



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 9, 2020 – 09:34 AM BST

PDB ID : 2AJ4
Title : Crystal structure of *Saccharomyces cerevisiae* Galactokinase in complex with galactose and Mg:AMPPNP
Authors : Thoden, J.B.; Sellick, C.A.; Timson, D.J.; Reece, R.J.; Holden, H.M.
Deposited on : 2005-08-01
Resolution : 2.40 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

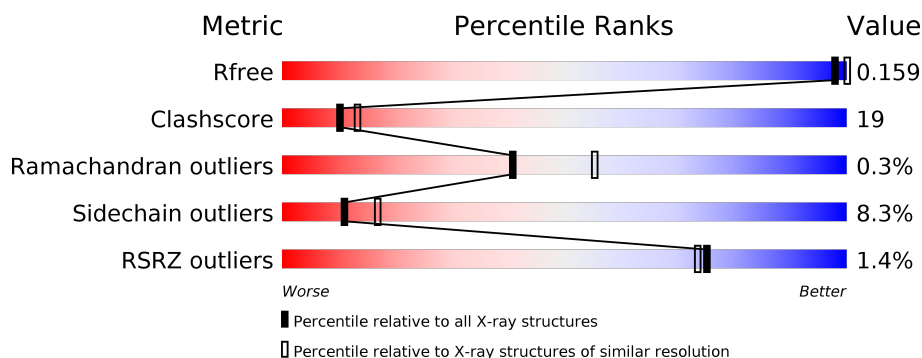
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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}	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria 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	548	<div> <div> <div>0%</div> <div>54%</div> <div>31%</div> <div>7%</div> <div>7%</div> </div> </div>
1	B	548	<div> <div>2%</div> <div>48%</div> <div>36%</div> <div>8%</div> <div>8%</div> </div>

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 8129 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 Galactokinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	509	Total	C	N	O	S	0	0	0
			3938	2517	656	742	23			
1	B	505	Total	C	N	O	S	0	0	0
			3910	2498	652	737	23			

There are 42 discrepancies between the modelled and reference sequences:

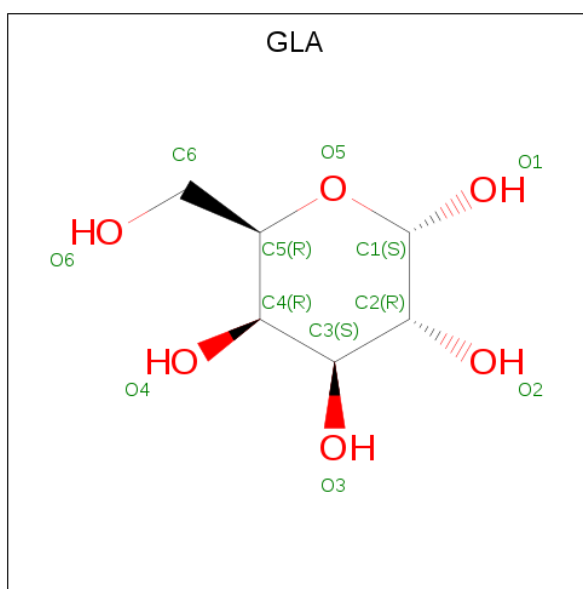
Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	cloning artifact	UNP P04385
A	-18	GLY	-	cloning artifact	UNP P04385
A	-17	SER	-	cloning artifact	UNP P04385
A	-16	SER	-	cloning artifact	UNP P04385
A	-15	HIS	-	expression tag	UNP P04385
A	-14	HIS	-	expression tag	UNP P04385
A	-13	HIS	-	expression tag	UNP P04385
A	-12	HIS	-	expression tag	UNP P04385
A	-11	HIS	-	expression tag	UNP P04385
A	-10	HIS	-	expression tag	UNP P04385
A	-9	SER	-	cloning artifact	UNP P04385
A	-8	SER	-	cloning artifact	UNP P04385
A	-7	GLU	-	cloning artifact	UNP P04385
A	-6	ASN	-	cloning artifact	UNP P04385
A	-5	LEU	-	cloning artifact	UNP P04385
A	-4	TYR	-	cloning artifact	UNP P04385
A	-3	PHE	-	cloning artifact	UNP P04385
A	-2	GLN	-	cloning artifact	UNP P04385
A	-1	GLY	-	cloning artifact	UNP P04385
A	0	HIS	-	cloning artifact	UNP P04385
A	1	MET	-	cloning artifact	UNP P04385
B	-19	MET	-	cloning artifact	UNP P04385
B	-18	GLY	-	cloning artifact	UNP P04385
B	-17	SER	-	cloning artifact	UNP P04385
B	-16	SER	-	cloning artifact	UNP P04385

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-15	HIS	-	expression tag	UNP P04385
B	-14	HIS	-	expression tag	UNP P04385
B	-13	HIS	-	expression tag	UNP P04385
B	-12	HIS	-	expression tag	UNP P04385
B	-11	HIS	-	expression tag	UNP P04385
B	-10	HIS	-	expression tag	UNP P04385
B	-9	SER	-	cloning artifact	UNP P04385
B	-8	SER	-	cloning artifact	UNP P04385
B	-7	GLU	-	cloning artifact	UNP P04385
B	-6	ASN	-	cloning artifact	UNP P04385
B	-5	LEU	-	cloning artifact	UNP P04385
B	-4	TYR	-	cloning artifact	UNP P04385
B	-3	PHE	-	cloning artifact	UNP P04385
B	-2	GLN	-	cloning artifact	UNP P04385
B	-1	GLY	-	cloning artifact	UNP P04385
B	0	HIS	-	cloning artifact	UNP P04385
B	1	MET	-	cloning artifact	UNP P04385

- Molecule 2 is alpha-D-galactopyranose (three-letter code: GLA) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			12	6	6		
2	B	1	Total	C	O	0	0
			12	6	6		

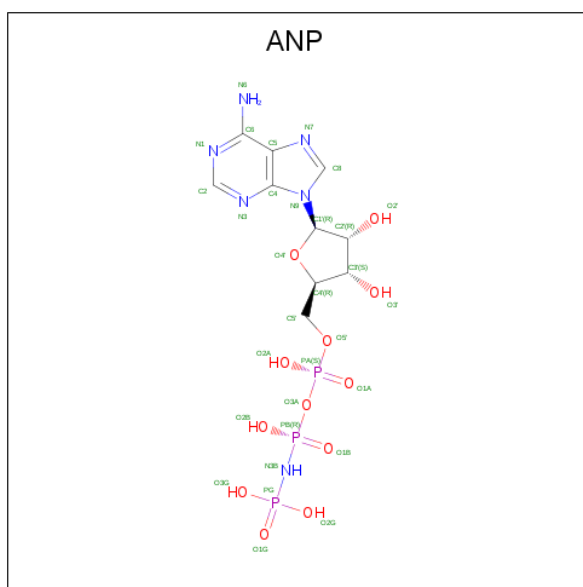
- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Mg 1 1	0	0
3	A	1	Total Mg 1 1	0	0

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total Cl 1 1	0	0
4	A	1	Total Cl 1 1	0	0

- Molecule 5 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (three-letter code: ANP) (formula: C₁₀H₁₇N₆O₁₂P₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C N O P 31 10 6 12 3	0	0
5	B	1	Total C N O P 31 10 6 12 3	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	106	Total O 106 106	0	0

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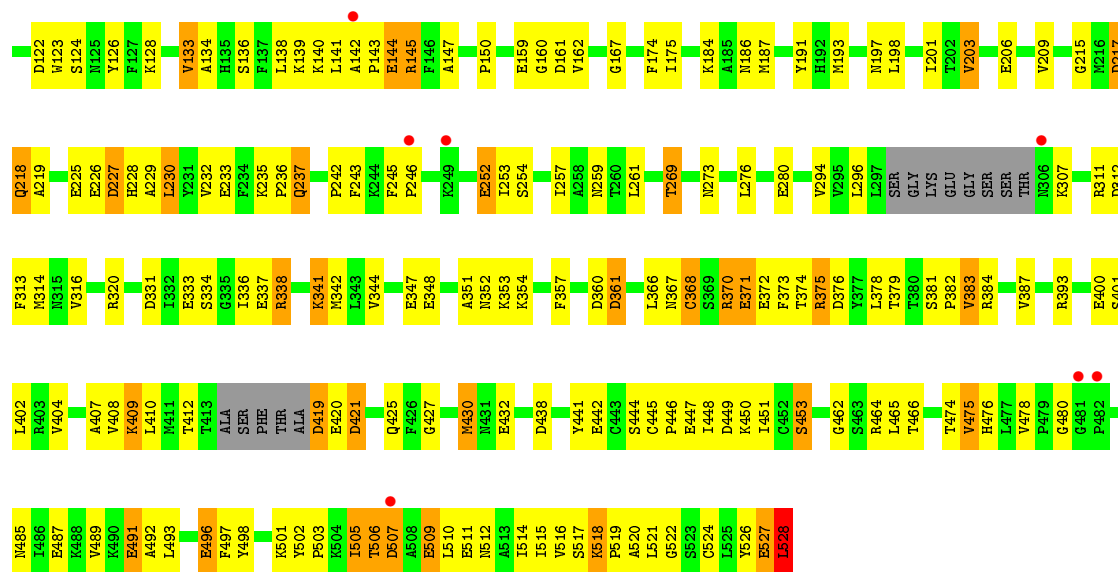
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	85	Total	O	0	0
			85	85		

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 ($\text{RSRZ} > 2$). 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.

