



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 06:32 PM UTC

PDB ID : 3UMM / pdb_00003umm
Title : Formylglycinamide ribonucleotide amidotransferase from *Salmonella typhimurium*: Role of the ATP complexation and glutaminase domain in catalytic coupling
Authors : Anand, R.; Morar, M.; Tanwar, A.S.; Panjekar, S.
Deposited on : 2011-11-14
Resolution : 3.20 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

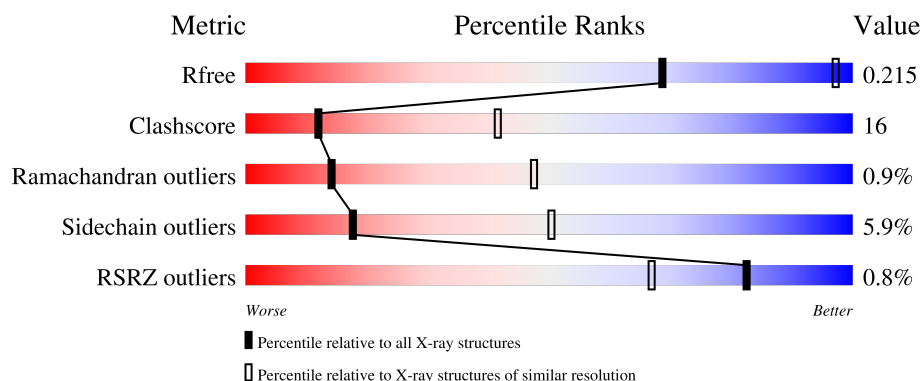
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1303	 65% 30% . .

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
1	CYG	A	1135	-	-	X	-
5	SO4	A	2009	-	-	X	-

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 10462 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.

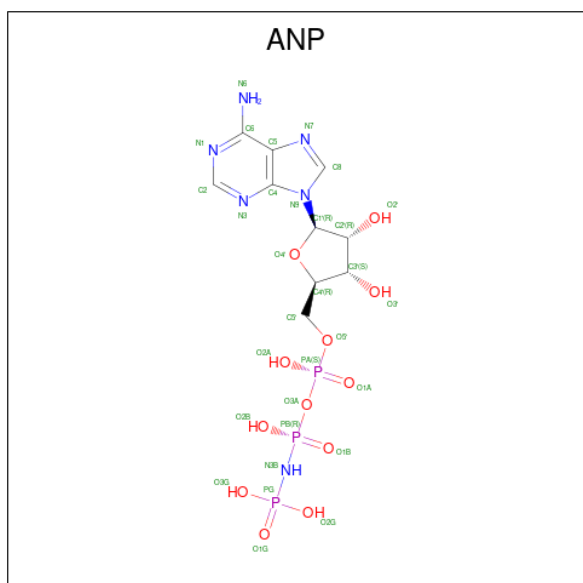
- Molecule 1 is a protein called Phosphoribosylformylglycinamide synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	1285	9909	6216	1769	1876	48	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

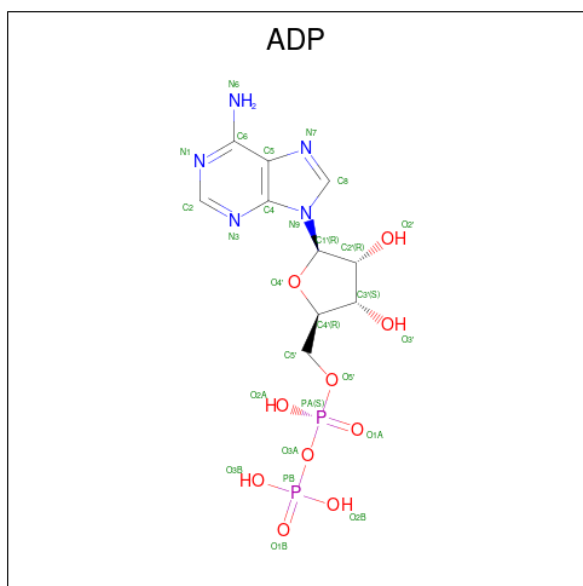
Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	GLY	-	expression tag	UNP P74881
A	-6	LEU	-	expression tag	UNP P74881
A	-5	VAL	-	expression tag	UNP P74881
A	-4	PRO	-	expression tag	UNP P74881
A	-3	ARG	-	expression tag	UNP P74881
A	-2	GLY	-	expression tag	UNP P74881
A	-1	SER	-	expression tag	UNP P74881
A	0	HIS	-	expression tag	UNP P74881

- Molecule 2 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (CCD ID: ANP) (formula: C₁₀H₁₇N₆O₁₂P₃).



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

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).

