NE1	1:E:49:LYS:HE3	2.08	0.69
1:E:87:ALA:HB2	1:E:127:ILE:HD12	1.75	0.69
1:C:66:VAL:HB	1:C:88:MET:HE1	1.74	0.68
1:A:3:ARG:CZ	1:A:22:GLU:HG3	2.24	0.68
1:B:242:GLY:HA3	3:B:3964:HOH:O	1.93	0.68
1:D:47:GLY:O	1:D:52:GLU:HB2	1.94	0.68
1:C:144:LYS:HD2	1:C:147:MET:HG3	1.76	0.67
1:C:245:LEU:O	1:C:246:GLU:HB2	1.95	0.67
1:B:114:ARG:HB3	3:B:4000:HOH:O	1.92	0.67
1:E:53:PRO:HB2	1:E:127:ILE:HG22	1.78	0.66
1:E:15:ILE:HG23	1:E:218:SER:HB3	1.77	0.66
1:D:113:ILE:N	1:D:113:ILE:HD12	2.11	0.66
1:E:206:SER:HB3	1:E:239:LEU:HD12	1.78	0.66
1:F:128:ASN:HB2	3:F:3945:HOH:O	1.96	0.66
1:A:221:ARG:NE	1:A:241:ARG:HD2	2.11	0.66
1:D:78:LYS:HB2	1:D:79:PRO:HD3	1.76	0.66
1:B:112:ASP:HB2	3:B:4000:HOH:O	1.96	0.66
1:E:109:ASP:OD1	1:E:111:THR:HB	1.96	0.65
1:E:186:HIS:ND1	3:E:3839:HOH:O	2.28	0.65
1:A:21:PRO:O	1:A:24:ASN:HB2	1.96	0.65
1:D:101:GLU:HG3	1:D:102:TYR:N	2.11	0.65
1:D:243:LYS:HG3	3:D:4008:HOH:O	1.96	0.65
1:D:157:ARG:HB3	1:D:157:ARG:CZ	2.27	0.64
1:D:157:ARG:NH1	1:D:157:ARG:HB3	2.12	0.64
1:D:120:LEU:O	1:D:124:ILE:HG13	1.97	0.64
1:C:193:ARG:NH1	3:C:3863:HOH:O	2.30	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:96:ILE:HG13	1:F:97:GLY:N	2.13	0.64
1:A:78:LYS:HB3	1:A:79:PRO:HD3	1.81	0.63
1:E:66:VAL:CB	1:E:88:MET:HE1	2.29	0.63
1:E:63:PRO:O	1:E:67:ARG:HG3	1.98	0.63
1:D:23:ARG:HD3	3:D:3949:HOH:O	1.98	0.63
1:A:104:LYS:HG2	1:A:105:TYR:CE2	2.33	0.63
1:B:144:LYS:HE3	1:B:147:MET:HG3	1.82	0.62
1:B:76:ASP:OD2	1:B:78:LYS:HE3	2.00	0.62
1:F:240:LYS:NZ	3:F:3895:HOH:O	2.32	0.61
1:F:96:ILE:HG13	1:F:97:GLY:H	1.65	0.61
1:F:104:LYS:HD2	1:F:104:LYS:N	2.05	0.61
1:A:102:TYR:CG	1:A:103:GLU:N	2.69	0.61
1:B:240:LYS:O	1:B:241:ARG:HG2	2.01	0.61
1:C:29:SER:O	1:C:193:ARG:HD2	2.00	0.60
1:A:118:GLU:O	1:A:122:GLN:HG2	2.01	0.60
1:C:81:GLU:HG3	1:C:86:PHE:HD2	1.67	0.60
1:A:114:ARG:HG3	1:A:114:ARG:HH11	1.65	0.60
1:C:3:ARG:NH1	1:C:23:ARG:HH22	1.99	0.60
1:E:27:LEU:HD11	1:E:170:SER:HB2	1.83	0.60
1:F:104:LYS:H	1:F:104:LYS:CD	2.02	0.60
1:A:206:SER:HB3	1:A:239:LEU:HD23	1.83	0.60
1:D:15:ILE:HG23	1:D:218:SER:HB3	1.83	0.60
1:F:136:SER:HB2	1:F:169:VAL:O	2.02	0.60
1:F:98:LYS:HG2	1:F:100:LYS:H	1.66	0.60
1:C:4:ARG:HG2	1:C:4:ARG:HH11	1.67	0.59
1:A:3:ARG:NE	1:A:22:GLU:HG3	2.17	0.59
1:F:23:ARG:HD2	1:F:160:ALA:O	2.02	0.59
1:B:64:VAL:HG12	1:B:68:GLN:NE2	2.17	0.59
1:C:111:THR:HG22	1:C:112:ASP:OD2	2.01	0.59
1:C:241:ARG:HH11	1:C:241:ARG:CG	2.14	0.59
1:E:22:GLU:HG2	1:E:23:ARG:HG2	1.84	0.59
1:E:3:ARG:NE	1:E:22:GLU:OE2	2.35	0.59
1:A:159:LEU:HD13	1:A:166:SER:OG	2.03	0.59
1:F:243:LYS:HD3	1:F:243:LYS:C	2.27	0.59
1:C:199:ILE:HD13	1:C:242:GLY:HA2	1.85	0.58
1:D:113:ILE:HG22	1:D:113:ILE:O	2.03	0.58
1:B:62:HIS:HB3	1:B:65:GLN:OE1	2.02	0.58
1:D:233:VAL:O	1:D:235:PRO:HD3	2.03	0.58
1:B:176:GLU:HG2	1:B:178:GLY:H	1.69	0.58
1:F:72:GLN:HE21	1:F:72:GLN:H	1.52	0.58
1:A:25:VAL:HG11	1:A:168:PHE:CE2	2.39	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:204:LYS:HE2	3:C:3902:HOH:O	2.02	0.58
1:F:152:ILE:HG13	1:F:184:VAL:HG13	1.85	0.58
1:E:78:LYS:HB2	1:E:79:PRO:HD3	1.85	0.58
1:E:127:ILE:HG22	1:E:127:ILE:O	2.03	0.58
1:A:55:ILE:HG12	1:A:87:ALA:HB3	1.85	0.57
1:F:112:ASP:HA	3:F:3949:HOH:O	2.04	0.57
1:D:3:ARG:NE	1:D:22:GLU:OE2	2.37	0.57
1:D:77:VAL:O	1:D:81:GLU:HG3	2.03	0.57
1:C:3:ARG:H	1:C:3:ARG:NE	2.00	0.57
1:A:200:ASP:HB3	3:B:3962:HOH:O	2.05	0.57
1:B:69:ASN:HB3	3:B:3905:HOH:O	2.05	0.57
1:B:184:VAL:HG13	1:B:185:GLU:N	2.20	0.57
1:E:66:VAL:CG1	1:E:88:MET:HE1	2.35	0.56
1:F:64:VAL:HG13	3:F:3964:HOH:O	2.04	0.56
1:E:171:GLN:HB3	1:F:186:HIS:CE1	2.40	0.56
1:B:150:SER:O	1:B:154:GLN:HG3	2.05	0.56
1:C:4:ARG:HH21	1:C:215:THR:CB	2.18	0.56
1:C:23:ARG:HA	1:C:164:CYS:O	2.06	0.56
1:C:102:TYR:HA	3:C:3921:HOH:O	2.06	0.56
1:A:62:HIS:HD2	1:A:93:THR:CG2	2.18	0.56
1:E:227:THR:HB	3:E:3986:HOH:O	2.05	0.56
1:F:128:ASN:HA	3:F:3952:HOH:O	2.06	0.56
1:A:157:ARG:HE	1:F:96:ILE:CD1	2.19	0.56
1:F:68:GLN:NE2	3:F:3982:HOH:O	2.36	0.56
1:A:77:VAL:O	1:A:81:GLU:HG3	2.06	0.56
1:A:3:ARG:CG	1:A:22:GLU:HG3	2.36	0.55
1:A:143:ASN:C	1:A:144:LYS:HD2	2.32	0.55
1:F:50:MET:HE3	3:F:3830:HOH:O	2.06	0.55
1:F:98:LYS:NZ	1:F:98:LYS:HB3	2.21	0.55
1:B:62:HIS:CE1	1:B:64:VAL:HG23	2.41	0.55
1:F:79:PRO:O	1:F:82:GLU:HG2	2.07	0.55
1:F:77:VAL:O	1:F:81:GLU:HG3	2.07	0.55
1:E:62:HIS:CE1	1:E:64:VAL:HG23	2.42	0.55
1:C:66:VAL:CG1	1:C:88:MET:HE1	2.37	0.55
1:D:47:GLY:O	1:D:52:GLU:N	2.36	0.55
1:F:193:ARG:HD2	1:F:195:ASP:CG	2.32	0.55
1:F:68:GLN:O	1:F:72:GLN:NE2	2.40	0.55
1:E:21:PRO:O	1:E:24:ASN:HB2	2.07	0.54
1:F:144:LYS:CE	1:F:147:MET:HG3	2.37	0.54
1:D:14:GLU:OE1	1:D:14:GLU:N	2.40	0.54
1:E:22:GLU:O	1:E:23:ARG:HB2	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:144:LYS:HE3	1:F:147:MET:HG3	1.90	0.54
1:B:80:TYR:HD1	1:B:85:MET:HE3	1.72	0.54
1:D:117:ILE:HG22	1:D:121:ARG:HD2	1.90	0.54
1:D:45:TRP:CE3	1:D:75:TRP:HB3	2.42	0.54
1:F:63:PRO:O	1:F:67:ARG:HG3	2.08	0.54
1:C:158:VAL:O	1:C:162:THR:HG23	2.07	0.54
1:B:229:LYS:HB2	3:B:4006:HOH:O	2.07	0.54
1:F:37:THR:O	1:F:41:GLN:HG3	2.08	0.53
1:F:112:ASP:OD2	1:F:114:ARG:HB2	2.08	0.53
1:C:15:ILE:HG23	1:C:218:SER:HB3	1.90	0.53
1:A:3:ARG:HG3	1:A:22:GLU:HG3	1.89	0.53
1:B:207:LEU:C	1:B:207:LEU:HD23	2.33	0.53
1:C:62:HIS:CE1	1:C:64:VAL:HG23	2.43	0.53
1:C:96:ILE:HG13	1:C:97:GLY:N	2.24	0.53
1:E:69:ASN:HB3	3:E:3864:HOH:O	2.08	0.53
1:E:97:GLY:O	1:E:98:LYS:HB2	2.08	0.53
1:D:240:LYS:NZ	3:D:3844:HOH:O	2.41	0.53
1:A:182:PRO:C	1:A:184:VAL:H	2.17	0.53