Chain A: 

Chain B:

Amino Acid	Category
P44	Green
P45	Green
F46	Green
V47	Green
A48	Green
R49	Green
S50	Green
P51	Green
G52	Green
R53	Green
V54	Green
E59	Green
D62	Green
D65	Green
V68	Green
L69	Green
P70	Green
L71	Green
A72	Green
I73	Green
D74	Green
F75	Green
D76	Green
M77	Green
L78	Green
V81	Green
K82	Green
E86	Green
P89	Green
S90	Green
I91	Green
N95	Green
A96	Green
D97	Green
P98	Green
K99	Green
F100	Green
R103	Green
K104	Green
P105	Green
D106	Green
L107	Green
P108	Green
L109	Green
D110	Green
G111	Green
S112	Green
D117	Green
P118	Green
L119	Green
K120	Green
V11	Yellow
P12	Yellow
E13	Yellow
F14	Yellow
M15	Yellow
S16	Yellow
S17	Yellow
A18	Yellow
L19	Yellow
E20	Yellow
L21	Yellow
P22	Yellow
R23	Yellow
P24	Yellow
L25	Yellow
A26	Yellow
E27	Yellow
K28	Yellow
C29	Yellow
P30	Yellow
S31	Yellow
I32	Yellow
I33	Yellow
F36	Yellow
I37	Yellow
D41	Yellow
A42	Yellow
K43	Yellow



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	63.30Å 85.00Å 112.30Å 90.00° 96.70° 90.00°	Depositor
Resolution (Å)	30.00 – 2.40 29.48 – 2.40	Depositor EDS
% Data completeness (in resolution range)	95.5 (30.00-2.40) 95.5 (29.48-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.75 (at 2.39Å)	Xtriage
Refinement program	TNT	Depositor
R, R_{free}	0.172 , 0.205 0.164 , 0.159	Depositor DCC
R_{free} test set	4490 reflections (10.12%)	wwPDB-VP
Wilson B-factor (Å ²)	25.1	Xtriage
Anisotropy	0.356	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 103.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	8129	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.44% 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: GLA, MG, ANP, CL

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	0.99	29/4022 (0.7%)	1.41	48/5451 (0.9%)
1	B	1.02	31/3993 (0.8%)	1.39	49/5411 (0.9%)
All	All	1.00	60/8015 (0.7%)	1.40	97/10862 (0.9%)

All (60) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	528	LEU	C-OXT	16.33	1.54	1.23
1	A	528	LEU	C-OXT	9.71	1.41	1.23
1	B	528	LEU	C-O	-8.77	1.06	1.23
1	A	333	GLU	CD-OE2	7.24	1.33	1.25
1	B	491	GLU	CD-OE2	7.23	1.33	1.25
1	A	144	GLU	CD-OE2	7.06	1.33	1.25
1	B	252	GLU	CD-OE2	6.85	1.33	1.25
1	A	20	GLU	CD-OE2	6.82	1.33	1.25
1	A	400	GLU	CD-OE2	6.71	1.33	1.25
1	A	159	GLU	CD-OE2	6.64	1.32	1.25
1	A	280	GLU	CD-OE2	6.57	1.32	1.25
1	A	527	GLU	CD-OE2	6.55	1.32	1.25
1	A	511	GLU	CD-OE2	6.53	1.32	1.25
1	B	206	GLU	CD-OE2	6.50	1.32	1.25
1	B	447	GLU	CD-OE2	6.47	1.32	1.25
1	A	27	GLU	CD-OE2	6.45	1.32	1.25
1	B	348	GLU	CD-OE2	6.45	1.32	1.25
1	A	372	GLU	CD-OE2	6.43	1.32	1.25
1	B	511	GLU	CD-OE2	6.43	1.32	1.25
1	B	337	GLU	CD-OE2	6.24	1.32	1.25
1	A	252	GLU	CD-OE2	6.23	1.32	1.25
1	A	13	GLU	CD-OE2	6.21	1.32	1.25
1	A	226	GLU	CD-OE2	6.20	1.32	1.25
1	B	159	GLU	CD-OE2	6.19	1.32	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	527	GLU	CD-OE2	6.19	1.32	1.25
1	B	400	GLU	CD-OE2	6.18	1.32	1.25
1	B	487	GLU	CD-OE2	6.17	1.32	1.25
1	B	333	GLU	CD-OE2	6.14	1.32	1.25
1	B	13	GLU	CD-OE2	6.12	1.32	1.25
1	B	20	GLU	CD-OE2	6.12	1.32	1.25
1	B	432	GLU	CD-OE2	6.12	1.32	1.25
1	A	206	GLU	CD-OE2	6.11	1.32	1.25
1	B	27	GLU	CD-OE2	6.08	1.32	1.25
1	A	432	GLU	CD-OE2	6.00	1.32	1.25
1	B	144	GLU	CD-OE2	5.90	1.32	1.25
1	A	348	GLU	CD-OE2	5.88	1.32	1.25
1	B	371	GLU	CD-OE2	5.88	1.32	1.25
1	A	233	GLU	CD-OE2	5.87	1.32	1.25
1	A	447	GLU	CD-OE2	5.85	1.32	1.25
1	A	420	GLU	CD-OE2	5.85	1.32	1.25
1	B	86	GLU	CD-OE2	5.84	1.32	1.25
1	A	225	GLU	CD-OE2	5.83	1.32	1.25
1	B	496	GLU	CD-OE2	5.82	1.32	1.25
1	B	420	GLU	CD-OE2	5.81	1.32	1.25
1	A	491	GLU	CD-OE2	5.78	1.32	1.25
1	B	225	GLU	CD-OE2	5.78	1.32	1.25
1	A	337	GLU	CD-OE2	5.78	1.32	1.25
1	B	226	GLU	CD-OE2	5.71	1.31	1.25
1	A	371	GLU	CD-OE2	5.69	1.31	1.25
1	B	528	LEU	CA-C	5.59	1.67	1.52
1	A	487	GLU	CD-OE2	5.56	1.31	1.25
1	A	86	GLU	CD-OE2	5.52	1.31	1.25
1	B	509	GLU	CD-OE2	5.39	1.31	1.25
1	B	372	GLU	CD-OE2	5.37	1.31	1.25
1	B	233	GLU	CD-OE2	5.30	1.31	1.25
1	A	496	GLU	CD-OE2	5.29	1.31	1.25
1	B	442	GLU	CD-OE2	5.14	1.31	1.25
1	A	268	GLU	CD-OE2	5.12	1.31	1.25
1	A	509	GLU	CD-OE2	5.03	1.31	1.25
1	B	280	GLU	CD-OE2	5.00	1.31	1.25