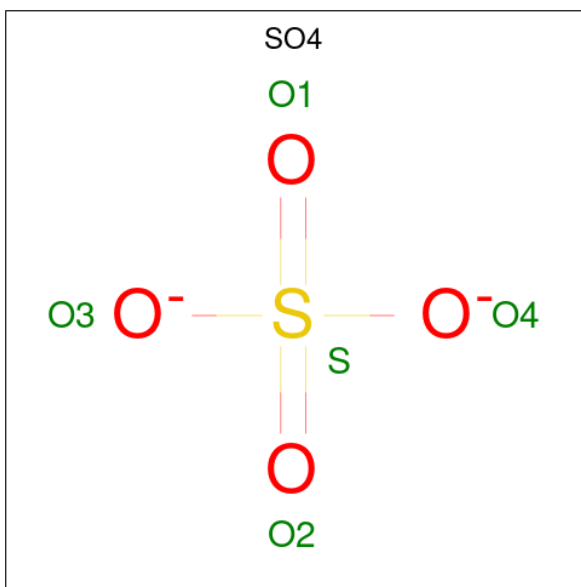


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	3	Total	Mg	0	0
			3	3		

- Molecule 5 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		

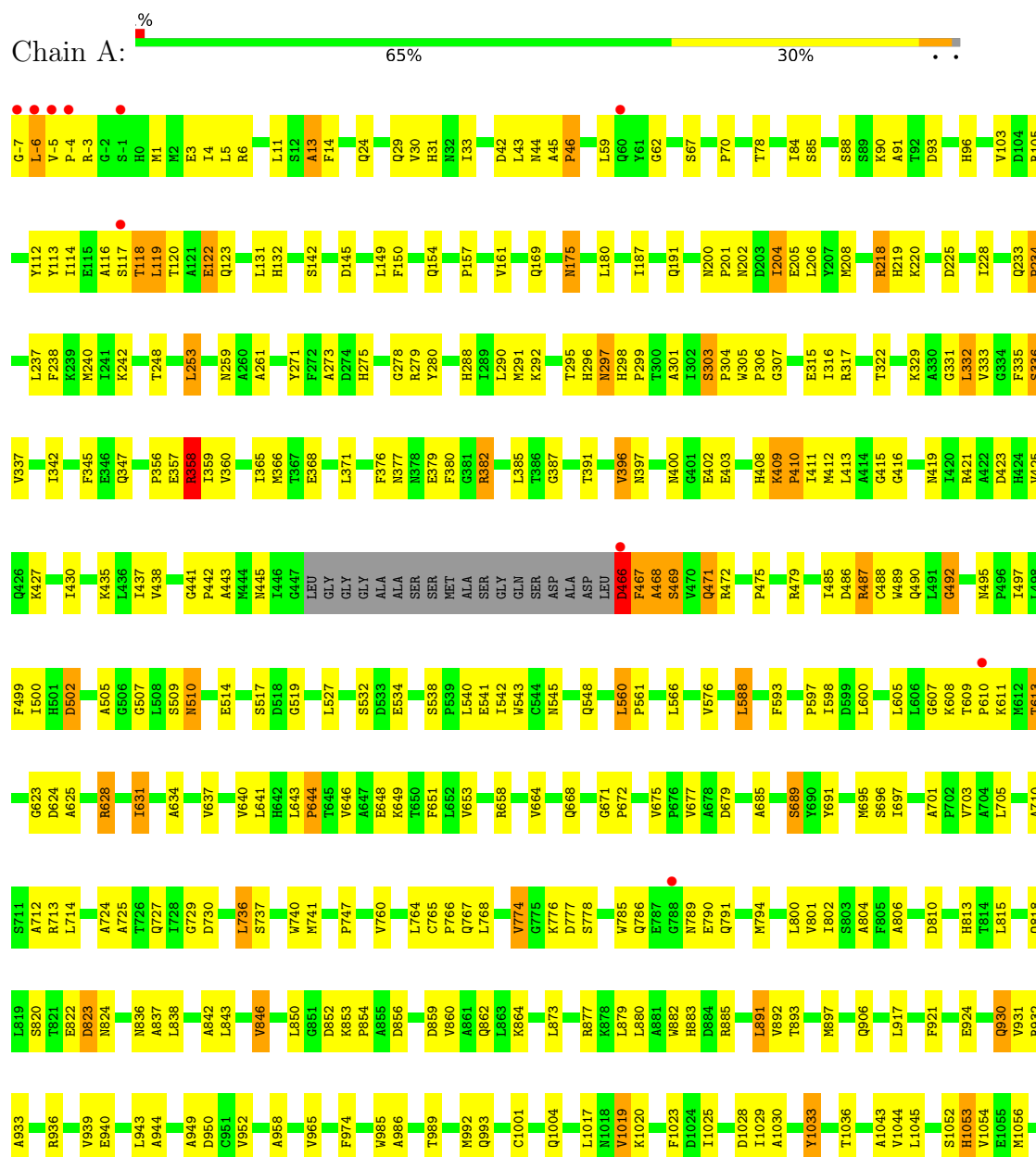
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	482	Total	O	0	0
			482	482		

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Phosphoribosylformylglycinamide synthase





4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	148.68Å 148.68Å 142.05Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.98 – 3.20 19.98 – 3.20	Depositor EDS
% Data completeness (in resolution range)	(Not available) (19.98-3.20) 97.9 (19.98-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.07 (at 3.22Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.196 , 0.276 0.216 , 0.215	Depositor DCC
R_{free} test set	1031 reflections (3.57%)	wwPDB-VP
Wilson B-factor (Å ²)	41.9	Xtriage
Anisotropy	0.035	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 29.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.030 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	10462	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.26% 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: CYG, ADP, MG, SO4, ANP

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	0.53	0/10106	1.05	53/13716 (0.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2

There are no bond length outliers.

All (53) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	466	ASP	CA-C-N	13.76	147.82	121.54
1	A	466	ASP	C-N-CA	13.76	147.82	121.54
1	A	1148	ILE	N-CA-C	10.21	117.66	107.55
1	A	409	LYS	CA-C-N	9.58	129.65	119.78
1	A	409	LYS	C-N-CA	9.58	129.65	119.78
1	A	303	SER	CA-C-N	7.75	129.52	119.84
1	A	303	SER	C-N-CA	7.75	129.52	119.84
1	A	1276	ASN	N-CA-C	7.49	122.06	113.15
1	A	628	ARG	N-CA-C	7.45	121.21	112.72
1	A	385	LEU	N-CA-C	7.45	122.55	113.17
1	A	485	ILE	N-CA-C	-6.74	103.76	110.30
1	A	1019	VAL	N-CA-C	6.51	119.29	109.20
1	A	701	ALA	N-CA-C	6.23	122.17	113.57
1	A	468	ALA	N-CA-C	-6.20	106.39	112.97
1	A	671	GLY	CA-C-N	6.19	125.87	119.56
1	A	671	GLY	C-N-CA	6.19	125.87	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1129	THR	N-CA-C	6.05	119.36	110.59
1	A	275	HIS	N-CA-C	6.01	117.84	111.28
1	A	410	PRO	N-CA-C	5.79	120.42	111.21
1	A	1053	HIS	N-CA-C	5.79	123.12	110.80
1	A	1158	VAL	N-CA-C	5.73	115.81	108.82
1	A	510	ASN	N-CA-C	-5.72	108.10	114.62
1	A	1238	ASN	N-CA-C	5.71	117.59	111.36
1	A	1117	ARG	N-CA-C	-5.70	104.76	110.97
1	A	1114	HIS	N-CA-C	5.68	117.92	111.11
1	A	777	ASP	N-CA-C	5.60	118.61	108.69
1	A	62	GLY	CA-C-N	5.59	125.77	119.90
1	A	62	GLY	C-N-CA	5.59	125.77	119.90
1	A	469	SER	N-CA-C	-5.58	105.82	113.30
1	A	724	ALA	N-CA-C	5.58	117.36	111.28
1	A	608	LYS	N-CA-C	5.58	118.66	109.85
1	A	409	LYS	N-CA-C	-5.55	97.51	109.01
1	A	441	GLY	CA-C-N	5.54	126.77	119.84
1	A	441	GLY	C-N-CA	5.54	126.77	119.84
1	A	534	GLU	CA-C-N	5.54	125.19	119.05
1	A	534	GLU	C-N-CA	5.54	125.19	119.05
1	A	789	ASN	N-CA-C	-5.50	106.34	113.16
1	A	740	TRP	N-CA-C	5.49	117.67	108.73
1	A	347	GLN	CA-C-N	5.42	125.75	119.47
1	A	347	GLN	C-N-CA	5.42	125.75	119.47
1	A	679	ASP	N-CA-C	5.33	118.01	111.82
1	A	297	ASN	N-CA-C	5.31	122.12	110.80
1	A	1036	THR	N-CA-C	-5.29	106.83	113.28
1	A	488	CYS	N-CA-C	5.23	116.79	111.14
1	A	806	ALA	N-CA-C	5.19	117.08	109.24
1	A	1236	ASN	N-CA-C	-5.19	98.23	108.71
1	A	495	ASN	CA-C-N	5.18	124.79	119.56
1	A	495	ASN	C-N-CA	5.18	124.79	119.56
1	A	689	SER	N-CA-C	5.14	116.89	109.07
1	A	1045	LEU	N-CA-C	5.11	117.62	109.96
1	A	1110	ILE	N-CA-C	-5.09	106.11	110.74
1	A	358	ARG	N-CA-C	5.08	119.23	113.19
1	A	187	ILE	N-CA-C	-5.06	104.77	111.09

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1135	CYG	Mainchain
1	A	466	ASP	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	9909	0	9695	309	0
2	A	31	0	13	3	0
3	A	27	0	11	0	0
4	A	3	0	0	0	0
5	A	10	0	0	5	0
6	A	482	0	0	3	0
All	All	10462	0	9719	310	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 16.