1:D:37:THR:O	1:D:41:GLN:HG3	2.09	0.53
1:F:113:ILE:HD11	1:F:155:LEU:HD21	1.91	0.53
1:F:125:ARG:HG2	1:F:125:ARG:HH11	1.74	0.53
1:D:63:PRO:O	1:D:67:ARG:HG3	2.09	0.53
1:A:113:ILE:O	1:A:117:ILE:HG22	2.09	0.52
1:E:113:ILE:HD13	1:E:151:ILE:HG23	1.91	0.52
1:D:128:ASN:O	1:D:130:LYS:HG2	2.09	0.52
1:E:79:PRO:O	1:E:83:LYS:HE2	2.08	0.52
1:D:64:VAL:HG12	1:D:68:GLN:HE21	1.73	0.52
1:A:22:GLU:O	1:A:23:ARG:HB2	2.08	0.52
1:D:113:ILE:N	1:D:113:ILE:CD1	2.73	0.52
1:A:171:GLN:HB3	1:B:186:HIS:CE1	2.44	0.52
1:B:32:PRO:HD2	1:B:174:VAL:CG2	2.39	0.52
1:E:98:LYS:HD2	1:E:98:LYS:N	2.24	0.52
1:B:80:TYR:CD1	1:B:85:MET:HE3	2.45	0.52
1:B:220:ARG:HG3	1:B:220:ARG:NH1	2.24	0.51
1:B:23:ARG:HA	1:B:164:CYS:O	2.10	0.51
1:D:53:PRO:HG2	1:D:128:ASN:CB	2.33	0.51
1:A:114:ARG:O	1:A:118:GLU:HG3	2.10	0.51
1:B:32:PRO:HG3	1:C:185:GLU:OE1	2.10	0.51
1:C:79:PRO:O	1:C:83:LYS:HG3	2.11	0.51
1:D:40:SER:HB3	1:D:133:VAL:HG11	1.92	0.51
1:D:53:PRO:HG2	1:D:128:ASN:C	2.35	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:22:GLU:O	1:C:23:ARG:HB2	2.11	0.51
1:B:27:LEU:HD11	1:B:170:SER:HB2	1.93	0.51
1:A:45:TRP:CE3	1:A:75:TRP:HB3	2.46	0.50
1:A:16:LEU:HD22	1:A:212:MET:HE3	1.93	0.50
1:B:111:THR:HG22	1:B:112:ASP:OD2	2.12	0.50
1:E:207:LEU:C	1:E:207:LEU:HD23	2.36	0.50
1:A:117:ILE:CD1	1:A:158:VAL:HG21	2.41	0.50
1:C:171:GLN:HB3	1:D:186:HIS:CE1	2.47	0.50
1:C:66:VAL:CB	1:C:88:MET:HE1	2.39	0.50
1:E:76:ASP:OD2	1:E:79:PRO:HD3	2.12	0.50
1:D:62:HIS:CE1	1:D:64:VAL:HG23	2.46	0.49
1:D:114:ARG:HB2	3:D:3965:HOH:O	2.13	0.49
1:B:181:GLY:O	1:B:184:VAL:HG12	2.13	0.49
1:F:193:ARG:HD2	1:F:195:ASP:OD1	2.12	0.49
1:A:117:ILE:HD11	1:A:158:VAL:CG1	2.41	0.49
1:D:140:LEU:O	1:D:144:LYS:HE2	2.13	0.49
1:E:41:GLN:HB3	1:E:70:MET:HE3	1.94	0.49
1:F:46:ASN:O	1:F:50:MET:HG2	2.12	0.49
1:B:32:PRO:HD2	1:B:174:VAL:HG23	1.94	0.49
1:F:3:ARG:HG3	1:F:3:ARG:HH11	1.77	0.49
1:A:114:ARG:HG3	1:A:114:ARG:NH1	2.28	0.48
1:D:157:ARG:NH1	1:D:157:ARG:CB	2.74	0.48
1:F:23:ARG:HA	1:F:164:CYS:O	2.14	0.48
1:B:184:VAL:HG13	1:B:185:GLU:H	1.76	0.48
1:D:22:GLU:O	1:D:23:ARG:HB2	2.14	0.48
1:F:21:PRO:O	1:F:24:ASN:HB2	2.13	0.48
1:A:152:ILE:HG13	1:A:184:VAL:HG22	1.95	0.48
1:B:243:LYS:HG2	3:B:3985:HOH:O	2.11	0.48
1:E:245:LEU:H	1:E:245:LEU:HG	1.47	0.48
1:E:201:GLY:HA3	1:F:240:LYS:HA	1.95	0.48
1:A:117:ILE:O	1:A:121:ARG:HG3	2.12	0.48
3:A:3848:HOH:O	1:F:98:LYS:HD3	2.13	0.48
1:E:62:HIS:HB3	1:E:65:GLN:OE1	2.13	0.48
1:A:76:ASP:OD1	1:A:79:PRO:HD3	2.14	0.48
1:C:66:VAL:HB	1:C:88:MET:CE	2.42	0.48
1:A:107:VAL:HG11	1:A:110:LEU:CD2	2.44	0.48
1:C:45:TRP:CE3	1:C:75:TRP:HB3	2.48	0.48
1:A:240:LYS:HB3	3:A:3934:HOH:O	2.14	0.47
1:E:84:GLY:O	1:E:127:ILE:HG23	2.13	0.47
1:A:189:ASP:O	1:A:213:ARG:HG2	2.14	0.47
1:C:48:LEU:C	1:C:50:MET:H	2.22	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:9:ILE:HG23	1:E:42:GLN:NE2	2.30	0.47
1:E:87:ALA:HB2	1:E:127:ILE:CD1	2.41	0.47
1:F:193:ARG:HD3	1:F:194:LEU:N	2.29	0.47
1:A:101:GLU:HA	3:A:3805:HOH:O	2.14	0.47
1:E:76:ASP:O	1:E:79:PRO:HD2	2.15	0.47
1:B:22:GLU:HG2	1:B:23:ARG:HG3	1.97	0.47
1:D:44:LEU:CD1	1:D:56:TYR:HB2	2.44	0.47
1:F:199:ILE:HD13	1:F:242:GLY:H	1.79	0.47
1:A:153:LEU:O	1:A:156:LYS:HB3	2.14	0.47
1:C:4:ARG:HG2	1:C:4:ARG:NH1	2.30	0.47
1:D:98:LYS:HG2	3:D:4017:HOH:O	2.15	0.47
1:E:45:TRP:CE3	1:E:75:TRP:HB3	2.49	0.47
1:E:111:THR:HG22	3:E:3963:HOH:O	2.14	0.47
1:F:4:ARG:HH12	1:F:215:THR:HG21	1.78	0.47
1:F:72:GLN:HE21	1:F:72:GLN:N	2.13	0.47
1:F:98:LYS:HG2	1:F:99:SER:N	2.30	0.47
1:B:32:PRO:CD	1:B:174:VAL:HG23	2.45	0.47
1:B:135:ASP:HA	1:B:136:SER:HA	1.54	0.47
1:A:120:LEU:O	1:A:124:ILE:HG13	2.15	0.47
1:C:3:ARG:CZ	1:C:23:ARG:HH12	2.27	0.47
1:C:241:ARG:CG	1:C:241:ARG:NH1	2.71	0.47
1:D:54:GLY:HA2	1:D:131:ARG:O	2.15	0.47
1:E:3:ARG:NE	1:E:22:GLU:CD	2.69	0.47
1:E:199:ILE:HB	1:E:204:LYS:NZ	2.29	0.47
1:A:107:VAL:HG11	1:A:110:LEU:HD23	1.96	0.47
1:D:90:ASP:HB3	1:D:106:ILE:HG12	1.97	0.46
1:A:233:VAL:O	1:A:235:PRO:HD3	2.14	0.46
1:E:127:ILE:O	1:E:127:ILE:CG2	2.63	0.46
1:D:135:ASP:HA	1:D:136:SER:HA	1.43	0.46
1:F:159:LEU:HD13	1:F:166:SER:OG	2.15	0.46
1:D:6:LYS:O	1:D:131:ARG:NH2	2.47	0.46
1:E:201:GLY:CA	1:F:240:LYS:HA	2.45	0.46
1:C:4:ARG:NH2	1:C:215:THR:CB	2.78	0.46
1:F:124:ILE:HG23	1:F:129:ALA:HB3	1.97	0.46
1:D:27:LEU:HD11	1:D:170:SER:HB2	1.97	0.46
1:F:101:GLU:CG	1:F:102:TYR:N	2.79	0.46
1:A:3:ARG:NE	1:A:22:GLU:OE2	2.49	0.46
1:C:135:ASP:HA	1:C:136:SER:HA	1.64	0.46
1:D:65:GLN:HG3	3:D:3817:HOH:O	2.15	0.45
1:D:101:GLU:CG	1:D:102:TYR:H	2.19	0.45
1:E:31:GLY:HA2	1:E:172:VAL:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:196:LEU:HD23	1:F:210:TRP:NE1	2.31	0.45
1:C:123:ALA:O	1:C:127:ILE:HG12	2.17	0.45
1:D:21:PRO:O	1:D:24:ASN:HB2	2.17	0.45
1:E:121:ARG:HH11	1:E:121:ARG:HG2	1.81	0.45
1:A:27:LEU:HD11	1:A:170:SER:HB2	1.99	0.45
1:C:109:ASP:OD2	1:C:111:THR:HB	2.16	0.45
1:F:135:ASP:HA	1:F:136:SER:HA	1.56	0.45
1:A:207:LEU:C	1:A:207:LEU:HD23	2.41	0.45
1:D:30:GLY:C	1:D:172:VAL:HG22	2.41	0.45
1:F:52:GLU:HG2	1:F:130:LYS:NZ	2.31	0.45
1:F:104:LYS:NZ	3:F:3905:HOH:O	2.50	0.45
1:B:144:LYS:CE	1:B:147:MET:HG3	2.46	0.45
1:E:6:LYS:HD3	1:E:50:MET:HE1	1.97	0.45
1:F:113:ILE:HG13	1:F:113:ILE:O	2.17	0.45
1:E:83:LYS:NZ	3:E:3974:HOH:O	2.50	0.45
1:D:83:LYS:HE3	1:D:85:MET:SD	2.56	0.45
1:D:124:ILE:HG23	1:D:129:ALA:CB	2.35	0.45
1:F:243:LYS:HA	3:F:3915:HOH:O	2.16	0.45
1:B:64:VAL:O	1:B:68:GLN:HG3	2.17	0.44
1:D:6:LYS:HE2	3:D:3945:HOH:O	2.17	0.44
1:D:67:ARG:HE	1:D:81:GLU:CD	2.25	0.44