All (97) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	53	ARG	NE-CZ-NH1	14.32	127.46	120.30
1	A	528	LEU	CB-CA-C	-11.15	89.02	110.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	393	ARG	NE-CZ-NH1	9.34	124.97	120.30
1	B	53	ARG	NE-CZ-NH1	9.32	124.96	120.30
1	B	117	ASP	CB-CG-OD1	9.12	126.50	118.30
1	A	62	ASP	CB-CG-OD1	8.52	125.96	118.30
1	B	62	ASP	CB-CG-OD2	-8.51	110.64	118.30
1	B	103	ARG	NE-CZ-NH1	8.47	124.53	120.30
1	B	528	LEU	CA-C-O	8.43	137.80	120.10
1	A	122	ASP	CB-CG-OD2	-8.36	110.78	118.30
1	B	117	ASP	CB-CG-OD2	-8.33	110.80	118.30
1	B	161	ASP	CB-CG-OD2	-8.17	110.95	118.30
1	A	62	ASP	CB-CG-OD2	-8.05	111.05	118.30
1	B	528	LEU	CB-CA-C	-8.03	94.95	110.20
1	A	53	ARG	NE-CZ-NH2	-8.01	116.29	120.30
1	A	277	ARG	NE-CZ-NH1	8.01	124.31	120.30
1	B	62	ASP	CB-CG-OD1	7.83	125.35	118.30
1	A	376	ASP	CB-CG-OD2	-7.82	111.26	118.30
1	B	122	ASP	CB-CG-OD2	-7.56	111.50	118.30
1	B	161	ASP	CB-CG-OD1	7.54	125.08	118.30
1	B	65	ASP	CB-CG-OD1	7.33	124.90	118.30
1	A	103	ARG	NE-CZ-NH1	7.22	123.91	120.30
1	A	393	ARG	NE-CZ-NH1	7.18	123.89	120.30
1	B	65	ASP	CB-CG-OD2	-7.17	111.84	118.30
1	A	331	ASP	CB-CG-OD1	7.15	124.73	118.30
1	A	376	ASP	CB-CG-OD1	7.14	124.73	118.30
1	B	368	CYS	N-CA-CB	-7.10	97.82	110.60
1	A	122	ASP	CB-CG-OD1	6.87	124.48	118.30
1	B	97	ASP	CB-CG-OD1	6.86	124.47	118.30
1	B	122	ASP	CB-CG-OD1	6.85	124.46	118.30
1	B	312	ASP	CB-CG-OD2	-6.77	112.21	118.30
1	B	376	ASP	CB-CG-OD2	-6.76	112.22	118.30
1	A	117	ASP	CB-CG-OD2	-6.65	112.32	118.30
1	B	421	ASP	CB-CG-OD2	-6.58	112.38	118.30
1	A	313	PHE	CB-CG-CD1	6.55	125.38	120.80
1	A	419	ASP	CB-CG-OD2	-6.46	112.49	118.30
1	B	421	ASP	CB-CG-OD1	6.43	124.09	118.30
1	A	97	ASP	CB-CG-OD2	-6.42	112.52	118.30
1	B	106	ASP	CB-CG-OD2	-6.41	112.53	118.30
1	A	421	ASP	CB-CG-OD2	-6.41	112.53	118.30
1	A	227	ASP	CB-CG-OD2	-6.33	112.60	118.30
1	B	438	ASP	CB-CG-OD2	-6.30	112.63	118.30
1	B	227	ASP	CB-CG-OD2	-6.25	112.67	118.30
1	A	106	ASP	CB-CG-OD2	-6.23	112.69	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	360	ASP	CB-CG-OD2	-6.23	112.70	118.30
1	A	384	ARG	NE-CZ-NH1	6.21	123.41	120.30
1	A	368	CYS	N-CA-CB	-6.18	99.48	110.60
1	A	507	ASP	CB-CG-OD2	-6.07	112.84	118.30
1	B	528	LEU	N-CA-CB	6.01	122.42	110.40
1	B	117	ASP	N-CA-CB	5.99	121.39	110.60
1	B	384	ARG	NE-CZ-NH1	5.96	123.28	120.30
1	A	312	ASP	CB-CG-OD1	5.92	123.63	118.30
1	A	45	ASP	CB-CG-OD2	-5.90	112.99	118.30
1	A	449	ASP	CB-CG-OD2	-5.89	113.00	118.30
1	B	331	ASP	CB-CG-OD1	5.88	123.59	118.30
1	A	331	ASP	CB-CG-OD2	-5.83	113.06	118.30
1	A	227	ASP	CB-CG-OD1	5.80	123.52	118.30
1	B	361	ASP	CB-CG-OD2	-5.79	113.08	118.30
1	A	117	ASP	CB-CG-OD1	5.76	123.49	118.30
1	A	161	ASP	CB-CG-OD2	-5.75	113.12	118.30
1	B	97	ASP	CB-CG-OD2	-5.75	113.13	118.30
1	B	45	ASP	CB-CG-OD2	-5.70	113.17	118.30
1	B	106	ASP	CB-CG-OD1	5.69	123.42	118.30
1	A	320	ARG	NE-CZ-NH1	5.68	123.14	120.30
1	A	449	ASP	CB-CG-OD1	5.68	123.41	118.30
1	B	217	ASP	CB-CG-OD1	5.67	123.40	118.30
1	B	320	ARG	NE-CZ-NH1	5.63	123.12	120.30
1	A	103	ARG	NE-CZ-NH2	-5.55	117.52	120.30
1	B	419	ASP	CB-CG-OD1	5.55	123.30	118.30
1	B	419	ASP	CB-CG-OD2	-5.49	113.36	118.30
1	A	512	ASN	CB-CA-C	5.48	121.37	110.40
1	A	528	LEU	N-CA-C	5.47	125.76	111.00
1	B	269	THR	CA-CB-CG2	-5.46	104.76	112.40
1	A	71	LEU	N-CA-CB	-5.44	99.52	110.40
1	A	507	ASP	CB-CG-OD1	5.43	123.19	118.30
1	A	419	ASP	CB-CG-OD1	5.42	123.18	118.30
1	A	311	ARG	NE-CZ-NH1	5.40	123.00	120.30
1	A	277	ARG	NE-CZ-NH2	-5.39	117.60	120.30
1	B	74	ASP	CB-CG-OD2	-5.39	113.45	118.30
1	B	507	ASP	CB-CG-OD2	-5.38	113.45	118.30
1	B	449	ASP	CB-CG-OD2	-5.35	113.48	118.30
1	A	217	ASP	CB-CG-OD2	-5.35	113.49	118.30
1	B	449	ASP	CB-CG-OD1	5.31	123.08	118.30
1	A	393	ARG	NE-CZ-NH2	-5.29	117.65	120.30
1	B	311	ARG	NE-CZ-NH1	5.20	122.90	120.30
1	B	376	ASP	CB-CG-OD1	5.17	122.96	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	110	ASP	CB-CG-OD1	5.11	122.90	118.30
1	A	515	ILE	CB-CA-C	-5.11	101.38	111.60
1	B	375	ARG	NE-CZ-NH2	-5.10	117.75	120.30
1	B	438	ASP	CB-CG-OD1	5.09	122.88	118.30
1	A	65	ASP	CB-CG-OD2	-5.08	113.73	118.30
1	B	312	ASP	CB-CG-OD1	5.08	122.87	118.30
1	B	338	ARG	NE-CZ-NH1	5.08	122.84	120.30
1	B	74	ASP	CB-CG-OD1	5.04	122.83	118.30
1	B	370	ARG	NE-CZ-NH1	5.04	122.82	120.30
1	A	65	ASP	CB-CG-OD1	5.02	122.82	118.30
1	A	384	ARG	NE-CZ-NH2	-5.01	117.79	120.30

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	3938	0	3924	130	0
1	B	3910	0	3898	166	0
2	A	12	0	12	1	0
2	B	12	0	12	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	31	0	13	2	0
5	B	31	0	13	3	0
6	A	106	0	0	2	0
6	B	85	0	0	1	0
All	All	8129	0	7872	297	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 19.