All (310) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:13:ALA:HB3	5:A:2009:SO4:O4	1.03	1.19
1:A:13:ALA:CB	5:A:2009:SO4:O4	1.96	1.13
1:A:466:ASP:C	6:A:1335:HOH:O	2.06	0.97
1:A:336:SER:HB2	1:A:411:ILE:HB	1.51	0.93
1:A:387:GLY:HA2	1:A:697:ILE:HD12	1.51	0.92
1:A:628:ARG:HA	1:A:631:ILE:HD13	1.52	0.90
1:A:329:LYS:HZ3	1:A:685:ALA:HA	1.39	0.87
1:A:120:THR:H	1:A:123:GLN:HE21	1.22	0.86
1:A:358:ARG:H	1:A:358:ARG:HD3	1.39	0.86
1:A:466:ASP:CA	6:A:1335:HOH:O	2.24	0.85
1:A:487:ARG:HG2	1:A:566:LEU:HD22	1.57	0.83
1:A:1076:LEU:HD23	1:A:1116:VAL:HG21	1.61	0.81
1:A:1175:THR:HG21	1:A:1221:ARG:HE	1.46	0.80
1:A:119:LEU:HB3	1:A:123:GLN:HB2	1.62	0.80
1:A:5:LEU:HD22	1:A:59:LEU:HD12	1.65	0.78
1:A:305:TRP:HB3	1:A:306:PRO:HD3	1.65	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:609:THR:HB	1:A:610:PRO:HD2	1.68	0.75
1:A:443:ALA:HB1	1:A:545:ASN:HD21	1.52	0.75
1:A:859:ASP:HB3	1:A:862:GLN:HB2	1.68	0.74
1:A:120:THR:HG23	1:A:123:GLN:HE21	1.52	0.74
1:A:1135:CYG:HB13	1:A:1136:ASN:HB2	1.70	0.73
1:A:329:LYS:NZ	1:A:685:ALA:HA	2.03	0.73
1:A:408:HIS:CD2	1:A:794:MET:HG2	2.24	0.72
1:A:466:ASP:HB2	1:A:467:PHE:HB2	1.71	0.72
1:A:510:ASN:O	1:A:514:GLU:HB2	1.89	0.72
1:A:588:LEU:HB2	1:A:598:ILE:HB	1.73	0.71
1:A:1106:TRP:CD2	1:A:1140:MET:HG3	2.27	0.70
1:A:443:ALA:HB1	1:A:545:ASN:ND2	2.06	0.70
1:A:1221:ARG:HA	1:A:1243:GLY:O	1.91	0.70
1:A:13:ALA:HB3	5:A:2009:SO4:S	2.29	0.69
1:A:466:ASP:HB2	1:A:467:PHE:CB	2.23	0.69
1:A:631:ILE:HD12	1:A:631:ILE:H	1.56	0.69
1:A:1262:GLU:O	1:A:1265:PHE:HD2	1.76	0.68
1:A:885:ARG:NH2	1:A:924:GLU:HB2	2.09	0.68
1:A:931:VAL:HG11	1:A:939:VAL:HG11	1.78	0.66
1:A:356:PRO:HG3	1:A:785:TRP:HB3	1.78	0.66
1:A:142:SER:O	1:A:145:ASP:HB2	1.95	0.66
1:A:84:ILE:HG13	1:A:105:ARG:NH1	2.11	0.66
1:A:823:ASP:HB3	1:A:933:ALA:CB	2.26	0.66
1:A:14:PHE:HB3	5:A:2009:SO4:O2	1.96	0.65
1:A:1056:MET:HE1	1:A:1134:VAL:HG21	1.78	0.65
1:A:1121:GLU:HG2	1:A:1125:HIS:CD2	2.32	0.65
1:A:175:ASN:ND2	1:A:180:LEU:HB2	2.11	0.65
1:A:541:GLU:O	1:A:545:ASN:HB3	1.96	0.65
1:A:1236:ASN:ND2	1:A:1243:GLY:HA2	2.12	0.65
1:A:588:LEU:HD12	1:A:598:ILE:HD12	1.79	0.65
1:A:-6:LEU:HG	1:A:1:MET:SD	2.36	0.64
1:A:1126:ARG:HG3	1:A:1127:PRO:HD2	1.79	0.64
1:A:1262:GLU:HG2	1:A:1263:ARG:N	2.12	0.64
1:A:396:VAL:HG21	1:A:850:LEU:HD13	1.78	0.64
1:A:1004:GLN:NE2	1:A:1233:TYR:H	1.95	0.64
1:A:120:THR:H	1:A:123:GLN:NE2	1.92	0.64
1:A:218:ARG:HH21	1:A:220:LYS:HE2	1.63	0.64
1:A:1135:CYG:O	1:A:1137:GLY:N	2.30	0.63
1:A:486:ASP:HA	1:A:489:TRP:NE1	2.13	0.63
1:A:1222:TYR:OH	1:A:1245:THR:HG21	1.97	0.63
1:A:609:THR:HB	1:A:610:PRO:CD	2.29	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:885:ARG:HH21	1:A:924:GLU:HB2	1.64	0.62
1:A:337:VAL:HG23	1:A:391:THR:HG22	1.81	0.62
1:A:637:VAL:HG22	1:A:891:LEU:CD2	2.28	0.62
1:A:435:LYS:HG3	1:A:560:LEU:HD22	1.82	0.62
1:A:357:GLU:H	1:A:358:ARG:HH11	1.48	0.62
1:A:111:LEU:HD11	1:A:112:TYR:HE1	1.65	0.61
1:A:161:VAL:O	1:A:200:ASN:HB3	2.00	0.61
1:A:430:ILE:HD12	1:A:519:GLY:HA3	1.82	0.61
1:A:696:SER:OG	1:A:804:ALA:HB3	2.00	0.61
1:A:335:PHE:CG	1:A:366:MET:HE1	2.36	0.61
1:A:356:PRO:HD2	1:A:359:ILE:HD11	1.80	0.61
1:A:-7:GLY:HA3	1:A:4:ILE:H	1.65	0.61
1:A:157:PRO:HA	1:A:593:PHE:CE2	2.35	0.60
1:A:1220:LEU:HB2	1:A:1246:ALA:HB3	1.83	0.60
1:A:815:LEU:HD21	1:A:879:LEU:HB2	1.83	0.60
1:A:332:LEU:HD12	1:A:695:MET:SD	2.42	0.60
1:A:161:VAL:HG21	1:A:206:LEU:HD22	1.83	0.60
1:A:315:GLU:HG3	1:A:415:GLY:HA2	1.84	0.60
1:A:96:HIS:HE1	1:A:103:VAL:O	1.84	0.59
1:A:396:VAL:HG22	1:A:850:LEU:HB2	1.83	0.59
1:A:517:SER:C	1:A:519:GLY:H	2.09	0.59
1:A:986:ALA:O	1:A:989:THR:HG22	2.01	0.59
1:A:357:GLU:H	1:A:358:ARG:NH1	2.00	0.59
1:A:317:ARG:HH22	1:A:548:GLN:NE2	2.01	0.59
1:A:466:ASP:N	6:A:1335:HOH:O	2.33	0.59
1:A:1044:VAL:HA	1:A:1089:VAL:CG1	2.33	0.58
1:A:527:LEU:HB2	1:A:588:LEU:HD22	1.85	0.58
1:A:118:THR:H	1:A:119:LEU:HD12	1.69	0.58
1:A:120:THR:HG23	1:A:123:GLN:NE2	2.19	0.58
1:A:466:ASP:N	1:A:468:ALA:H	2.01	0.58
1:A:631:ILE:HD12	1:A:631:ILE:N	2.18	0.58
1:A:943:LEU:HD13	1:A:952:VAL:HG21	1.85	0.58
1:A:1033:TYR:N	1:A:1033:TYR:CD2	2.72	0.58
1:A:640:VAL:HG21	1:A:921:PHE:CE1	2.38	0.58
1:A:335:PHE:HB3	1:A:366:MET:HE1	1.85	0.58
1:A:238:PHE:HE2	1:A:242:LYS:HE3	1.68	0.57
1:A:1071:HIS:O	1:A:1074:ASP:HB2	2.04	0.57
1:A:329:LYS:NZ	1:A:419:ASN:HD21	2.02	0.57
1:A:1196:HIS:CD2	1:A:1199:GLY:HA3	2.40	0.57
1:A:358:ARG:HD3	1:A:358:ARG:N	2.15	0.57
1:A:815:LEU:CD2	1:A:879:LEU:HB2	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:14:PHE:HD2	5:A:2009:SO4:O3	1.89	0.56
1:A:78:THR:HB	1:A:149:LEU:HD11	1.87	0.56
1:A:317:ARG:HH22	1:A:548:GLN:HE22	1.53	0.56
1:A:736:LEU:HG	1:A:802:ILE:HG23	1.87	0.56
1:A:1135:CYG:O	1:A:1136:ASN:C	2.49	0.56