1:F:86:PHE:HE2	1:F:88:MET:HG2	1.81	0.44
1:A:186:HIS:CE1	1:F:171:GLN:HB3	2.52	0.44
1:A:202:GLU:HB2	1:B:220:ARG:HD3	1.99	0.44
1:A:62:HIS:HD2	1:A:93:THR:HG23	1.82	0.44
1:F:30:GLY:HA2	1:F:193:ARG:HE	1.83	0.44
1:F:120:LEU:O	1:F:124:ILE:HG13	2.17	0.44
1:C:4:ARG:NH2	1:C:215:THR:OG1	2.51	0.44
1:C:241:ARG:HG2	1:C:241:ARG:NH1	2.28	0.44
1:C:243:LYS:HE3	1:C:243:LYS:CA	2.33	0.44
1:A:3:ARG:HG2	1:A:3:ARG:HH11	1.82	0.44
1:E:240:LYS:HB3	1:E:240:LYS:HE3	1.66	0.44
1:B:103:GLU:HB3	1:B:106:ILE:CG1	2.48	0.44
1:D:203:LEU:HG	1:E:208:ILE:HD11	2.00	0.44
1:A:206:SER:HB3	1:A:239:LEU:CD2	2.46	0.44
1:C:199:ILE:HG21	1:C:242:GLY:CA	2.46	0.44
1:D:101:GLU:OE1	1:D:101:GLU:HA	2.17	0.44
1:D:189:ASP:HA	1:D:213:ARG:HH11	1.83	0.44
1:A:39:PHE:C	1:A:39:PHE:CD1	2.95	0.44
1:C:159:LEU:HD13	1:C:166:SER:OG	2.17	0.44
1:F:22:GLU:HG2	1:F:23:ARG:HG3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:10:PRO:HA	3:D:3850:HOH:O	2.18	0.43
1:D:23:ARG:HH11	1:D:23:ARG:HG3	1.83	0.43
1:F:4:ARG:HH12	1:F:215:THR:CB	2.30	0.43
1:E:140:LEU:O	1:E:144:LYS:HE3	2.18	0.43
1:F:78:LYS:N	1:F:79:PRO:CD	2.81	0.43
1:A:102:TYR:CD2	1:A:102:TYR:C	2.96	0.43
1:D:207:LEU:HD23	1:D:207:LEU:C	2.43	0.43
1:A:207:LEU:HD23	1:A:208:ILE:N	2.34	0.43
1:B:120:LEU:O	1:B:124:ILE:HG13	2.18	0.43
1:D:52:GLU:HA	1:D:53:PRO:HD3	1.76	0.43
1:A:117:ILE:O	1:A:117:ILE:HD12	2.18	0.43
1:A:135:ASP:HA	1:A:136:SER:HA	1.45	0.43
1:D:7:THR:C	1:D:9:ILE:H	2.27	0.43
1:D:55:ILE:HG12	1:D:87:ALA:HB3	1.99	0.43
1:D:62:HIS:O	1:D:66:VAL:HG23	2.19	0.43
1:A:117:ILE:HD13	1:A:158:VAL:HG21	2.00	0.43
1:B:53:PRO:HB2	1:B:129:ALA:HA	1.99	0.43
1:F:66:VAL:CG1	1:F:88:MET:HE1	2.49	0.43
1:F:100:LYS:O	1:F:101:GLU:HB2	2.19	0.43
1:B:237:LYS:HE3	3:B:4011:HOH:O	2.17	0.43
1:D:41:GLN:HB3	1:D:70:MET:HE3	2.01	0.43
1:F:199:ILE:CG2	1:F:242:GLY:HA2	2.35	0.43
1:E:40:SER:O	1:E:43:PHE:HB3	2.18	0.42
1:E:120:LEU:O	1:E:124:ILE:HG13	2.19	0.42
1:F:22:GLU:O	1:F:23:ARG:HB2	2.19	0.42
1:F:68:GLN:HE21	1:F:68:GLN:HA	1.84	0.42
1:A:23:ARG:HA	1:A:164:CYS:O	2.19	0.42
1:F:3:ARG:HD3	3:F:3980:HOH:O	2.20	0.42
1:F:241:ARG:HA	1:F:241:ARG:HD3	1.47	0.42
1:C:30:GLY:O	1:C:172:VAL:HG22	2.17	0.42
1:C:117:ILE:HD12	3:C:3927:HOH:O	2.19	0.42
1:C:202:GLU:HB2	1:D:220:ARG:NE	2.35	0.42
1:E:121:ARG:HG2	1:E:121:ARG:NH1	2.34	0.42
1:E:135:ASP:HA	1:E:136:SER:HA	1.46	0.42
1:F:66:VAL:HG12	1:F:88:MET:HE1	2.02	0.42
1:C:3:ARG:NH1	1:C:23:ARG:NH2	2.67	0.42
1:D:112:ASP:C	1:D:113:ILE:HD12	2.44	0.42
1:F:78:LYS:N	1:F:79:PRO:HD2	2.35	0.42
1:C:150:SER:O	1:C:154:GLN:HG3	2.19	0.42
1:F:243:LYS:C	1:F:243:LYS:CD	2.92	0.42
1:D:99:SER:HB2	3:D:4023:HOH:O	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:27:LEU:HB2	1:A:188:VAL:HG11	2.01	0.42
1:A:78:LYS:HA	1:A:81:GLU:OE1	2.20	0.42
1:B:90:ASP:HB2	1:B:103:GLU:HG2	2.02	0.42
1:D:206:SER:HB3	1:D:239:LEU:HD23	2.01	0.42
1:A:183:GLY:O	1:A:187:GLY:N	2.51	0.41
1:B:103:GLU:HB3	1:B:106:ILE:HG12	2.01	0.41
1:C:48:LEU:HD11	1:C:86:PHE:CD1	2.56	0.41
1:C:207:LEU:HD23	1:C:208:ILE:N	2.35	0.41
1:F:53:PRO:HA	1:F:85:MET:O	2.20	0.41
1:B:67:ARG:HD3	1:B:78:LYS:HD2	2.02	0.41
1:B:83:LYS:HD3	1:B:85:MET:HE2	2.02	0.41
1:B:240:LYS:NZ	3:B:4012:HOH:O	2.46	0.41
1:E:52:GLU:HA	1:E:53:PRO:HD2	1.94	0.41
1:E:77:VAL:O	1:E:81:GLU:HG3	2.20	0.41
1:E:85:MET:HE3	3:E:3893:HOH:O	2.20	0.41
1:A:23:ARG:HG2	1:A:23:ARG:HH11	1.85	0.41
1:B:63:PRO:O	1:B:67:ARG:HG3	2.20	0.41
1:D:64:VAL:HG12	1:D:68:GLN:NE2	2.35	0.41
1:A:3:ARG:O	1:A:4:ARG:HD3	2.19	0.41
1:A:125:ARG:NH1	3:A:3957:HOH:O	2.48	0.41
1:E:45:TRP:HE1	1:E:49:LYS:CE	2.27	0.41
1:A:3:ARG:HG3	1:A:22:GLU:CG	2.51	0.41
1:C:207:LEU:HD23	1:C:207:LEU:C	2.46	0.41
1:E:62:HIS:ND1	1:E:63:PRO:HD2	2.35	0.41
1:F:78:LYS:HB3	1:F:79:PRO:CD	2.44	0.41
1:D:31:GLY:HA2	1:D:172:VAL:O	2.20	0.41
1:A:56:TYR:HE1	1:A:58:ALA:HB2	1.86	0.41
1:A:112:ASP:OD1	1:A:114:ARG:HB2	2.20	0.41
1:A:208:ILE:HD11	1:F:203:LEU:HG	2.03	0.41
1:B:228:ASP:OD1	1:B:228:ASP:N	2.53	0.41
1:C:78:LYS:HB3	1:C:79:PRO:CD	2.44	0.41
1:E:67:ARG:NH1	1:E:81:GLU:OE2	2.53	0.41
1:A:63:PRO:O	1:A:67:ARG:HG3	2.21	0.41
1:F:199:ILE:HD13	1:F:242:GLY:N	2.36	0.41
1:A:196:LEU:HD23	1:B:210:TRP:NE1	2.36	0.41
1:D:81:GLU:HG2	1:D:86:PHE:HD2	1.86	0.41
1:E:67:ARG:HD2	3:E:3894:HOH:O	2.21	0.41
1:E:69:ASN:O	1:E:72:GLN:HB3	2.21	0.41
1:E:215:THR:OG1	1:E:216:SER:N	2.53	0.41
1:F:31:GLY:HA2	1:F:172:VAL:O	2.21	0.41
1:A:5:VAL:CG2	1:A:22:GLU:OE1	2.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:57:VAL:HG11	1:B:116:PHE:CZ	2.56	0.41
1:F:125:ARG:HG2	1:F:125:ARG:NH1	2.35	0.41
1:A:42:GLN:HG3	1:A:75:TRP:CZ2	2.56	0.40
1:A:56:TYR:CE1	1:A:58:ALA:HB2	2.56	0.40
1:C:243:LYS:CE	1:C:244:VAL:H	2.35	0.40
1:A:157:ARG:NH2	1:F:92:PHE:HE2	2.20	0.40
1:B:31:GLY:HA2	1:B:172:VAL:O	2.20	0.40
1:A:23:ARG:N	1:A:23:ARG:HD2	2.36	0.40
1:B:233:VAL:O	1:B:235:PRO:HD3	2.22	0.40
1:C:121:ARG:HD2	3:C:3854:HOH:O	2.21	0.40
1:E:90:ASP:OD2	1:E:90:ASP:C	2.62	0.40
1:B:204:LYS:NZ	1:B:242:GLY:HA2	2.36	0.40
1:E:14:GLU:OE2	1:E:14:GLU:N	2.52	0.40
1:A:114:ARG:O	1:A:117:ILE:CG2	2.70	0.40
1:D:124:ILE:CG2	1:D:129:ALA:HB3	2.36	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	224/247 (91%)	217 (97%)	7 (3%)	0	100	100
1	B	236/247 (96%)	228 (97%)	7 (3%)	1 (0%)	30	27
1	C	227/247 (92%)	217 (96%)	10 (4%)	0	100	100
1	D	240/247 (97%)	228 (95%)	9 (4%)	3 (1%)	9	5
1	E	230/247 (93%)	221 (96%)	9 (4%)	0	100	100
1	F	230/247 (93%)	215 (94%)	15 (6%)	0	100	100
All	All	1387/1482 (94%)	1326 (96%)	57 (4%)	4 (0%)	36	35