All (297) 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:203:VAL:HG22	1:B:215:GLY:HA3	1.42	0.98
1:B:218:GLN:HE21	1:B:218:GLN:H	1.11	0.95
1:A:218:GLN:NE2	1:A:218:GLN:H	1.67	0.93
1:B:218:GLN:NE2	1:B:218:GLN:H	1.66	0.92
1:B:505:ILE:HD13	1:B:510:LEU:HD12	1.53	0.89
1:B:353:LYS:NZ	1:B:361:ASP:HB3	1.89	0.88
1:A:218:GLN:HE21	1:A:218:GLN:H	1.13	0.88
1:A:480:GLY:HA2	1:A:486:ILE:HD12	1.60	0.82
1:B:353:LYS:HZ2	1:B:361:ASP:HB3	1.45	0.80
1:B:404:VAL:O	1:B:408:VAL:HG23	1.82	0.79
1:A:49:ARG:HB2	1:A:78:LEU:CD2	2.13	0.78
1:B:334:SER:O	1:B:338:ARG:HG3	1.84	0.77
1:B:245:PHE:HB3	1:B:246:PRO:HD2	1.66	0.77
1:A:21:LEU:HD22	1:A:22:PRO:HD2	1.67	0.75
1:B:506:THR:HG23	1:B:509:GLU:OE1	1.87	0.75
1:B:374:THR:O	1:B:379:THR:HG23	1.87	0.74
1:B:36:PHE:CZ	1:B:82:LYS:HB2	2.23	0.74
1:A:117:ASP:OD1	1:A:119:SER:HB3	1.88	0.73
1:B:29:CYS:O	1:B:33:ILE:HD12	1.88	0.73
1:A:412:THR:HG22	1:A:413:THR:HG23	1.70	0.72
1:B:445:CYS:HB2	1:B:446:PRO:HD2	1.71	0.71
1:B:193:MET:HE3	1:B:198:LEU:HD13	1.72	0.71
1:A:296:LEU:O	1:A:297:LEU:HD23	1.90	0.71
1:B:12:PRO:HB2	1:B:14:PHE:CE1	2.26	0.71
1:B:276:LEU:HD13	1:B:383:VAL:HG13	1.72	0.71
1:B:49:ARG:HG2	1:B:50:SER:N	2.05	0.71
1:B:43:LYS:O	1:B:82:LYS:HE3	1.91	0.70
1:B:49:ARG:HB2	1:B:78:LEU:CD2	2.20	0.70
1:A:332:ILE:HD11	1:A:408:VAL:HG11	1.72	0.70
1:A:23:ARG:HB3	1:A:24:PRO:HD3	1.72	0.69
1:B:505:ILE:HD13	1:B:510:LEU:CD1	2.21	0.69
1:B:108:PRO:HG2	1:B:112:SER:O	1.93	0.69
1:B:485:ASN:O	1:B:489:VAL:HG23	1.91	0.68
1:A:408:VAL:O	1:A:412:THR:HB	1.92	0.68
1:A:54:VAL:CG2	1:A:73:ILE:HG21	2.24	0.67
1:B:10:ILE:O	1:B:10:ILE:HD12	1.95	0.67
1:A:330:GLY:O	1:A:331:ASP:C	2.32	0.66
1:A:466:THR:HB	1:A:475:VAL:HG22	1.78	0.66
1:A:49:ARG:HB2	1:A:78:LEU:HD21	1.78	0.66
1:B:111:GLY:O	1:B:139:LYS:NZ	2.29	0.65
1:B:421:ASP:O	1:B:425:GLN:HG3	1.96	0.65
1:B:53:ARG:NH2	1:B:167:GLY:O	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:502:TYR:O	1:B:505:ILE:HB	1.97	0.65
1:B:36:PHE:HZ	1:B:82:LYS:HB2	1.59	0.65
1:A:53:ARG:NH2	1:A:167:GLY:O	2.30	0.64
1:A:45:ASP:O	1:A:528:LEU:HB2	1.98	0.64
1:A:466:THR:HB	1:A:475:VAL:CG2	2.27	0.64
1:B:448:ILE:HD13	1:B:465:LEU:HB3	1.79	0.64
1:B:498:TYR:CE1	1:B:514:ILE:HD11	2.32	0.64
1:B:184:LYS:NZ	1:B:527:GLU:HG2	2.12	0.64
1:A:110:ASP:OD1	1:A:112:SER:N	2.30	0.64
1:A:187:MET:HB3	1:A:191:TYR:CB	2.27	0.63
1:A:184:LYS:NZ	1:A:191:TYR:O	2.31	0.63
1:A:21:LEU:CD2	1:A:22:PRO:HD2	2.28	0.63
1:B:126:TYR:CE2	5:B:532:ANP:H4'	2.34	0.63
1:B:22:PRO:O	1:B:25:LEU:HB2	1.99	0.62
1:B:493:LEU:O	1:B:497:PHE:N	2.30	0.62
1:B:498:TYR:HE1	1:B:514:ILE:HD11	1.65	0.62
1:A:336:ILE:HG23	1:A:402:LEU:HD11	1.82	0.62
1:B:197:ASN:O	1:B:201:ILE:HG12	1.98	0.62
1:B:86:GLU:OE1	1:B:89:PRO:HA	2.00	0.62
1:A:111:GLY:O	1:A:139:LYS:NZ	2.33	0.61
1:B:336:ILE:HG23	1:B:402:LEU:HD11	1.83	0.60
1:B:109:LEU:O	1:B:150:PRO:HD3	2.01	0.60
1:A:12:PRO:HB2	1:A:14:PHE:CE1	2.37	0.60
1:A:480:GLY:HA2	1:A:486:ILE:CD1	2.30	0.60
1:A:109:LEU:HA	1:A:150:PRO:HG3	1.82	0.59
1:B:29:CYS:C	1:B:33:ILE:HD12	2.23	0.59
1:B:51:PRO:HG3	1:B:521:LEU:O	2.02	0.59
1:B:341:LYS:O	1:B:344:VAL:HB	2.01	0.59
1:B:184:LYS:HZ3	1:B:527:GLU:HG2	1.65	0.59
1:A:31:SER:O	1:A:35:LYS:HG3	2.01	0.59
1:A:54:VAL:HG21	1:A:73:ILE:HG21	1.85	0.58
1:A:30:PRO:O	1:A:34:LYS:HG3	2.02	0.58
1:B:506:THR:O	1:B:509:GLU:HB2	2.04	0.58
1:A:218:GLN:HE21	1:A:218:GLN:N	1.95	0.57
1:B:501:LYS:C	1:B:503:PRO:HD3	2.24	0.57
1:B:466:THR:HB	1:B:475:VAL:HG22	1.86	0.57
1:B:526:TYR:CE2	1:B:528:LEU:HD23	2.39	0.57
1:B:218:GLN:HE21	1:B:218:GLN:N	1.94	0.56
1:A:44:PRO:HG2	1:A:528:LEU:HD12	1.87	0.56
1:A:332:ILE:HD11	1:A:408:VAL:CG1	2.36	0.56
1:A:44:PRO:HG2	1:A:528:LEU:CD1	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:46:PHE:CD1	1:A:525:LEU:HD21	2.40	0.56
1:B:97:ASP:OD2	1:B:98:PRO:HD2	2.06	0.56
1:A:123:TRP:CE3	5:A:532:ANP:H2	2.41	0.56
1:B:218:GLN:NE2	1:B:218:GLN:N	2.47	0.56
1:B:314:MET:HA	1:B:342:MET:CE	2.36	0.55
1:B:53:ARG:NH1	1:B:217:ASP:OD1	2.38	0.55
1:B:140:LYS:O	1:B:143:PRO:HD3	2.06	0.55
1:B:126:TYR:HD1	1:B:175:ILE:HD11	1.71	0.55
1:A:410:LEU:HD22	1:A:416:PHE:CZ	2.42	0.55
1:B:139:LYS:HE3	1:B:147:ALA:HA	1.89	0.55
1:B:123:TRP:CE3	5:B:532:ANP:H2	2.42	0.55
1:A:77:MET:HG2	1:A:174:PHE:HA	1.89	0.55
1:A:338:ARG:O	1:A:341:LYS:HB3	2.07	0.55
1:A:51:PRO:HG3	1:A:521:LEU:O	2.06	0.55
1:A:122:ASP:O	1:A:125:ASN:HB2	2.07	0.55
1:B:59:GLU:HB2	1:B:464:ARG:NH2	2.22	0.55
1:A:49:ARG:HG2	1:A:50:SER:N	2.22	0.54
1:B:237:GLN:OE1	1:B:237:GLN:HA	2.07	0.54
1:A:54:VAL:HG23	1:A:73:ILE:HG21	1.87	0.54
1:B:68:VAL:HG23	1:B:232:VAL:HB	1.89	0.54
1:A:49:ARG:HB2	1:A:78:LEU:HD23	1.90	0.54
1:B:371:GLU:O	1:B:375:ARG:HG3	2.07	0.54
1:B:75:PHE:HB3	1:B:162:VAL:HG22	1.90	0.54
1:B:9:VAL:HG12	1:B:10:ILE:N	2.23	0.54
1:A:412:THR:CG2	1:A:413:THR:HG23	2.37	0.53
1:B:141:LEU:C	1:B:143:PRO:HD3	2.29	0.53
1:A:29:CYS:HB2	1:A:30:PRO:HD3	1.88	0.53
1:B:117:ASP:OD1	1:B:119:SER:N	2.33	0.53
1:B:68:VAL:C	1:B:70:PRO:HD3	2.29	0.53
1:B:91:ILE:O	1:B:104:LYS:HA	2.07	0.53
1:A:97:ASP:OD2	1:A:98:PRO:HD2	2.09	0.53
1:B:23:ARG:O	1:B:24:PRO:C	2.46	0.53
1:B:276:LEU:HD13	1:B:383:VAL:CG1	2.38	0.53
1:B:444:SER:HB3	6:B:570:HOH:O	2.08	0.53
1:A:69:LEU:HD12	1:A:230:LEU:O	2.09	0.52
1:B:466:THR:HB	1:B:475:VAL:CG2	2.38	0.52
1:B:44:PRO:O	1:B:528:LEU:HD12	2.08	0.52
1:B:54:VAL:HG21	1:B:257:ILE:CD1	2.40	0.52
1:A:234:PHE:O	1:A:235:LYS:HG2	2.08	0.52
1:B:12:PRO:O	1:B:524:CYS:HB2	2.09	0.52
1:B:95:ASN:HB2	1:B:123:TRP:CH2	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:526:TYR:HE2	1:B:528:LEU:CD2	2.23	0.52
1:A:18:ALA:O	1:A:20:GLU:N	2.43	0.51
1:A:203:VAL:HB	1:A:215:GLY:HA3	1.92	0.51
1:A:54:VAL:HG23	1:A:73:ILE:CG2	2.41	0.51
1:B:313:PHE:CD2	1:B:342:MET:HE3	2.46	0.51
1:B:526:TYR:HE2	1:B:528:LEU:HD23	1.76	0.51
1:A:86:GLU:OE1	1:A:89:PRO:HA	2.11	0.51
1:A:351:ALA:O	1:A:354:LYS:HG3	2.11	0.51
1:B:259:ASN:OD1	1:B:261:LEU:N	2.30	0.51
1:A:277:ARG:HD2	1:A:441:TYR:CE2	2.47	0.50
1:A:229:ALA:O	1:A:242:PRO:HA	2.12	0.50
1:A:254:SER:OG	1:A:480:GLY:HA3	2.11	0.50
1:A:86:GLU:OE1	1:A:153:GLY:HA3	2.11	0.50
1:A:29:CYS:N	1:A:30:PRO:HD2	2.26	0.50
1:B:54:VAL:HG21	1:B:257:ILE:HD11	1.94	0.50
1:A:200:ARG:HG2	1:A:200:ARG:HH11	1.77	0.50
1:A:410:LEU:HD22	1:A:416:PHE:HZ	1.76	0.50
1:B:29:CYS:N	1:B:30:PRO:HD2	2.27	0.50
1:A:356:GLY:HA3	1:A:387:VAL:HG21	1.94	0.50
1:B:353:LYS:HZ3	1:B:361:ASP:HB3	1.75	0.50
1:A:91:ILE:HD12	1:A:107:LEU:HD21	1.94	0.49
1:A:124:SER:O	1:A:128:LYS:HG3	2.12	0.49
1:B:72:ALA:HB3	1:B:520:ALA:O	2.12	0.49
1:A:61:ILE:HB	1:A:66:PHE:HB2	1.94	0.49
1:A:69:LEU:N	1:A:70:PRO:HD3	2.26	0.49
1:B:294:VAL:HB	1:B:316:VAL:HG11	1.95	0.49