1:A:823:ASP:HB3	1:A:933:ALA:HB2	1.86	0.55
1:A:1060:PHE:O	1:A:1065:PHE:HB2	2.05	0.55
1:A:1138:CYS:HB2	1:A:1257:MET:O	2.06	0.55
1:A:204:ILE:HD11	1:A:543:TRP:CD1	2.42	0.55
1:A:261:ALA:HB2	1:A:774:VAL:HG13	1.88	0.55
1:A:658:ARG:HD2	1:A:668:GLN:OE1	2.07	0.55
1:A:238:PHE:CE2	1:A:242:LYS:HE3	2.42	0.55
1:A:30:VAL:HA	1:A:116:ALA:HB2	1.89	0.55
1:A:843:LEU:HD21	1:A:917:LEU:HD21	1.89	0.55
1:A:1192:ILE:HG13	1:A:1193:ALA:H	1.72	0.54
1:A:-6:LEU:HG	1:A:1:MET:CE	2.36	0.54
1:A:640:VAL:HG21	1:A:921:PHE:HE1	1.71	0.54
1:A:824:ASN:HD21	1:A:958:ALA:H	1.54	0.54
1:A:445:ASN:C	1:A:445:ASN:HD22	2.16	0.54
1:A:301:ALA:HB2	1:A:410:PRO:HD2	1.90	0.53
1:A:33:ILE:HG13	1:A:114:ILE:HG12	1.89	0.53
1:A:29:GLN:HG3	1:A:31:HIS:HE1	1.73	0.53
1:A:288:HIS:O	1:A:419:ASN:HA	2.08	0.53
1:A:823:ASP:HB3	1:A:933:ALA:HB3	1.91	0.53
1:A:175:ASN:HD22	1:A:180:LEU:HB2	1.72	0.53
1:A:204:ILE:HD13	1:A:540:LEU:HA	1.89	0.53
1:A:1033:TYR:H	1:A:1033:TYR:HD2	1.56	0.53
1:A:1056:MET:HE1	1:A:1134:VAL:CG2	2.39	0.53
1:A:1192:ILE:HG13	1:A:1193:ALA:N	2.23	0.53
1:A:989:THR:O	1:A:993:GLN:HG3	2.08	0.53
1:A:637:VAL:HG22	1:A:891:LEU:HD21	1.89	0.52
1:A:737:SER:HB2	1:A:774:VAL:HG23	1.92	0.52
1:A:1134:VAL:O	1:A:1135:CYG:O	2.26	0.52
1:A:497:ILE:HG21	1:A:500:ILE:HB	1.91	0.52
1:A:1135:CYG:O	1:A:1138:CYS:N	2.37	0.52
1:A:1004:GLN:NE2	1:A:1232:THR:HG23	2.25	0.52
1:A:1023:PHE:CE1	1:A:1025:ILE:HG22	2.44	0.52
1:A:91:ALA:HB2	1:A:1099:VAL:HG11	1.92	0.52
1:A:675:VAL:HG12	1:A:677:VAL:HG13	1.91	0.52
1:A:906:GLN:OE1	1:A:965:VAL:HB	2.10	0.52
1:A:893:THR:O	1:A:897:MET:HG3	2.09	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:396:VAL:CG2	1:A:850:LEU:HB2	2.40	0.51
1:A:219:HIS:HE1	2:A:2001:ANP:O2A	1.94	0.51
1:A:225:ASP:HB2	1:A:613:THR:HG23	1.93	0.51
1:A:605:LEU:C	1:A:607:GLY:H	2.19	0.51
1:A:873:LEU:HD13	1:A:879:LEU:HD21	1.93	0.51
1:A:408:HIS:NE2	1:A:794:MET:HE3	2.26	0.51
1:A:-5:VAL:HG12	1:A:-4:PRO:HD2	1.94	0.50
1:A:-7:GLY:O	1:A:3:GLU:HG3	2.11	0.50
1:A:1019:VAL:CG1	1:A:1020:LYS:N	2.74	0.50
1:A:1033:TYR:N	1:A:1033:TYR:HD2	2.10	0.50
1:A:202:ASN:HB2	1:A:205:GLU:HG3	1.94	0.50
1:A:201:PRO:HB2	1:A:206:LEU:HD13	1.94	0.49
1:A:413:LEU:HD13	1:A:801:VAL:HG11	1.93	0.49
1:A:765:CYS:HB2	1:A:766:PRO:HD3	1.93	0.49
1:A:1052:SER:O	1:A:1054:VAL:N	2.45	0.49
1:A:259:ASN:HA	2:A:2001:ANP:O1B	2.13	0.49
1:A:304:PRO:HB2	1:A:368:GLU:HB2	1.95	0.49
1:A:1139:GLN:O	1:A:1143:ASN:ND2	2.46	0.49
1:A:218:ARG:NH2	1:A:220:LYS:HE2	2.26	0.49
1:A:648:GLU:HB2	1:A:985:TRP:CE3	2.48	0.49
1:A:725:ALA:HB2	1:A:882:TRP:CD1	2.47	0.49
1:A:228:ILE:HD13	1:A:233:GLN:HG3	1.94	0.49
1:A:1019:VAL:HG12	1:A:1020:LYS:N	2.28	0.48
1:A:335:PHE:CB	1:A:366:MET:HE1	2.43	0.48
1:A:337:VAL:O	1:A:391:THR:HA	2.13	0.48
1:A:161:VAL:HB	1:A:201:PRO:HG2	1.93	0.48
1:A:1135:CYG:HB3	1:A:1260:HIS:CE1	2.49	0.48
1:A:1101:GLY:O	1:A:1104:GLU:HB2	2.14	0.48
1:A:301:ALA:O	1:A:360:VAL:HG22	2.13	0.48
1:A:1236:ASN:HD21	1:A:1243:GLY:HA2	1.76	0.48
1:A:278:GLY:O	1:A:1068:ILE:HG23	2.14	0.48
1:A:486:ASP:O	1:A:490:GLN:HG3	2.13	0.48
1:A:710:ALA:HA	1:A:856:ASP:OD1	2.14	0.48
1:A:295:THR:HB	1:A:297:ASN:HD21	1.79	0.48
1:A:1166:GLU:O	1:A:1195:SER:HA	2.14	0.48
1:A:400:ASN:HB3	1:A:403:GLU:OE1	2.14	0.47
1:A:842:ALA:O	1:A:846:VAL:HB	2.14	0.47
1:A:471:GLN:HE21	1:A:472:ARG:H	1.61	0.47
1:A:1080:ILE:HG22	1:A:1081:GLY:N	2.30	0.47
1:A:1194:VAL:HG13	1:A:1196:HIS:CE1	2.49	0.47
1:A:29:GLN:HG3	1:A:31:HIS:CE1	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:466:ASP:CB	1:A:467:PHE:HB2	2.41	0.47
1:A:631:ILE:HG21	1:A:917:LEU:HD21	1.97	0.47
1:A:936:ARG:O	1:A:940:GLU:HG3	2.15	0.47
1:A:1170:SER:HB2	1:A:1194:VAL:HG21	1.96	0.47
1:A:1088:LEU:HG	1:A:1089:VAL:N	2.29	0.46
1:A:379:GLU:HB3	1:A:475:PRO:HB2	1.96	0.46
1:A:411:ILE:HG12	1:A:741:MET:HG2	1.97	0.46
1:A:637:VAL:HG22	1:A:891:LEU:HD22	1.96	0.46
1:A:689:SER:HG	1:A:691:TYR:HD2	1.63	0.46
1:A:1101:GLY:HA3	1:A:1104:GLU:HG3	1.97	0.46
1:A:1203:VAL:HG21	1:A:1209:LEU:HB2	1.97	0.46
1:A:427:LYS:HB3	1:A:499:PHE:CD1	2.50	0.46
1:A:712:ALA:HA	1:A:800:LEU:HD23	1.97	0.46
1:A:517:SER:C	1:A:519:GLY:N	2.70	0.46
1:A:837:ALA:HB1	1:A:853:LYS:O	2.14	0.46
1:A:298:HIS:HB3	1:A:299:PRO:HD3	1.96	0.46
1:A:335:PHE:CD1	1:A:366:MET:HE1	2.50	0.46
1:A:944:ALA:HA	1:A:949:ALA:HB2	1.97	0.46
1:A:471:GLN:NE2	1:A:472:ARG:H	2.13	0.46
1:A:880:LEU:HB2	1:A:930:GLN:O	2.15	0.45
1:A:387:GLY:HA2	1:A:697:ILE:CD1	2.35	0.45
1:A:880:LEU:HD11	1:A:932:ARG:HG2	1.98	0.45
1:A:90:LYS:O	1:A:93:ASP:HB2	2.16	0.45
1:A:380:PHE:O	1:A:479:ARG:HD3	2.17	0.45
1:A:767:GLN:HB3	1:A:860:VAL:HG11	1.98	0.45
1:A:296:HIS:HD2	1:A:307:GLY:O	2.00	0.45
1:A:813:HIS:CD2	1:A:877:ARG:HD3	2.52	0.45
1:A:1194:VAL:HG11	1:A:1237:PRO:HG3	1.99	0.45