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	184	VAL
1	D	103	GLU
1	D	180	GLY
1	B	180	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	197/209 (94%)	194 (98%)	3 (2%)	57	64
1	B	202/209 (97%)	197 (98%)	5 (2%)	42	45
1	C	199/209 (95%)	193 (97%)	6 (3%)	36	38
1	D	204/209 (98%)	199 (98%)	5 (2%)	42	45
1	E	201/209 (96%)	195 (97%)	6 (3%)	36	38
1	F	200/209 (96%)	192 (96%)	8 (4%)	28	27
All	All	1203/1254 (96%)	1170 (97%)	33 (3%)	39	42

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	83	LYS
1	A	102	TYR
1	A	136	SER
1	B	78	LYS
1	B	122	GLN
1	B	137	VAL
1	B	166	SER
1	B	177	ARG
1	C	3	ARG
1	C	34	THR
1	C	111	THR
1	C	113	ILE
1	C	136	SER
1	C	243	LYS
1	D	113	ILE

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Mol	Chain	Res	Type
1	D	136	SER
1	D	166	SER
1	D	200	ASP
1	D	240	LYS
1	E	130	LYS
1	E	137	VAL
1	E	213	ARG
1	E	239	LEU
1	E	240	LYS
1	E	245	LEU
1	F	14	GLU
1	F	72	GLN
1	F	98	LYS
1	F	104	LYS
1	F	144	LYS
1	F	193	ARG
1	F	240	LYS
1	F	241	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	62	HIS
1	A	108	HIS
1	B	68	GLN
1	B	72	GLN
1	B	186	HIS
1	C	68	GLN
1	D	46	ASN
1	D	68	GLN
1	D	69	ASN
1	E	72	GLN
1	E	108	HIS
1	F	68	GLN
1	F	72	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

6 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	ADP	D	3804	-	28,29,29	1.15	1 (3%)	43,45,45	1.74	8 (18%)
2	ADP	A	3801	-	28,29,29	1.08	2 (7%)	43,45,45	1.68	8 (18%)
2	ADP	B	3802	-	28,29,29	1.12	2 (7%)	43,45,45	1.72	8 (18%)
2	ADP	E	3805	-	28,29,29	1.12	3 (10%)	43,45,45	1.69	8 (18%)
2	ADP	C	3803	-	28,29,29	1.07	2 (7%)	43,45,45	1.69	8 (18%)
2	ADP	F	3806	-	28,29,29	1.16	3 (10%)	43,45,45	1.70	8 (18%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ADP	D	3804	-	-	1/16/32/32	0/3/3/3
2	ADP	A	3801	-	-	1/16/32/32	0/3/3/3
2	ADP	B	3802	-	-	1/16/32/32	0/3/3/3
2	ADP	E	3805	-	-	1/16/32/32	0/3/3/3
2	ADP	C	3803	-	-	1/16/32/32	0/3/3/3
2	ADP	F	3806	-	-	1/16/32/32	0/3/3/3

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	3803	ADP	C5-N7	-3.09	1.33	1.39
2	B	3802	ADP	C5-N7	-2.99	1.33	1.39
2	F	3806	ADP	C5-N7	-2.90	1.33	1.39
2	A	3801	ADP	C5-N7	-2.82	1.33	1.39
2	D	3804	ADP	C5-N7	-2.81	1.33	1.39
2	E	3805	ADP	C5-N7	-2.78	1.34	1.39
2	F	3806	ADP	PA-O3A	2.41	1.62	1.59
2	C	3803	ADP	C4-N9	-2.31	1.32	1.37
2	E	3805	ADP	PA-O3A	2.31	1.62	1.59
2	E	3805	ADP	C4-N9	-2.18	1.33	1.37
2	A	3801	ADP	C4-N9	-2.11	1.33	1.37
2	B	3802	ADP	C4-N9	-2.09	1.33	1.37
2	F	3806	ADP	C4-N9	-2.03	1.33	1.37