1:B:81:VAL:HG12	1:B:82:LYS:N	2.27	0.49
1:B:44:PRO:HG2	1:B:528:LEU:HD11	1.95	0.49
1:B:124:SER:O	1:B:128:LYS:HG3	2.12	0.49
1:B:187:MET:HB3	1:B:191:TYR:HB2	1.94	0.49
1:B:410:LEU:HA	1:B:410:LEU:HD23	1.60	0.49
1:A:363:ALA:HB1	1:A:368:CYS:HB3	1.94	0.48
1:B:100:PHE:HB3	1:B:123:TRP:CE2	2.48	0.48
1:B:526:TYR:CE2	1:B:528:LEU:CD2	2.97	0.48
1:A:374:THR:HG23	1:A:378:LEU:HB2	1.95	0.48
1:B:193:MET:CE	1:B:198:LEU:HD13	2.43	0.48
1:A:313:PHE:CD2	1:A:342:MET:HE1	2.49	0.48
1:A:417:THR:HG22	1:A:418:ALA:N	2.28	0.48
1:A:276:LEU:HA	1:A:383:VAL:HG21	1.95	0.48
1:A:64:CYS:O	1:A:65:ASP:HB2	2.12	0.48
1:B:245:PHE:HB3	1:B:253:ILE:CD1	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:136:SER:HB3	6:A:635:HOH:O	2.14	0.48
1:A:445:CYS:HB2	1:A:446:PRO:CD	2.44	0.47
1:B:23:ARG:HB3	1:B:24:PRO:HD3	1.96	0.47
1:A:59:GLU:HB2	1:A:464:ARG:NH2	2.29	0.47
1:B:445:CYS:HB2	1:B:446:PRO:CD	2.40	0.47
1:A:248:LEU:HB3	1:A:419:ASP:CG	2.34	0.47
1:B:47:VAL:HB	1:B:526:TYR:HB3	1.96	0.47
1:B:49:ARG:HB2	1:B:78:LEU:HD23	1.95	0.47
1:A:444:SER:OG	1:A:445:CYS:N	2.47	0.47
1:B:70:PRO:HD2	1:B:230:LEU:O	2.15	0.47
1:A:296:LEU:HA	1:A:296:LEU:HD23	1.55	0.47
1:B:462:GLY:O	1:B:476:HIS:HA	2.14	0.47
1:A:109:LEU:O	1:A:150:PRO:HD3	2.15	0.47
1:A:23:ARG:HB3	1:A:24:PRO:CD	2.41	0.47
1:B:235:LYS:HA	1:B:236:PRO:C	2.35	0.47
1:B:515:ILE:HG22	1:B:516:VAL:N	2.30	0.47
1:B:142:ALA:HB1	1:B:145:ARG:HB2	1.96	0.47
1:B:77:MET:HG2	1:B:174:PHE:HA	1.95	0.47
1:A:55:ASN:HA	1:A:70:PRO:HA	1.97	0.47
1:B:229:ALA:HB3	1:B:243:PHE:CZ	2.50	0.47
1:A:218:GLN:NE2	1:A:218:GLN:N	2.49	0.46
1:A:505:ILE:HA	1:A:509:GLU:OE1	2.14	0.46
1:A:23:ARG:O	1:A:26:ALA:HB3	2.16	0.46
1:A:29:CYS:O	1:A:32:ILE:HG22	2.15	0.46
1:A:381:SER:HA	1:A:382:PRO:HD3	1.70	0.46
1:A:332:ILE:HG21	1:A:409:LYS:HD2	1.97	0.46
1:B:252:GLU:HB2	1:B:480:GLY:C	2.36	0.46
1:B:109:LEU:HA	1:B:150:PRO:HG3	1.97	0.46
1:B:228:HIS:O	1:B:519:PRO:HB3	2.16	0.46
1:B:296:LEU:HD23	1:B:296:LEU:HA	1.76	0.46
1:A:226:GLU:O	1:A:227:ASP:HB2	2.14	0.46
1:B:69:LEU:N	1:B:70:PRO:HD3	2.31	0.46
1:B:228:HIS:H	1:B:519:PRO:HB2	1.81	0.46
1:A:142:ALA:N	1:A:143:PRO:HD3	2.31	0.45
1:A:23:ARG:HG2	1:A:27:GLU:OE2	2.16	0.45
1:A:316:VAL:O	1:A:317:TYR:C	2.55	0.45
1:B:351:ALA:O	1:B:354:LYS:HG3	2.16	0.45
1:A:187:MET:HB3	1:A:191:TYR:HB2	1.98	0.45
1:A:256:VAL:HG22	1:A:516:VAL:HG22	1.96	0.45
1:B:313:PHE:CD2	1:B:342:MET:CE	3.00	0.45
1:B:506:THR:N	1:B:509:GLU:OE1	2.43	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:515:ILE:CG2	1:B:516:VAL:N	2.80	0.45
1:A:229:ALA:HB3	1:A:243:PHE:CZ	2.52	0.45
1:A:270:ALA:N	1:A:271:PRO:CD	2.80	0.45
1:A:29:CYS:N	1:A:30:PRO:CD	2.80	0.45
1:A:313:PHE:CD2	1:A:342:MET:CE	3.00	0.45
1:B:307:LYS:HD2	1:B:307:LYS:HA	1.65	0.45
1:A:260:THR:O	1:A:261:LEU:HB2	2.17	0.45
1:A:271:PRO:O	1:A:383:VAL:HG22	2.16	0.45
1:B:254:SER:HB2	1:B:478:VAL:O	2.17	0.45
1:A:75:PHE:HD2	1:A:161:ASP:O	2.00	0.44
1:B:77:MET:HA	1:B:160:GLY:HA2	1.99	0.44
1:B:141:LEU:O	1:B:143:PRO:HD3	2.18	0.44
1:B:252:GLU:HB2	1:B:480:GLY:O	2.18	0.44
1:B:37:ILE:O	1:B:41:ASP:N	2.43	0.44
1:A:53:ARG:NH1	1:A:217:ASP:OD1	2.48	0.44
1:A:126:TYR:CE2	5:A:532:ANP:H4'	2.52	0.44
1:B:15:ASN:HA	1:B:15:ASN:HD22	1.53	0.44
1:B:41:ASP:O	1:B:42:ALA:HB2	2.16	0.44
1:B:138:LEU:HD11	1:B:186:ASN:HB2	2.00	0.44
1:B:117:ASP:OD1	1:B:118:PRO:N	2.50	0.44
1:B:21:LEU:HD23	1:B:26:ALA:HA	2.00	0.44
1:B:44:PRO:HG2	1:B:528:LEU:CD1	2.48	0.44
1:A:225:GLU:O	1:A:228:HIS:HB2	2.18	0.44
1:B:518:LYS:O	1:B:519:PRO:C	2.55	0.44
1:A:313:PHE:HD2	1:A:342:MET:CE	2.32	0.43
1:B:184:LYS:NZ	1:B:527:GLU:CG	2.80	0.43
1:B:269:THR:O	1:B:273:ASN:N	2.46	0.43
1:B:43:LYS:O	1:B:82:LYS:HG3	2.18	0.43
1:B:9:VAL:CG1	1:B:10:ILE:N	2.81	0.43
1:A:207:HIS:HD2	1:A:211:VAL:O	2.02	0.43
1:B:227:ASP:HA	1:B:519:PRO:HG2	1.99	0.43
1:B:229:ALA:O	1:B:242:PRO:HA	2.18	0.43
1:B:46:PHE:CB	1:B:184:LYS:HZ2	2.31	0.43
1:B:512:ASN:O	1:B:515:ILE:HD11	2.18	0.43
1:B:133:VAL:HG12	1:B:134:ALA:N	2.34	0.43
1:B:23:ARG:O	1:B:26:ALA:N	2.52	0.43
1:B:75:PHE:CB	1:B:162:VAL:HG22	2.49	0.43
1:B:54:VAL:O	1:B:71:LEU:N	2.50	0.43
1:A:265:ASN:HB2	6:A:563:HOH:O	2.19	0.42
1:B:492:ALA:O	1:B:496:GLU:HB2	2.20	0.42
1:A:418:ALA:O	1:A:421:ASP:HB2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:366:LEU:HB2	1:B:368:CYS:HB2	2.02	0.42
1:B:408:VAL:O	1:B:409:LYS:C	2.58	0.42
1:A:276:LEU:HD13	1:A:383:VAL:HG13	2.02	0.42
1:A:320:ARG:HG3	1:A:320:ARG:O	2.19	0.42
1:A:505:ILE:HG13	1:A:509:GLU:OE1	2.19	0.42
1:B:53:ARG:HH11	1:B:217:ASP:CG	2.21	0.42
1:B:69:LEU:HD12	1:B:230:LEU:O	2.19	0.42
1:B:50:SER:HA	1:B:51:PRO:HD3	1.90	0.42
1:A:257:ILE:HA	1:A:474:THR:O	2.20	0.41
5:B:532:ANP:O1A	5:B:532:ANP:O3G	2.37	0.41
1:A:10:ILE:HA	1:A:194:SER:HA	2.01	0.41
1:A:59:GLU:HB2	1:A:464:ARG:HH22	1.83	0.41
1:B:314:MET:HA	1:B:342:MET:HE1	2.01	0.41
1:B:450:LYS:O	1:B:451:ILE:C	2.56	0.41
1:B:493:LEU:HD23	1:B:493:LEU:HA	1.88	0.41
1:A:47:VAL:HB	1:A:526:TYR:HB3	2.02	0.41
1:B:374:THR:O	1:B:375:ARG:C	2.57	0.41
1:B:381:SER:HA	1:B:382:PRO:HD3	1.85	0.41
1:A:410:LEU:HD11	1:A:425:GLN:HB3	2.02	0.41
1:B:521:LEU:HG	1:B:522:GLY:N	2.34	0.41
1:A:21:LEU:HA	1:A:21:LEU:HD23	1.68	0.41
1:A:266:LYS:HE3	2:A:529:GLA:O2	2.20	0.41
1:A:374:THR:O	1:A:379:THR:HG23	2.21	0.41
1:B:117:ASP:HA	1:B:118:PRO:HD2	1.90	0.41
1:A:141:LEU:HA	1:A:141:LEU:HD12	1.79	0.41
1:A:215:GLY:O	1:A:216:MET:C	2.58	0.41
1:A:94:ILE:HG22	1:A:157:PHE:CE1	2.55	0.41
1:A:174:PHE:O	1:A:178:VAL:HG23	2.21	0.41
1:A:68:VAL:C	1:A:70:PRO:HD3	2.41	0.41
1:A:141:LEU:C	1:A:143:PRO:HD3	2.41	0.41
1:A:493:LEU:HD23	1:A:493:LEU:HA	1.85	0.41
1:B:245:PHE:HB3	1:B:253:ILE:HD13	2.03	0.41
1:B:408:VAL:H	1:B:408:VAL:HG23	1.56	0.41
1:B:404:VAL:O	1:B:407:ALA:HB3	2.20	0.41
1:B:491:GLU:O	1:B:492:ALA:C	2.60	0.41
1:A:169:SER:OG	1:A:172:ALA:HB3	2.22	0.41
1:B:126:TYR:CD1	1:B:175:ILE:HD11	2.53	0.40
1:B:218:GLN:O	1:B:219:ALA:C	2.58	0.40
1:B:373:PHE:CE2	1:B:378:LEU:HD21	2.55	0.40
1:A:141:LEU:HG	1:A:187:MET:HE1	2.03	0.40
1:B:187:MET:HB3	1:B:191:TYR:CB	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:360:ASP:OD1	1:B:370:ARG:HD2	2.21	0.40
1:B:257:ILE:HG23	1:B:474:THR:O	2.21	0.40
1:A:14:PHE:HB3	1:A:21:LEU:HD21	2.03	0.40
1:A:331:ASP:HB3	1:A:334:SER:HG	1.85	0.40
1:B:10:ILE:C	1:B:10:ILE:HD12	2.41	0.40
1:B:245:PHE:HB3	1:B:246:PRO:CD	2.45	0.40
1:A:97:ASP:HB3	1:A:100:PHE:HD1	1.87	0.40
1:B:276:LEU:CD1	1:B:383:VAL:CG1	2.99	0.40
1:B:427:GLY:HA2	1:B:430:MET:HG3	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	501/548 (91%)	483 (96%)	17 (3%)	1 (0%)	47	62
1	B	497/548 (91%)	460 (93%)	35 (7%)	2 (0%)	34	48
All	All	998/1096 (91%)	943 (94%)	52 (5%)	3 (0%)	41	55