2:A:2001:ANP:O5'	2:A:2001:ANP:H8	2.17	0.45
1:A:437:ILE:HG22	1:A:438:VAL:N	2.32	0.45
1:A:505:ALA:C	1:A:507:GLY:H	2.24	0.45
1:A:116:ALA:HB1	1:A:119:LEU:HD11	1.98	0.45
1:A:1134:VAL:HG12	1:A:1135:CYG:N	2.32	0.45
1:A:1222:TYR:CZ	1:A:1245:THR:HG21	2.52	0.45
1:A:1135:CYG:C	1:A:1137:GLY:N	2.81	0.45
1:A:14:PHE:CD1	1:A:14:PHE:C	2.94	0.44
1:A:377:ASN:OD1	1:A:382:ARG:HD2	2.17	0.44
1:A:815:LEU:N	1:A:815:LEU:HD12	2.32	0.44
1:A:208:MET:HG3	1:A:509:SER:O	2.16	0.44
1:A:332:LEU:HD13	1:A:416:GLY:HA2	1.98	0.44
1:A:44:ASN:OD1	1:A:45:ALA:N	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:220:LYS:NZ	1:A:220:LYS:HB3	2.32	0.44
1:A:292:LYS:HB3	1:A:315:GLU:OE2	2.18	0.44
1:A:119:LEU:HD12	1:A:119:LEU:N	2.32	0.44
1:A:1028:ASP:C	1:A:1030:ALA:H	2.25	0.44
1:A:421:ARG:NH1	1:A:492:GLY:HA2	2.33	0.44
1:A:271:TYR:CZ	1:A:280:TYR:HB3	2.53	0.44
1:A:297:ASN:OD1	1:A:411:ILE:HA	2.17	0.44
1:A:643:LEU:HD12	1:A:644:PRO:HD2	1.98	0.44
1:A:741:MET:SD	1:A:778:SER:HB2	2.58	0.44
1:A:337:VAL:CG1	1:A:366:MET:HE3	2.48	0.44
1:A:472:ARG:O	1:A:548:GLN:HG3	2.18	0.44
1:A:342:ILE:HB	1:A:345:PHE:HB3	1.99	0.44
1:A:672:PRO:HG3	1:A:1272:TRP:NE1	2.32	0.44
1:A:1043:ALA:HB2	1:A:1085:PHE:CD2	2.53	0.44
1:A:120:THR:N	1:A:123:GLN:HE21	2.03	0.44
1:A:259:ASN:ND2	1:A:502:ASP:HB3	2.33	0.44
1:A:290:LEU:HD12	1:A:290:LEU:C	2.43	0.44
1:A:760:VAL:O	1:A:765:CYS:HB2	2.18	0.44
1:A:1155:PRO:CB	1:A:1201:VAL:HG13	2.48	0.44
1:A:316:ILE:HD13	1:A:380:PHE:CD2	2.53	0.43
1:A:499:PHE:C	1:A:499:PHE:CD2	2.96	0.43
1:A:1044:VAL:HA	1:A:1089:VAL:HG13	1.99	0.43
1:A:45:ALA:HB1	1:A:46:PRO:HD2	1.99	0.43
1:A:634:ALA:HA	1:A:974:PHE:HE1	1.84	0.43
1:A:376:PHE:CD1	1:A:475:PRO:HG3	2.53	0.43
1:A:631:ILE:H	1:A:631:ILE:CD1	2.29	0.43
1:A:625:ALA:HA	1:A:852:ASP:HB2	2.00	0.43
1:A:298:HIS:HB2	1:A:409:LYS:HE3	2.01	0.43
1:A:120:THR:OG1	1:A:122:GLU:HB2	2.19	0.43
1:A:736:LEU:HG	1:A:802:ILE:CG2	2.49	0.43
1:A:1099:VAL:O	1:A:1100:LEU:HB2	2.19	0.42
1:A:208:MET:HE3	1:A:605:LEU:HD13	2.01	0.42
1:A:930:GLN:HE21	1:A:930:GLN:HB3	1.63	0.42
1:A:253:LEU:HB3	1:A:425:VAL:HG11	2.01	0.42
1:A:273:ALA:HA	1:A:280:TYR:HA	2.01	0.42
1:A:786:GLN:HA	1:A:786:GLN:OE1	2.19	0.42
1:A:1192:ILE:HD12	1:A:1283:TRP:CE2	2.53	0.42
1:A:437:ILE:HG12	1:A:576:VAL:HG12	2.01	0.42
1:A:658:ARG:O	1:A:664:VAL:HG11	2.19	0.42
1:A:729:GLY:O	1:A:730:ASP:C	2.62	0.42
1:A:70:PRO:HB3	1:A:113:TYR:CZ	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:637:VAL:O	1:A:641:LEU:HG	2.20	0.42
1:A:768:LEU:CD2	1:A:864:LYS:HB2	2.49	0.42
1:A:42:ASP:HB2	1:A:150:PHE:CD1	2.55	0.42
1:A:379:GLU:OE2	1:A:475:PRO:HD2	2.19	0.42
1:A:331:GLY:HA2	1:A:416:GLY:HA3	2.02	0.42
1:A:1017:LEU:HD22	1:A:1191:PRO:HB3	2.02	0.42
1:A:114:ILE:HD11	1:A:131:LEU:HD11	2.02	0.42
1:A:154:GLN:OE1	1:A:154:GLN:HA	2.20	0.42
1:A:397:ASN:HA	1:A:402:GLU:HA	2.02	0.41
1:A:560:LEU:HD12	1:A:560:LEU:HA	1.85	0.41
1:A:560:LEU:N	1:A:561:PRO:CD	2.83	0.41
1:A:646:VAL:HG13	1:A:892:VAL:HG11	2.02	0.41
1:A:1192:ILE:CG1	1:A:1193:ALA:N	2.83	0.41
1:A:11:LEU:HD11	1:A:112:TYR:CE1	2.52	0.41
1:A:228:ILE:HD13	1:A:233:GLN:CG	2.50	0.41
1:A:295:THR:HB	1:A:297:ASN:ND2	2.35	0.41
1:A:333:VAL:O	1:A:387:GLY:HA3	2.19	0.41
1:A:486:ASP:HA	1:A:489:TRP:CD1	2.54	0.41
1:A:290:LEU:HD22	1:A:322:THR:HG21	2.01	0.41
1:A:538:SER:OG	1:A:541:GLU:HG3	2.20	0.41
1:A:1001:CYS:HB3	1:A:1233:TYR:CD2	2.55	0.41
1:A:1081:GLY:HA2	1:A:1119:GLU:OE2	2.19	0.41
1:A:233:GLN:HA	1:A:234:PRO:HD3	1.79	0.41
1:A:838:LEU:HD23	1:A:838:LEU:HA	1.85	0.41
1:A:1196:HIS:CG	1:A:1258:MET:HE2	2.55	0.41
1:A:649:LYS:O	1:A:653:VAL:HG23	2.20	0.41
1:A:713:ARG:HG2	1:A:764:LEU:HD22	2.01	0.41
1:A:786:GLN:NE2	1:A:791:GLN:HG2	2.35	0.41
1:A:1102:ALA:HB1	1:A:1139:GLN:OE1	2.21	0.41
1:A:1146:GLU:HG3	1:A:1147:LEU:HD13	2.02	0.41
1:A:85:SER:O	1:A:88:SER:HB3	2.20	0.41
1:A:1148:ILE:HA	1:A:1149:PRO:HD3	1.85	0.41
1:A:237:LEU:HD23	1:A:240:MET:CE	2.50	0.41
1:A:538:SER:O	1:A:542:ILE:HG13	2.20	0.41
1:A:303:SER:O	1:A:306:PRO:HD2	2.19	0.41
1:A:365:ILE:HD13	1:A:410:PRO:HG3	2.03	0.41
1:A:371:LEU:HD21	1:A:1164:ARG:HD2	2.02	0.41
1:A:651:PHE:CE1	1:A:992:MET:HE2	2.56	0.41
1:A:882:TRP:CG	1:A:883:HIS:N	2.89	0.41
1:A:1017:LEU:CD2	1:A:1171:LEU:HB2	2.51	0.41
1:A:356:PRO:HB2	1:A:359:ILE:HG12	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:703:VAL:HG21	1:A:714:LEU:HD12	2.02	0.41
1:A:727:GLN:OE1	1:A:810:ASP:HB3	2.21	0.40
1:A:776:LYS:HD2	1:A:776:LYS:HA	1.81	0.40
1:A:305:TRP:HB3	1:A:306:PRO:CD	2.44	0.40
1:A:396:VAL:HG11	1:A:705:LEU:HD13	2.02	0.40
1:A:820:SER:OG	1:A:822:GLU:HG2	2.22	0.40
1:A:1128:GLN:OE1	1:A:1128:GLN:HA	2.21	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	1280/1303 (98%)	1152 (90%)	116 (9%)	12 (1%)	14 47