All (48) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	3804	ADP	C5-C4-N3	-5.22	119.53	126.72
2	B	3802	ADP	C5-C4-N3	-5.15	119.63	126.72
2	C	3803	ADP	N3-C2-N1	-5.10	120.86	128.58
2	F	3806	ADP	C5-C4-N3	-5.10	119.69	126.72
2	A	3801	ADP	N3-C2-N1	-5.09	120.88	128.58
2	E	3805	ADP	C5-C4-N3	-5.08	119.72	126.72
2	F	3806	ADP	N3-C2-N1	-5.06	120.92	128.58
2	D	3804	ADP	N3-C2-N1	-5.05	120.94	128.58
2	B	3802	ADP	N3-C2-N1	-5.01	121.00	128.58
2	C	3803	ADP	C5-C4-N3	-4.95	119.89	126.72
2	E	3805	ADP	N3-C2-N1	-4.94	121.10	128.58
2	A	3801	ADP	C5-C4-N3	-4.93	119.93	126.72
2	B	3802	ADP	N3-C4-N9	3.99	133.95	127.17
2	D	3804	ADP	N3-C4-N9	3.98	133.94	127.17
2	F	3806	ADP	N3-C4-N9	3.93	133.85	127.17
2	E	3805	ADP	N3-C4-N9	3.80	133.63	127.17
2	D	3804	ADP	C2-N3-C4	3.79	121.08	111.83
2	C	3803	ADP	N3-C4-N9	3.70	133.47	127.17
2	E	3805	ADP	C2-N3-C4	3.69	120.85	111.83
2	C	3803	ADP	C2-N3-C4	3.66	120.78	111.83
2	B	3802	ADP	C2-N3-C4	3.65	120.75	111.83
2	A	3801	ADP	N3-C4-N9	3.63	133.34	127.17
2	F	3806	ADP	C2-N3-C4	3.62	120.66	111.83
2	A	3801	ADP	C2-N3-C4	3.61	120.65	111.83
2	A	3801	ADP	N9-C8-N7	-2.95	109.75	113.94
2	C	3803	ADP	N9-C8-N7	-2.83	109.91	113.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	3805	ADP	N9-C8-N7	-2.81	109.94	113.94
2	D	3804	ADP	N9-C8-N7	-2.75	110.03	113.94
2	F	3806	ADP	N9-C8-N7	-2.67	110.14	113.94
2	D	3804	ADP	C5-N7-C8	2.67	107.64	103.45
2	B	3802	ADP	N9-C8-N7	-2.62	110.21	113.94
2	E	3805	ADP	C5-N7-C8	2.52	107.41	103.45
2	F	3806	ADP	C5-N7-C8	2.49	107.36	103.45
2	B	3802	ADP	C5-N7-C8	2.49	107.36	103.45
2	C	3803	ADP	C5-N7-C8	2.48	107.35	103.45
2	A	3801	ADP	C5-N7-C8	2.48	107.34	103.45
2	D	3804	ADP	C4-C5-N7	-2.45	107.78	110.58
2	E	3805	ADP	C4-C5-N7	-2.36	107.88	110.58
2	A	3801	ADP	C4-N9-C8	2.28	108.13	105.74
2	E	3805	ADP	C4-N9-C8	2.27	108.12	105.74
2	B	3802	ADP	C4-C5-N7	-2.26	108.00	110.58
2	C	3803	ADP	C4-N9-C8	2.25	108.10	105.74
2	C	3803	ADP	C4-C5-N7	-2.22	108.04	110.58
2	A	3801	ADP	C4-C5-N7	-2.20	108.07	110.58
2	B	3802	ADP	C4-N9-C8	2.19	108.04	105.74
2	F	3806	ADP	C4-C5-N7	-2.17	108.10	110.58
2	D	3804	ADP	C4-N9-C8	2.17	108.02	105.74
2	F	3806	ADP	C4-N9-C8	2.12	107.96	105.74

There are no chirality outliers.

All (6) torsion outliers are listed below:

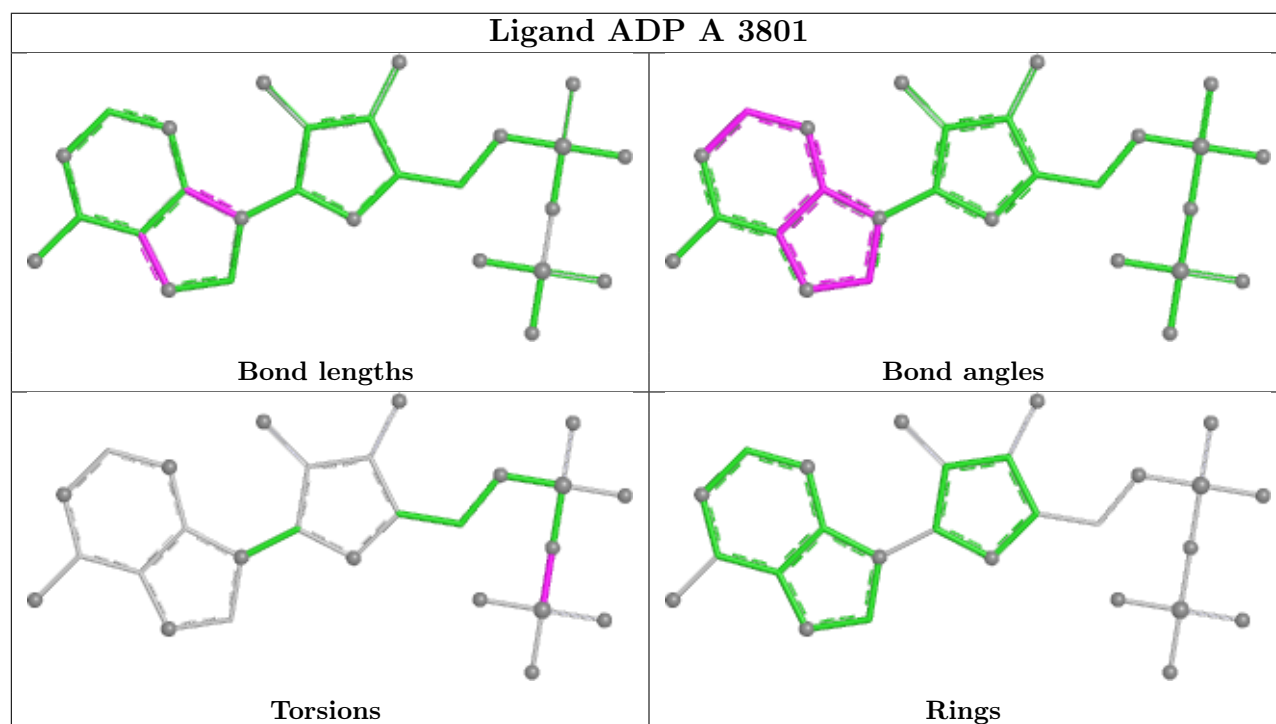
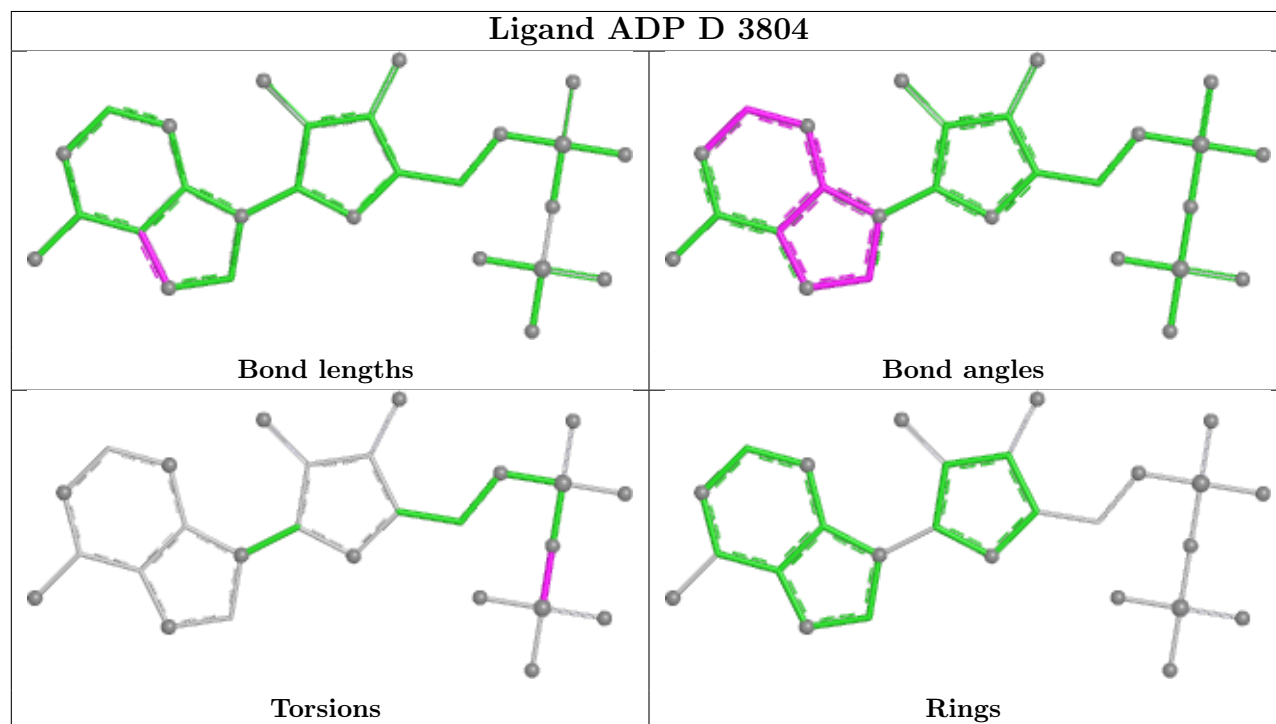
Mol	Chain	Res	Type	Atoms
2	C	3803	ADP	PA-O3A-PB-O2B
2	A	3801	ADP	PA-O3A-PB-O2B
2	D	3804	ADP	PA-O3A-PB-O2B
2	F	3806	ADP	PA-O3A-PB-O3B
2	B	3802	ADP	PA-O3A-PB-O1B
2	E	3805	ADP	PA-O3A-PB-O3B

There are no ring outliers.