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	74	ASP
1	B	23	ARG
1	B	453	SER

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	433/467 (93%)	401 (93%)	32 (7%)	13	22
1	B	431/467 (92%)	391 (91%)	40 (9%)	9	13
All	All	864/934 (92%)	792 (92%)	72 (8%)	11	17

All (72) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	VAL
1	A	15	ASN
1	A	23	ARG
1	A	50	SER
1	A	53	ARG
1	A	74	ASP
1	A	103	ARG
1	A	104	LYS
1	A	119	SER
1	A	136	SER
1	A	139	LYS
1	A	148	SER
1	A	193	MET
1	A	200	ARG
1	A	218	GLN
1	A	226	GLU
1	A	254	SER
1	A	307	LYS
1	A	352	ASN
1	A	364	GLN
1	A	367	ASN
1	A	368	CYS
1	A	375	ARG
1	A	383	VAL
1	A	409	LYS
1	A	412	THR
1	A	441	TYR
1	A	457	SER
1	A	475	VAL
1	A	518	LYS
1	A	525	LEU
1	A	527	GLU
1	B	15	ASN

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Mol	Chain	Res	Type
1	B	25	LEU
1	B	32	ILE
1	B	43	LYS
1	B	50	SER
1	B	53	ARG
1	B	71	LEU
1	B	74	ASP
1	B	103	ARG
1	B	119	SER
1	B	133	VAL
1	B	136	SER
1	B	144	GLU
1	B	145	ARG
1	B	203	VAL
1	B	209	VAL
1	B	218	GLN
1	B	230	LEU
1	B	237	GLN
1	B	341	LYS
1	B	347	GLU
1	B	352	ASN
1	B	357	PHE
1	B	367	ASN
1	B	383	VAL
1	B	387	VAL
1	B	401	SER
1	B	409	LYS
1	B	412	THR
1	B	419	ASP
1	B	430	MET
1	B	441	TYR
1	B	453	SER
1	B	475	VAL
1	B	505	ILE
1	B	506	THR
1	B	507	ASP
1	B	517	SER
1	B	518	LYS
1	B	528	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	102	GLN
1	A	155	GLN
1	A	218	GLN
1	A	251	HIS
1	A	273	ASN
1	A	364	GLN
1	B	15	ASN
1	B	102	GLN
1	B	155	GLN
1	B	192	HIS
1	B	197	ASN
1	B	218	GLN
1	B	273	ASN
1	B	364	GLN
1	B	425	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 for Mogul analysis.