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	13	ALA
1	A	117	SER
1	A	623	GLY
1	A	1053	HIS
1	A	1136	ASN
1	A	467	PHE
1	A	-6	LEU
1	A	836	ASN
1	A	818	GLN
1	A	423	ASP
1	A	492	GLY
1	A	234	PRO

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	1030/1040 (99%)	969 (94%)	61 (6%)	18 50

All (61) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	-3	ARG
1	A	6	ARG
1	A	24	GLN
1	A	43	LEU
1	A	46	PRO
1	A	67	SER
1	A	118	THR
1	A	119	LEU
1	A	122	GLU
1	A	132	HIS
1	A	169	GLN
1	A	175	ASN
1	A	191	GLN
1	A	204	ILE
1	A	218	ARG
1	A	248	THR
1	A	253	LEU
1	A	279	ARG
1	A	291	MET
1	A	332	LEU
1	A	336	SER
1	A	358	ARG
1	A	382	ARG
1	A	396	VAL
1	A	412	MET
1	A	442	PRO
1	A	469	SER
1	A	471	GLN
1	A	487	ARG
1	A	502	ASP

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Mol	Chain	Res	Type
1	A	532	SER
1	A	560	LEU
1	A	588	LEU
1	A	597	PRO
1	A	600	LEU
1	A	611	LYS
1	A	613	THR
1	A	624	ASP
1	A	631	ILE
1	A	644	PRO
1	A	736	LEU
1	A	747	PRO
1	A	774	VAL
1	A	790	GLU
1	A	823	ASP
1	A	846	VAL
1	A	854	PRO
1	A	891	LEU
1	A	930	GLN
1	A	950	ASP
1	A	1029	ILE
1	A	1033	TYR
1	A	1116	VAL
1	A	1117	ARG
1	A	1182	LEU
1	A	1183	GLN
1	A	1186	VAL
1	A	1190	MET
1	A	1203	VAL
1	A	1245	THR
1	A	1279	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (38) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	31	HIS
1	A	39	HIS
1	A	52	GLN
1	A	54	GLN
1	A	96	HIS
1	A	123	GLN
1	A	153	HIS

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Mol	Chain	Res	Type
1	A	175	ASN
1	A	219	HIS
1	A	259	ASN
1	A	283	HIS
1	A	296	HIS
1	A	298	HIS
1	A	339	ASN
1	A	347	GLN
1	A	397	ASN
1	A	408	HIS
1	A	419	ASN
1	A	426	GLN
1	A	445	ASN
1	A	471	GLN
1	A	501	HIS
1	A	545	ASN
1	A	548	GLN
1	A	584	GLN
1	A	589	HIS
1	A	739	ASN
1	A	767	GLN
1	A	818	GLN
1	A	824	ASN
1	A	902	HIS
1	A	953	HIS
1	A	969	ASN
1	A	993	GLN
1	A	1004	GLN
1	A	1026	ASN
1	A	1125	HIS
1	A	1176	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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
1	CYG	A	1135	1	12,14,15	0.99	1 (8%)	10,17,19	3.65	4 (40%)

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
1	CYG	A	1135	1	-	8/14/16/18	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1135	CYG	O1-C1	2.68	1.30	1.22

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1135	CYG	OE2-CD1-CG1	-7.76	115.02	123.98
1	A	1135	CYG	CG1-CD1-SG	6.40	121.03	113.40
1	A	1135	CYG	CB-SG-CD1	-3.97	95.31	100.76
1	A	1135	CYG	O2-C1-O1	-3.03	117.20	124.08

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	1135	CYG	C-CA-CB-SG
1	A	1135	CYG	OE2-CD1-SG-CB
1	A	1135	CYG	N-CA-CB-SG
1	A	1135	CYG	SG-CD1-CG1-CB1
1	A	1135	CYG	OE2-CD1-CG1-CB1
1	A	1135	CYG	CG1-CD1-SG-CB
1	A	1135	CYG	CA-CB-SG-CD1
1	A	1135	CYG	O1-C1-CA1-N1

There are no ring outliers.