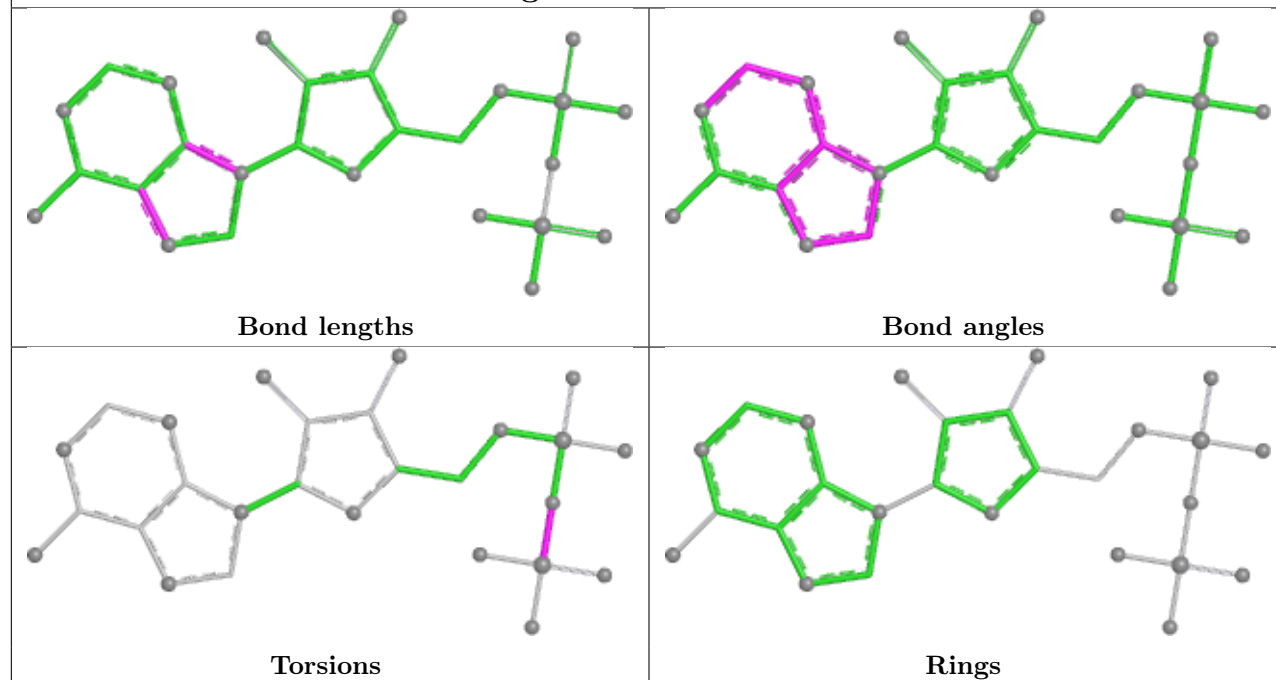
No monomer is involved in short contacts.

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.

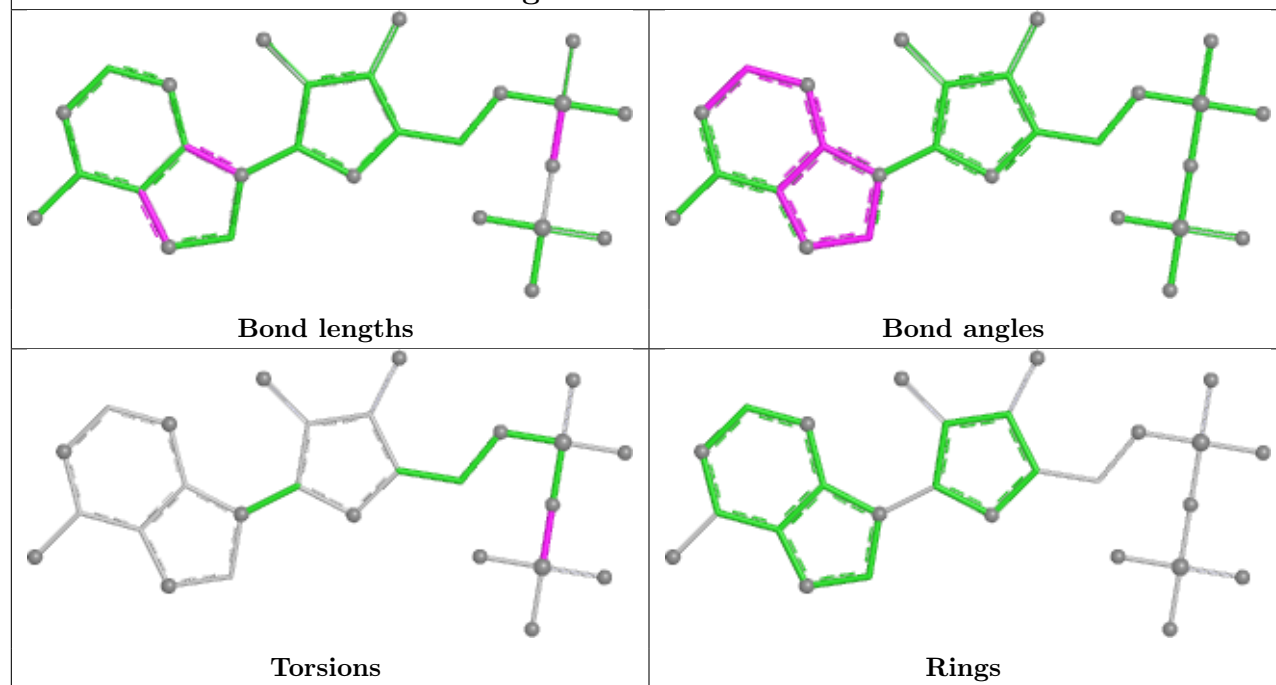
Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD 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.