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
5	ANP	A	532	3	29,33,33	1.34	4 (13%)	31,52,52	1.73	6 (19%)
5	ANP	B	532	3	29,33,33	1.48	5 (17%)	31,52,52	1.84	8 (25%)
2	GLA	B	529	-	12,12,12	0.61	0	17,17,17	0.92	1 (5%)
2	GLA	A	529	-	12,12,12	0.70	0	17,17,17	1.27	1 (5%)

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
5	ANP	A	532	3	-	4/14/38/38	0/3/3/3
5	ANP	B	532	3	-	3/14/38/38	0/3/3/3
2	GLA	B	529	-	-	1/2/22/22	0/1/1/1
2	GLA	A	529	-	-	1/2/22/22	0/1/1/1

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	532	ANP	PB-O1B	3.93	1.52	1.46
5	A	532	ANP	PB-O1B	3.52	1.51	1.46
5	A	532	ANP	PG-O1G	3.15	1.51	1.46
5	B	532	ANP	PG-O1G	2.69	1.50	1.46
5	A	532	ANP	C6-N6	-2.59	1.24	1.34
5	B	532	ANP	C6-N6	-2.54	1.24	1.34
5	B	532	ANP	PG-O2G	-2.45	1.50	1.56
5	A	532	ANP	C2-N1	2.36	1.38	1.33
5	B	532	ANP	C2-N1	2.02	1.37	1.33

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	532	ANP	C5-C6-N6	5.59	128.85	120.35
5	A	532	ANP	C5-C6-N6	4.23	126.77	120.35
5	A	532	ANP	O1B-PB-N3B	-3.67	106.37	111.77
5	B	532	ANP	C2-N1-C6	3.60	124.92	118.75
5	A	532	ANP	C2-N1-C6	3.47	124.70	118.75
5	B	532	ANP	N3-C2-N1	-3.41	123.35	128.68
5	A	532	ANP	C5-C6-N1	-3.31	112.84	120.35
5	A	532	ANP	N3-C2-N1	-3.27	123.57	128.68
2	A	529	GLA	O4-C4-C3	3.17	117.67	110.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	532	ANP	C5-C6-N1	-3.10	113.33	120.35
5	A	532	ANP	O1G-PG-N3B	-2.85	107.58	111.77
5	B	532	ANP	O1G-PG-N3B	-2.54	108.03	111.77
2	B	529	GLA	O4-C4-C3	2.44	115.98	110.35
5	B	532	ANP	O3'-C3'-C2'	2.25	119.10	111.82
5	B	532	ANP	O2G-PG-O1G	-2.17	107.99	113.45
5	B	532	ANP	PA-O5'-C5'	-2.15	109.08	121.68

There are no chirality outliers.

All (9) torsion outliers are listed below:

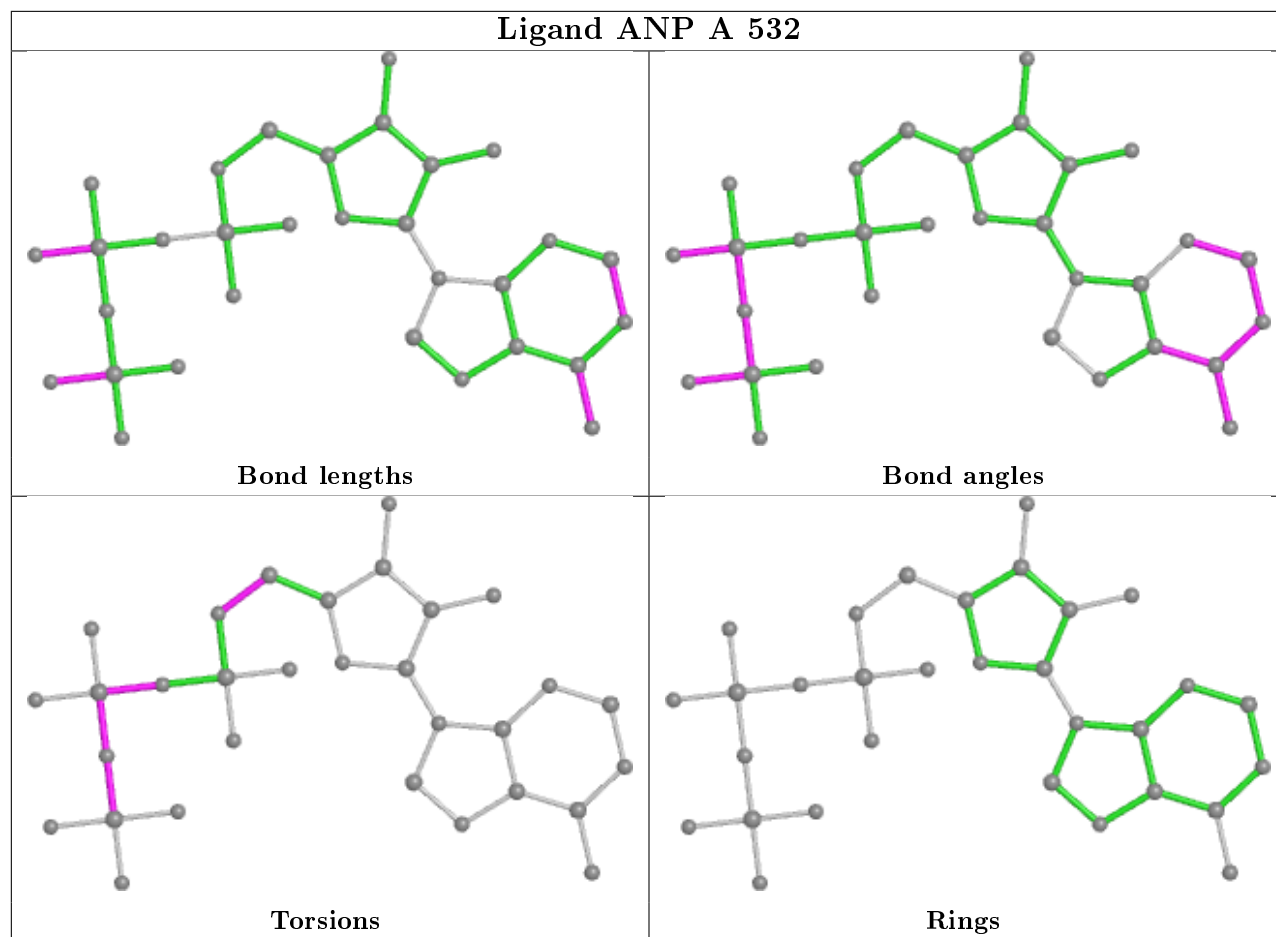
Mol	Chain	Res	Type	Atoms
5	A	532	ANP	PB-N3B-PG-O1G
5	A	532	ANP	PG-N3B-PB-O1B
5	A	532	ANP	PA-O3A-PB-O1B
5	B	532	ANP	PB-N3B-PG-O1G
5	B	532	ANP	PG-N3B-PB-O1B
5	B	532	ANP	PA-O3A-PB-O1B
2	A	529	GLA	O5-C5-C6-O6
2	B	529	GLA	O5-C5-C6-O6
5	A	532	ANP	C4'-C5'-O5'-PA

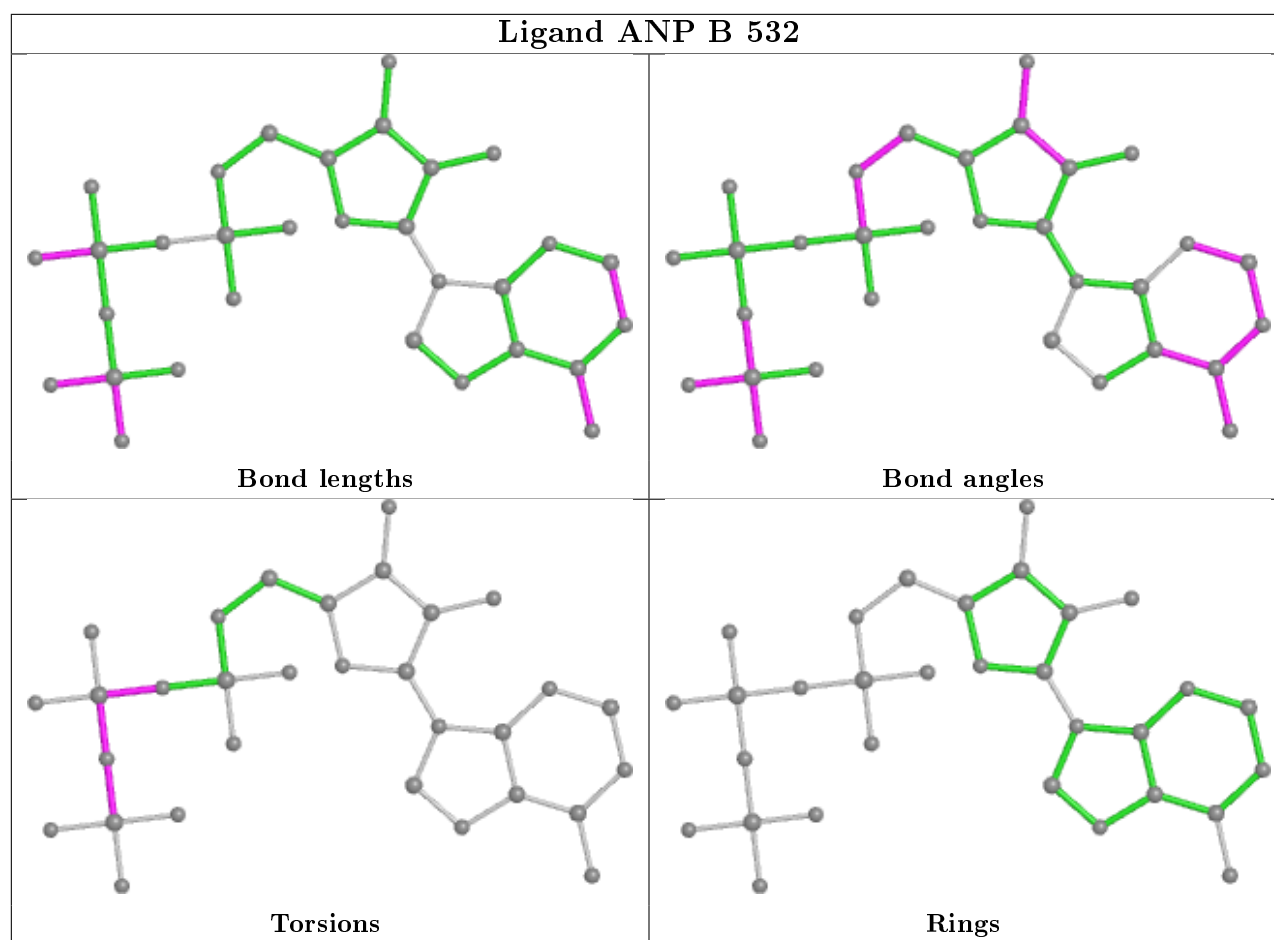
There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	532	ANP	2	0
5	B	532	ANP	3	0
2	A	529	GLA	1	0