1 monomer is involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1135	CYG	8	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 3 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	SO4	A	2002	-	4,4,4	0.53	0	6,6,6	0.20	0
3	ADP	A	2005	4	28,29,29	2.06	4 (14%)	43,45,45	1.38	6 (13%)
2	ANP	A	2001	-	33,33,33	5.00	12 (36%)	45,52,52	2.83	11 (24%)
5	SO4	A	2009	-	4,4,4	0.53	0	6,6,6	0.20	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	ADP	A	2005	4	-	0/16/32/32	0/3/3/3
2	ANP	A	2001	-	-	7/18/38/38	0/3/3/3

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	2001	ANP	PG-O1G	15.96	1.70	1.46
2	A	2001	ANP	PB-O1B	13.98	1.67	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	2001	ANP	PB-O3A	11.94	1.73	1.59
2	A	2001	ANP	PA-O3A	11.05	1.71	1.59
3	A	2005	ADP	O4'-C4'	-7.95	1.27	1.45
2	A	2001	ANP	PA-O1A	5.21	1.68	1.50
3	A	2005	ADP	O3'-C3'	-4.72	1.31	1.43
2	A	2001	ANP	PG-O3G	4.22	1.68	1.56
2	A	2001	ANP	C5'-C4'	3.36	1.61	1.51
2	A	2001	ANP	C2-N1	2.53	1.38	1.33
2	A	2001	ANP	C5-N7	-2.37	1.34	1.39
3	A	2005	ADP	C6-N6	-2.36	1.28	1.34
2	A	2001	ANP	C4-N3	2.34	1.38	1.34
3	A	2005	ADP	PB-O2B	-2.08	1.47	1.54
2	A	2001	ANP	C5-C4	2.05	1.42	1.39
2	A	2001	ANP	C6-N1	2.03	1.41	1.35

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	2001	ANP	O1B-PB-N3B	-12.36	93.57	111.77
2	A	2001	ANP	O5'-PA-O1A	-6.91	81.54	108.94
2	A	2001	ANP	O5'-C5'-C4'	5.84	128.87	108.99
2	A	2001	ANP	O2B-PB-O3A	4.44	119.47	104.64
2	A	2001	ANP	O3A-PB-N3B	4.18	118.19	106.59
3	A	2005	ADP	C2-N1-C6	3.70	124.80	118.73
2	A	2001	ANP	N3-C2-N1	-3.54	123.22	128.58
3	A	2005	ADP	N3-C2-N1	-3.22	123.71	128.58
2	A	2001	ANP	O3A-PA-O1A	-2.91	101.94	110.70
2	A	2001	ANP	C6-C5-C4	-2.85	113.28	117.18
3	A	2005	ADP	C5-C4-N3	2.80	130.57	126.72
2	A	2001	ANP	C5'-C4'-C3'	-2.61	105.82	115.21
2	A	2001	ANP	PA-O5'-C5'	-2.46	107.24	121.35
3	A	2005	ADP	O4'-C4'-C5'	2.29	116.67	109.33
2	A	2001	ANP	N9-C8-N7	2.14	116.98	113.94
3	A	2005	ADP	C4'-O4'-C1'	2.14	114.20	109.47
3	A	2005	ADP	O2A-PA-O1A	2.04	121.92	112.44

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	2001	ANP	PB-N3B-PG-O1G
2	A	2001	ANP	PA-O3A-PB-O2B

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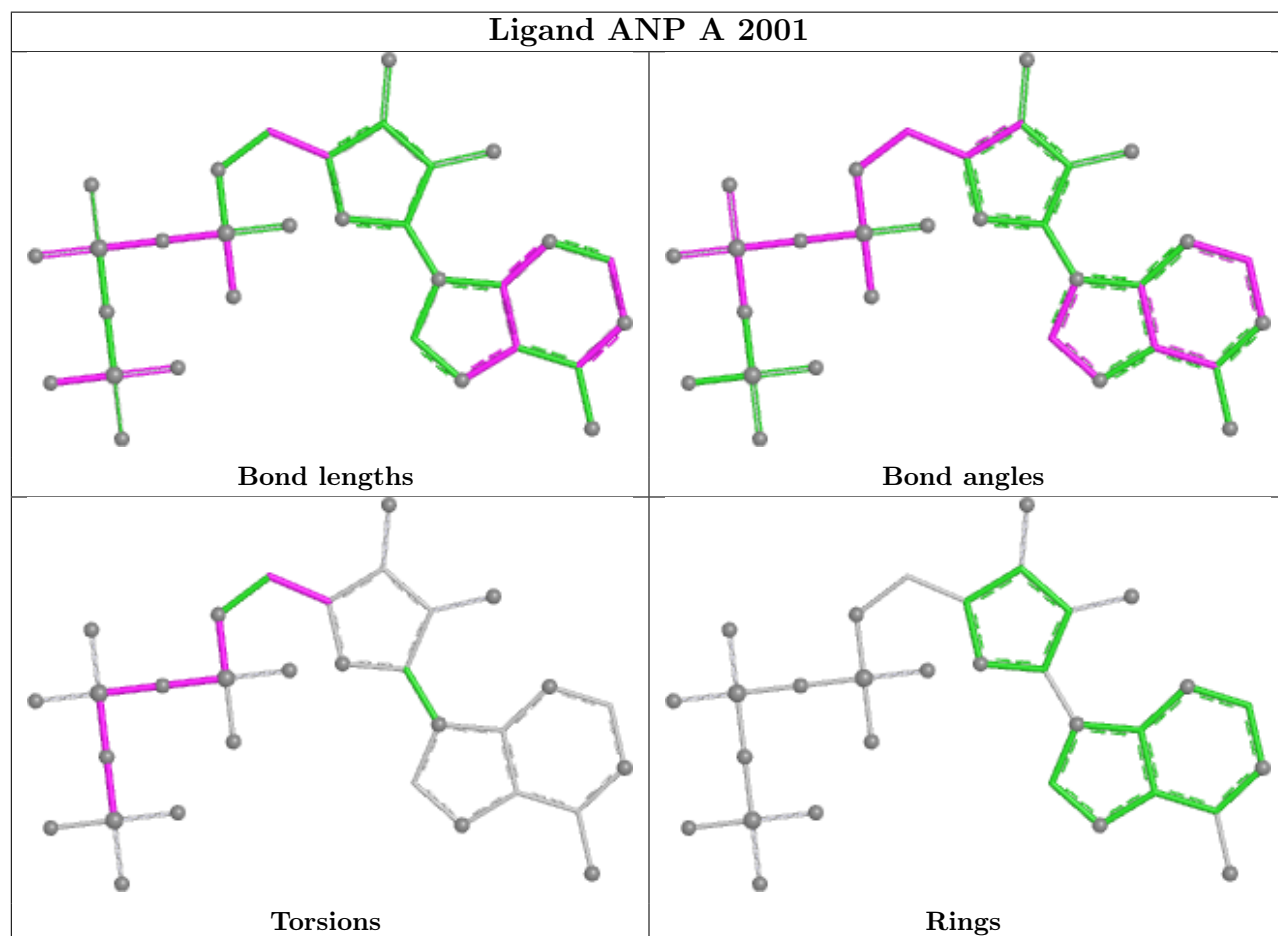
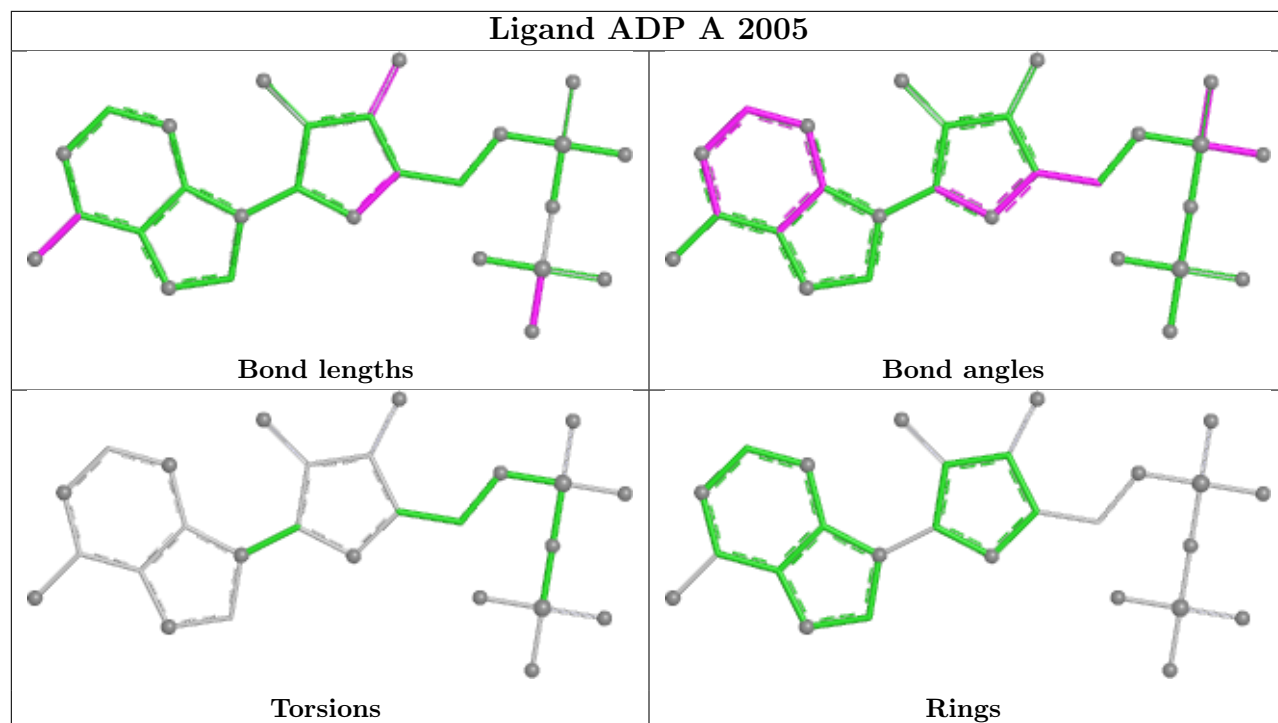
Mol	Chain	Res	Type	Atoms
2	A	2001	ANP	C5'-O5'-PA-O3A
2	A	2001	ANP	PG-N3B-PB-O3A
2	A	2001	ANP	O4'-C4'-C5'-O5'
2	A	2001	ANP	C5'-O5'-PA-O1A
2	A	2001	ANP	PB-O3A-PA-O1A