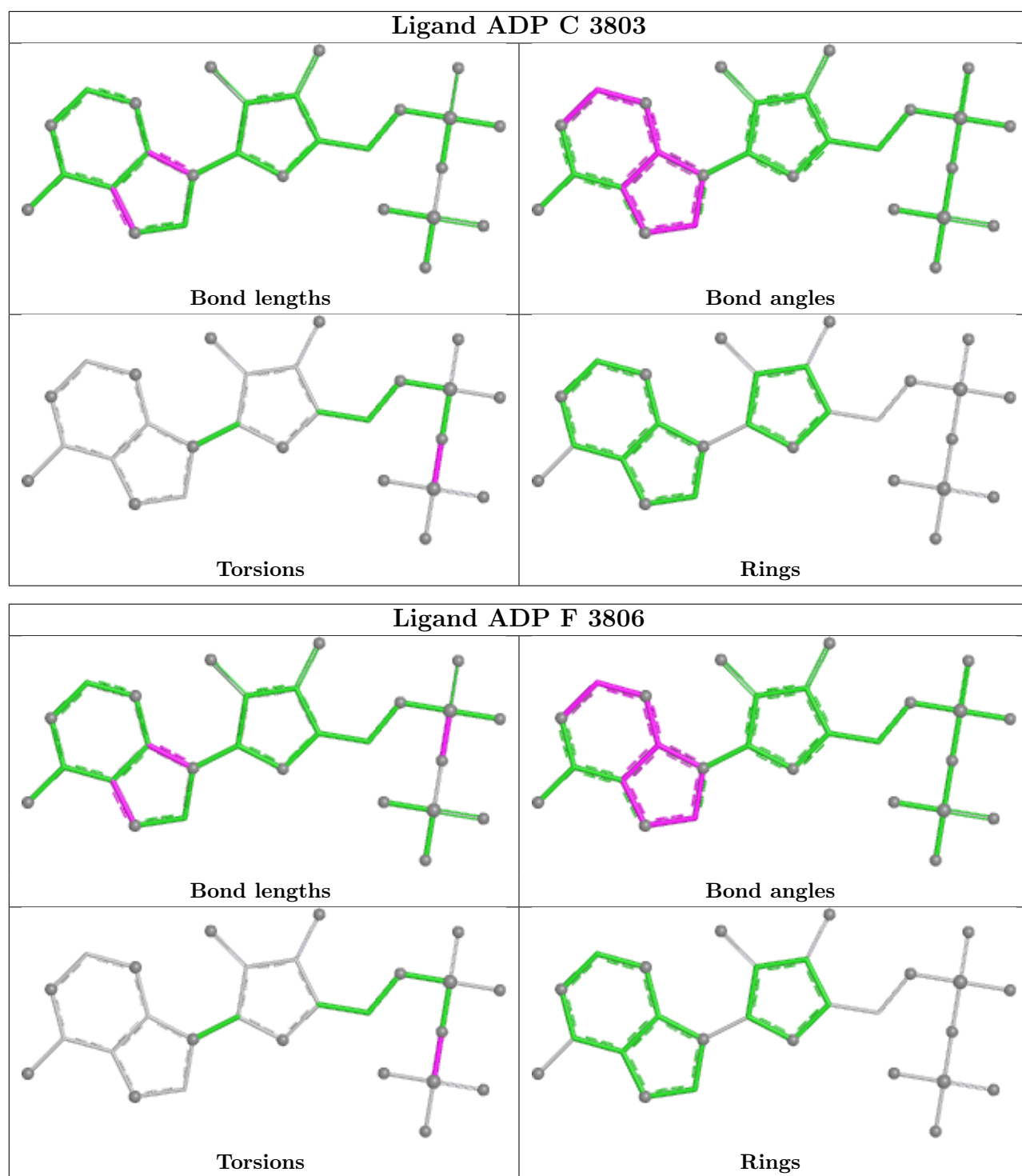


Ligand ADP B 3802



Ligand ADP E 3805





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	232/247 (93%)	1.20	52 (22%) 2 2	27, 50, 77, 97	0
1	B	240/247 (97%)	0.72	22 (9%) 14 13	26, 40, 63, 78	0
1	C	233/247 (94%)	0.69	14 (6%) 27 26	24, 40, 64, 80	0
1	D	242/247 (97%)	1.16	46 (19%) 3 3	27, 49, 74, 93	0
1	E	236/247 (95%)	0.95	33 (13%) 6 5	23, 43, 66, 83	0
1	F	236/247 (95%)	0.94	31 (13%) 7 6	27, 44, 69, 92	0
All	All	1419/1482 (95%)	0.94	198 (13%) 6 5	23, 44, 71, 97	0

All (198) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	174	VAL	6.0
1	F	182	PRO	5.9
1	A	183	GLY	5.4
1	E	183	GLY	5.3
1	B	174	VAL	5.1
1	D	71	ALA	5.0
1	E	244	VAL	5.0
1	D	128	ASN	4.7
1	B	182	PRO	4.7
1	D	182	PRO	4.6
1	C	102	TYR	4.4
1	D	174	VAL	4.4
1	E	175	GLY	4.2
1	A	102	TYR	4.2
1	F	243	LYS	4.2
1	E	245	LEU	4.2
1	F	102	TYR	4.0
1	E	243	LYS	3.9
1	D	69	ASN	3.7

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Mol	Chain	Res	Type	RSRZ
1	D	45	TRP	3.7
1	C	68	GLN	3.6
1	F	124	ILE	3.6
1	C	2	THR	3.6
1	F	129	ALA	3.6
1	F	128	ASN	3.6
1	A	182	PRO	3.6
1	D	129	ALA	3.5
1	A	110	LEU	3.5
1	B	175	GLY	3.5
1	C	97	GLY	3.4
1	A	69	ASN	3.4
1	C	213	ARG	3.4
1	D	85	MET	3.4
1	D	87	ALA	3.3
1	D	20	ILE	3.2
1	D	50	MET	3.2
1	B	183	GLY	3.2
1	B	244	VAL	3.2
1	D	102	TYR	3.2
1	B	213	ARG	3.2
1	A	22	GLU	3.2
1	E	182	PRO	3.2
1	A	5	VAL	3.2
1	A	105	TYR	3.2
1	A	161	GLY	3.2
1	D	51	GLY	3.2
1	A	53	PRO	3.2
1	C	112	ASP	3.1
1	B	243	LYS	3.1
1	E	128	ASN	3.1
1	F	66	VAL	3.1
1	D	48	LEU	3.1
1	A	85	MET	3.1
1	D	183	GLY	3.0
1	A	132	VAL	3.0
1	C	183	GLY	3.0
1	F	242	GLY	3.0
1	D	52	GLU	2.9
1	F	183	GLY	2.9
1	E	97	GLY	2.9
1	D	157	ARG	2.9

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Mol	Chain	Res	Type	RSRZ
1	E	82	GLU	2.9
1	A	124	ILE	2.9
1	B	173	SER	2.9
1	F	184	VAL	2.8
1	D	106	ILE	2.8
1	D	124	ILE	2.8
1	F	241	ARG	2.8
1	F	180	GLY	2.8
1	F	113	ILE	2.8
1	B	177	ARG	2.8
1	E	184	VAL	2.8
1	D	201	GLY	2.8
1	E	129	ALA	2.8
1	F	87	ALA	2.8
1	A	96	ILE	2.8
1	B	122	GLN	2.7
1	A	109	ASP	2.7
1	A	59	LEU	2.7
1	C	193	ARG	2.7
1	D	96	ILE	2.7
1	A	97	GLY	2.7
1	A	55	ILE	2.7
1	D	127	ILE	2.7
1	E	93	THR	2.7
1	A	80	TYR	2.7
1	E	102	TYR	2.7
1	A	113	ILE	2.7
1	D	242	GLY	2.7
1	D	2	THR	2.6
1	D	88	MET	2.6
1	D	9	ILE	2.6
1	A	123	ALA	2.6
1	A	184	VAL	2.6
1	A	98	LYS	2.6
1	D	120	LEU	2.6
1	F	112	ASP	2.6
1	A	166	SER	2.6
1	F	106	ILE	2.5
1	D	97	GLY	2.5
1	F	161	GLY	2.5
1	A	93	THR	2.5
1	A	136	SER	2.5

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Mol	Chain	Res	Type	RSRZ
1	D	103	GLU	2.5
1	F	77	VAL	2.5
1	A	71	ALA	2.5
1	A	235	PRO	2.5
1	C	79	PRO	2.5
1	F	160	ALA	2.5
1	E	78	LYS	2.5
1	D	238	VAL	2.5
1	D	176	GLU	2.5
1	A	104	LYS	2.5
1	B	242	GLY	2.5
1	D	46	ASN	2.5
1	A	107	VAL	2.4
1	A	103	GLU	2.4
1	A	120	LEU	2.4
1	E	18	GLY	2.4
1	A	106	ILE	2.4
1	E	110	LEU	2.4
1	D	84	GLY	2.4
1	D	112	ASP	2.4
1	E	79	PRO	2.4
1	B	71	ALA	2.4
1	A	95	GLY	2.4
1	D	113	ILE	2.4
1	A	111	THR	2.4
1	B	245	LEU	2.3
1	C	76	ASP	2.3
1	A	117	ILE	2.3
1	C	134	VAL	2.3
1	E	77	VAL	2.3
1	B	19	GLY	2.3
1	C	241	ARG	2.3
1	E	96	ILE	2.3
1	E	113	ILE	2.3
1	A	64	VAL	2.3
1	D	5	VAL	2.3
1	A	180	GLY	2.3
1	F	142	ILE	2.3
1	C	129	ALA	2.3
1	D	123	ALA	2.3
1	A	108	HIS	2.2
1	D	61	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	113	ILE	2.2
1	A	137	VAL	2.2
1	E	64	VAL	2.2
1	E	8	GLY	2.2
1	F	88	MET	2.2
1	E	105	TYR	2.2
1	B	108	HIS	2.2
1	A	86	PHE	2.2
1	D	104	LYS	2.2
1	E	22	GLU	2.2
1	F	162	THR	2.2
1	D	40	SER	2.2
1	E	49	LYS	2.2
1	A	20	ILE	2.1
1	B	246	GLU	2.1
1	E	124	ILE	2.1
1	F	51	GLY	2.1
1	D	80	TYR	2.1
1	A	210	TRP	2.1
1	A	116	PHE	2.1
1	D	55	ILE	2.1
1	D	86	PHE	2.1
1	A	158	VAL	2.1
1	B	160	ALA	2.1
1	F	94	ALA	2.1
1	D	44	LEU	2.1
1	D	99	SER	2.1
1	F	99	SER	2.1
1	B	72	GLN	2.1
1	B	97	GLY	2.1
1	E	127	ILE	2.1
1	F	96	ILE	2.1
1	E	73	PHE	2.1
1	B	184	VAL	2.1
1	E	25	VAL	2.1
1	E	123	ALA	2.1
1	A	173	SER	2.1
1	F	48	LEU	2.1
1	F	185	GLU	2.1
1	B	2	THR	2.1
1	F	240	LYS	2.1
1	A	87	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	147	MET	2.0
1	C	239	LEU	2.0
1	A	19	GLY	2.0
1	A	163	GLY	2.0
1	D	181	GLY	2.0
1	E	80	TYR	2.0
1	E	173	SER	2.0
1	A	91	ALA	2.0
1	F	75	TRP	2.0
1	A	3	ARG	2.0
1	F	63	PRO	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](#)