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





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	509/548 (92%)	-0.63	5 (0%) 82 80	12, 28, 67, 96	0
1	B	505/548 (92%)	-0.31	9 (1%) 68 66	13, 39, 85, 98	0
All	All	1014/1096 (92%)	-0.47	14 (1%) 75 73	12, 33, 80, 98	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	18	ALA	3.5
1	A	120	VAL	3.4
1	B	249	LYS	3.2
1	B	142	ALA	2.9
1	B	306	ASN	2.7
1	A	416	PHE	2.7
1	A	20	GLU	2.7
1	B	482	PRO	2.6
1	A	417	THR	2.5
1	B	20	GLU	2.5
1	B	481	GLY	2.5
1	B	246	PRO	2.4
1	B	507	ASP	2.4
1	B	21	LEU	2.1

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](#)

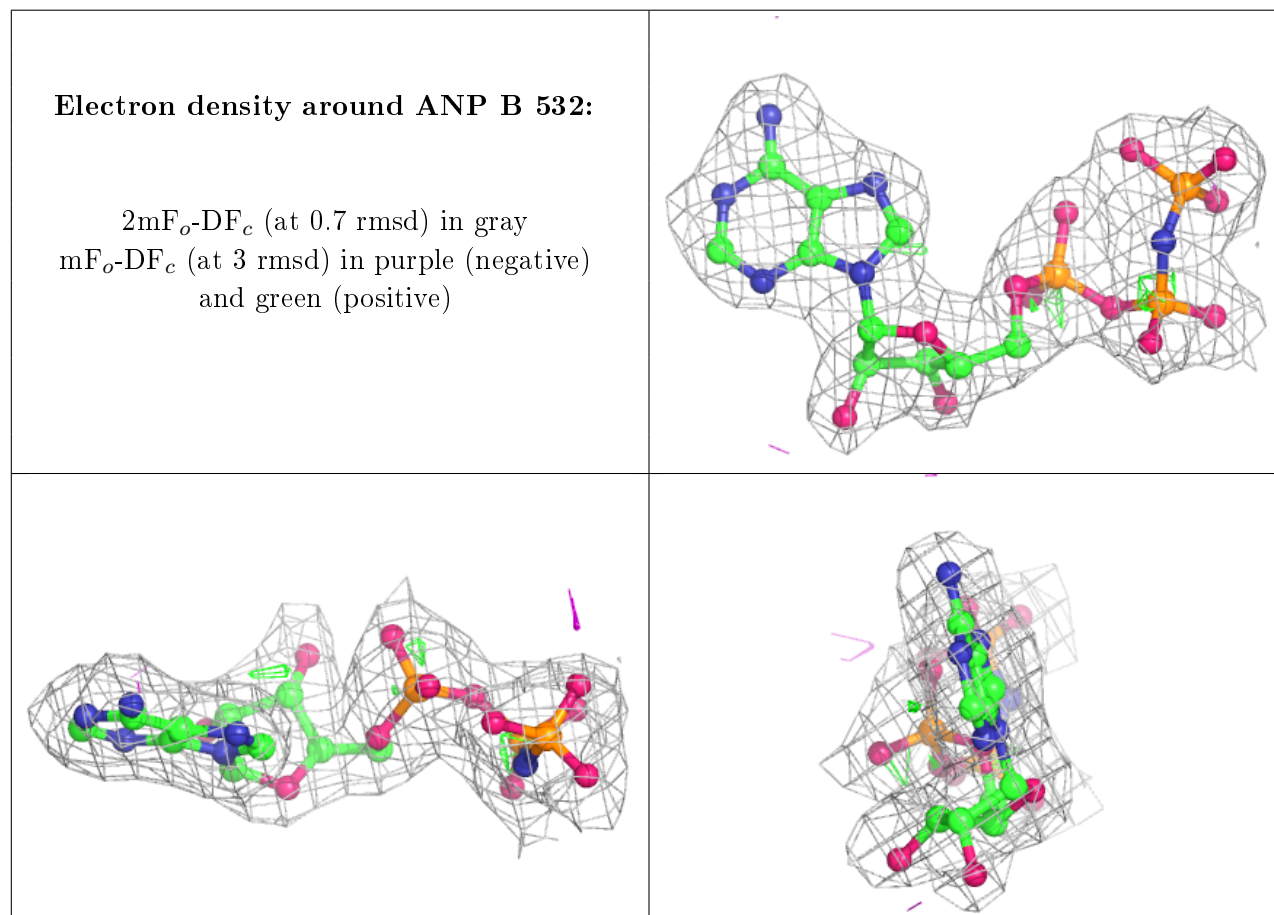
There are no monosaccharides in this entry.

6.4 Ligands ⓘ

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.

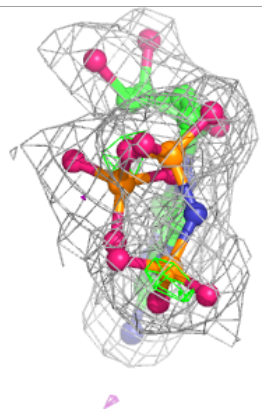
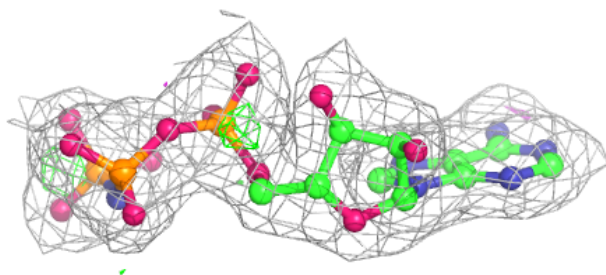
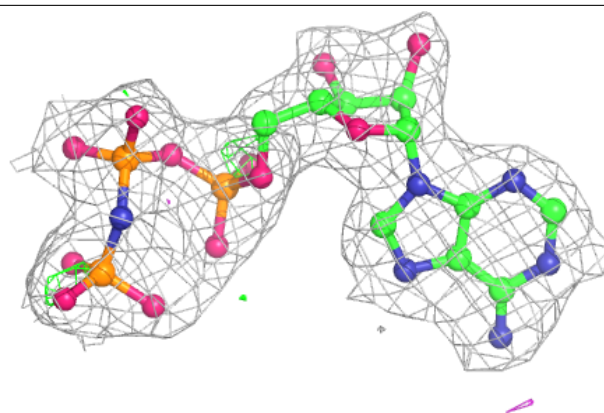
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	MG	B	530	1/1	0.91	0.22	44,44,44,44	0
3	MG	A	530	1/1	0.93	0.22	34,34,34,34	0
4	CL	A	531	1/1	0.97	0.06	33,33,33,33	0
4	CL	B	531	1/1	0.97	0.08	48,48,48,48	0
2	GLA	B	529	12/12	0.98	0.15	11,17,30,33	0
2	GLA	A	529	12/12	0.98	0.15	5,14,22,27	0
5	ANP	B	532	31/31	0.98	0.10	9,28,51,95	0
5	ANP	A	532	31/31	0.99	0.11	10,22,36,51	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 ANP A 532:

$2mF_o-DF_c$ (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.