There are no ring outliers.

2 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	2001	ANP	3	0
5	A	2009	SO4	5	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	1284/1303 (98%)	-0.18	10 (0%) 82 67	11, 28, 52, 95	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	466	ASP	5.1
1	A	-6	LEU	4.8
1	A	-7	GLY	4.4
1	A	-4	PRO	3.5
1	A	-5	VAL	3.2
1	A	788	GLY	2.5
1	A	610	PRO	2.4
1	A	117	SER	2.2
1	A	-1	SER	2.1
1	A	60	GLN	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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(Å ²)	Q<0.9
1	CYG	A	1135	15/16	0.92	0.14	43,45,46,48	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

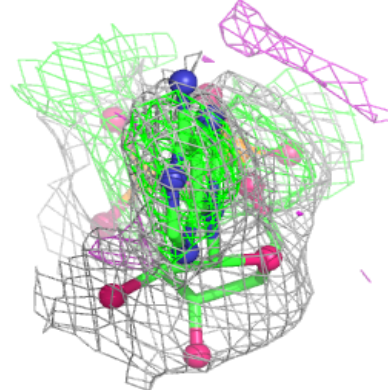
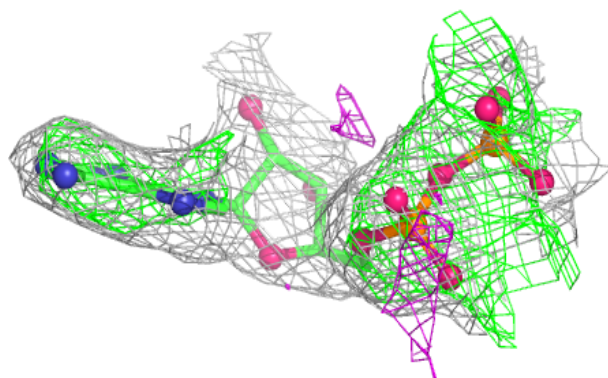
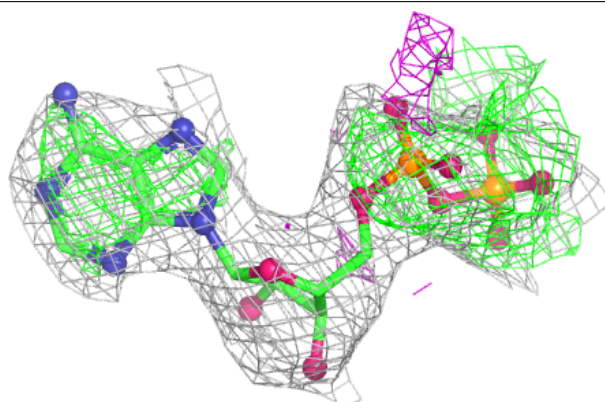
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
5	SO4	A	2009	5/5	0.67	0.39	30,30,30,30	0
3	ADP	A	2005	27/27	0.88	0.25	30,30,30,30	18
5	SO4	A	2002	5/5	0.89	0.11	30,30,30,30	0
2	ANP	A	2001	31/31	0.92	0.11	30,30,30,30	0
4	MG	A	2007	1/1	0.93	0.39	30,30,30,30	0
4	MG	A	2006	1/1	0.94	0.31	30,30,30,30	0
4	MG	A	2008	1/1	0.98	0.17	30,30,30,30	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.

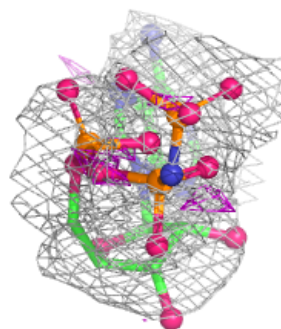
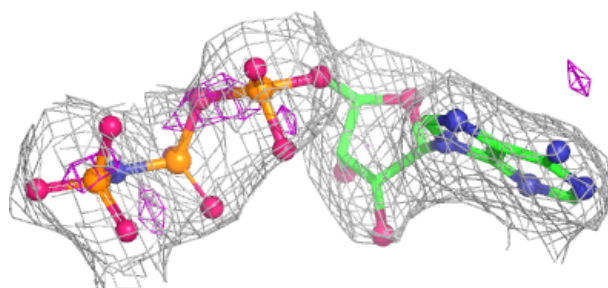
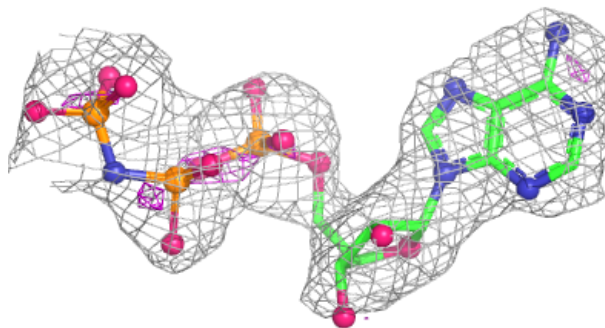
Electron density around ADP A 2005:

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 ANP A 2001:

$2mF_o - DF_c$ (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.