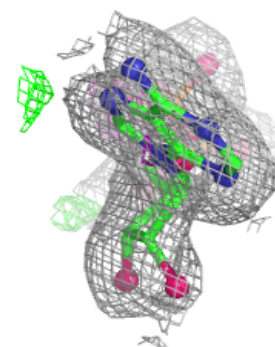
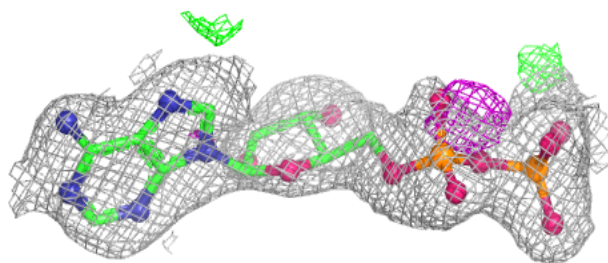
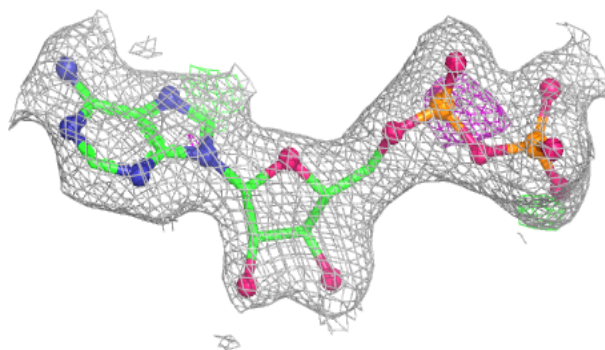
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists 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
2	ADP	D	3804	27/27	0.87	0.12	44,50,60,61	0
2	ADP	B	3802	27/27	0.88	0.13	36,55,63,63	0
2	ADP	E	3805	27/27	0.93	0.09	31,41,45,45	0
2	ADP	F	3806	27/27	0.93	0.09	35,44,48,49	0
2	ADP	A	3801	27/27	0.94	0.08	31,36,40,42	0
2	ADP	C	3803	27/27	0.95	0.07	30,35,40,42	0

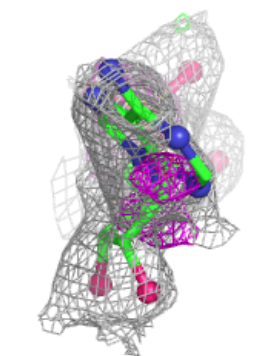
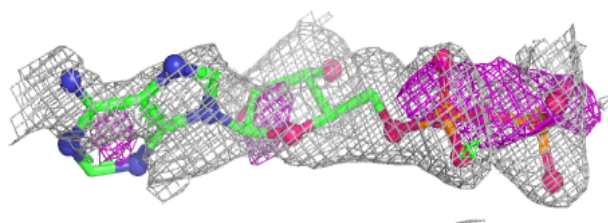
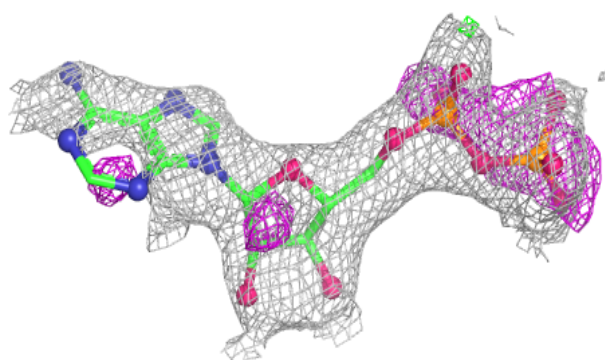
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around ADP D 3804:

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

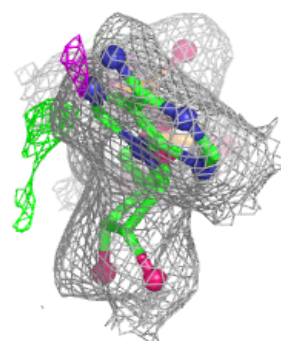
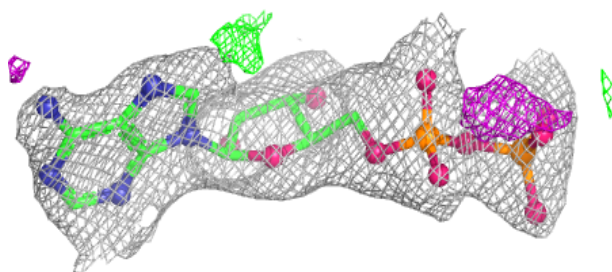
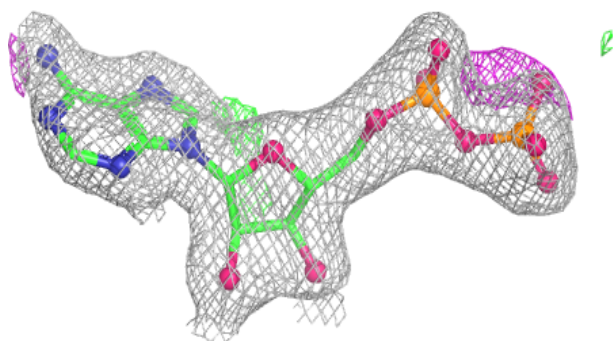
**Electron density around ADP B 3802:**

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

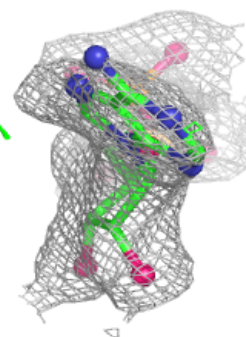
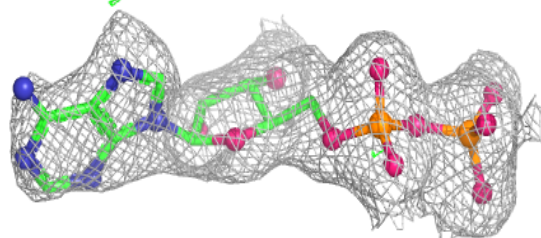
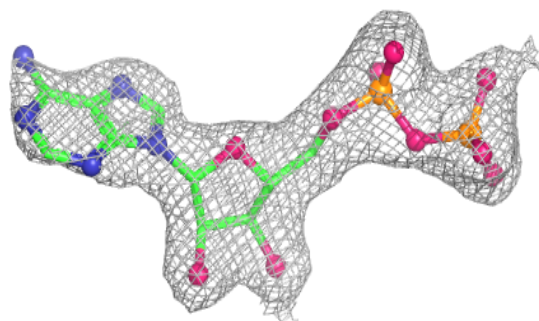


Electron density around ADP E 3805:

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

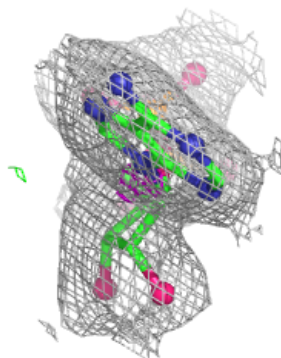
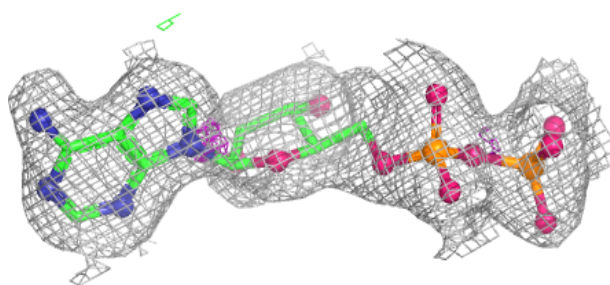
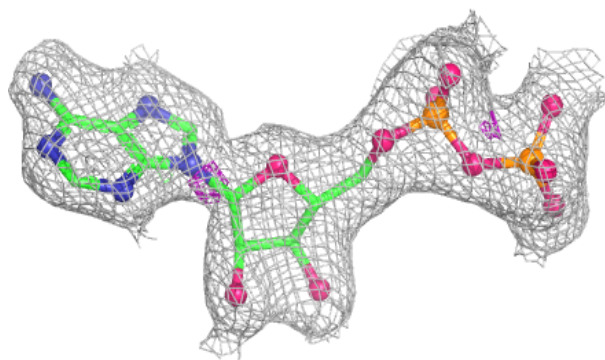
**Electron density around ADP F 3806:**

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

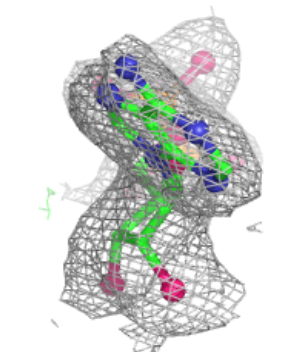
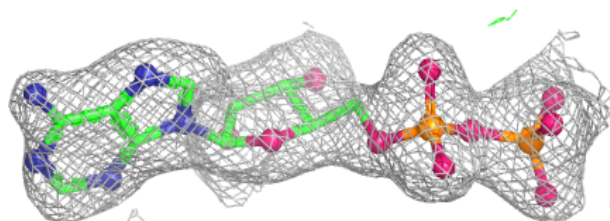
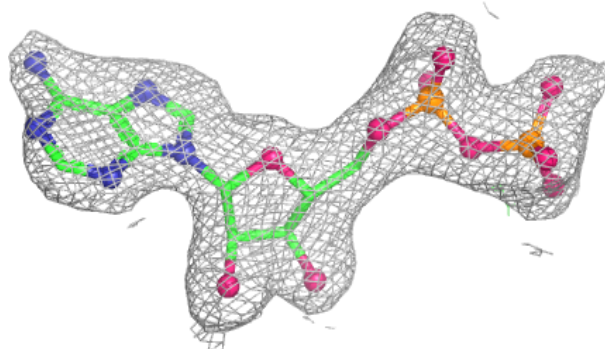


Electron density around ADP A 3801:

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

**Electron density around ADP C 3803:**

$2mF_o-DF_c$ (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.