



# Full wwPDB X-ray Structure Validation Report ⓘ

May 24, 2020 – 10:44 pm BST

PDB ID : 2IOA  
Title : E. coli Bifunctional glutathionylspermidine synthetase/amidase Incomplex with Mg<sup>2+</sup> and ADP and phosphinate inhibitor  
Authors : Pai, C.H.; Chiang, B.Y.; Ko, T.P.; Chou, C.C.; Chong, C.M.; Yen, F.J.; Coward, J.K.; Wang, A.H.-J.; Lin, C.H.  
Deposited on : 2006-10-10  
Resolution : 2.80 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](mailto: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.

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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 : 2.11  
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) : 2.11

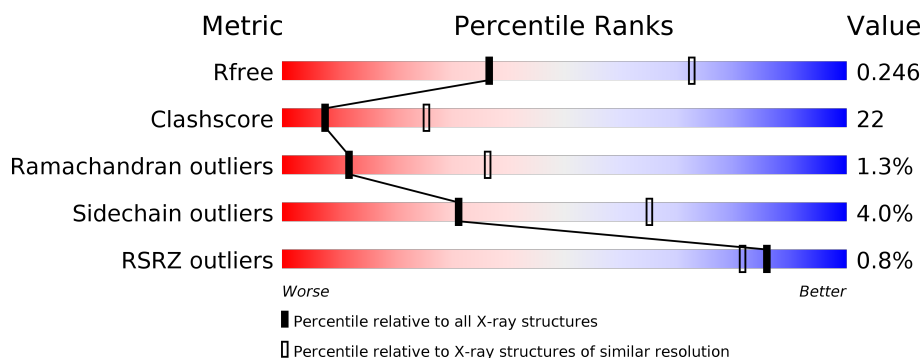
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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  $\geq 3$ , 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	619	<div> <div>%</div> <div> <div></div> <div>56%</div> <div>37%</div> <div>• 5%</div> </div> </div>
1	B	619	<div> <div>%</div> <div> <div></div> <div>58%</div> <div>34%</div> <div>• 5%</div> </div> </div>

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 10089 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.

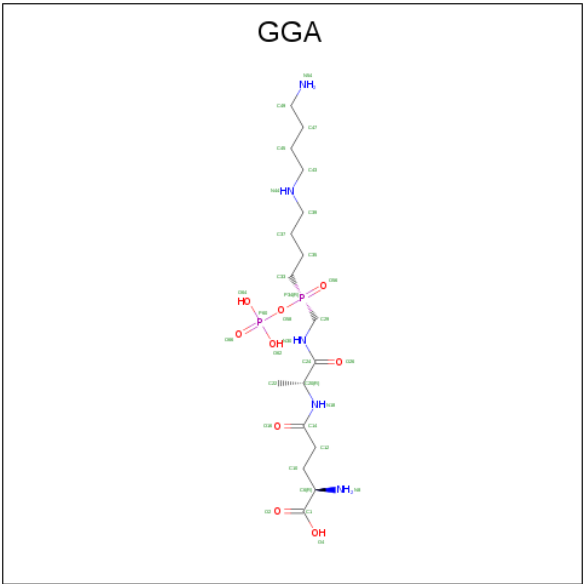
- Molecule 1 is a protein called Bifunctional glutathionylspermidine synthetase/amidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	589	Total	C	N	O	S	0	0	0
			4755	3051	813	872	19			
1	B	589	Total	C	N	O	S	0	0	0
			4753	3048	813	873	19			

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

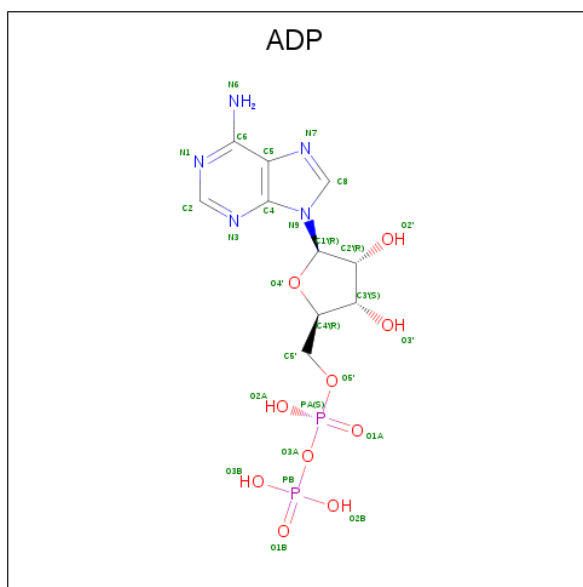
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total	Mg	0	0
			2	2		
2	A	2	Total	Mg	0	0
			2	2		

- Molecule 3 is D-GAMMA-GLUTAMYL-N-{|(R)-{4-[(4-AMINOBTUTYL)AMINO]BTUTYL } (PHOSPHONOOXY)PHOSPHORYL|METHYL}-D-ALANINAMIDE (three-letter code: GGA) (formula: C<sub>17</sub>H<sub>37</sub>N<sub>5</sub>O<sub>9</sub>P<sub>2</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			33	17	5	9	2		
3	B	1	Total	C	N	O	P	0	0
			33	17	5	9	2		

- Molecule 4 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula:  $C_{10}H_{15}N_5O_{10}P_2$ ).



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

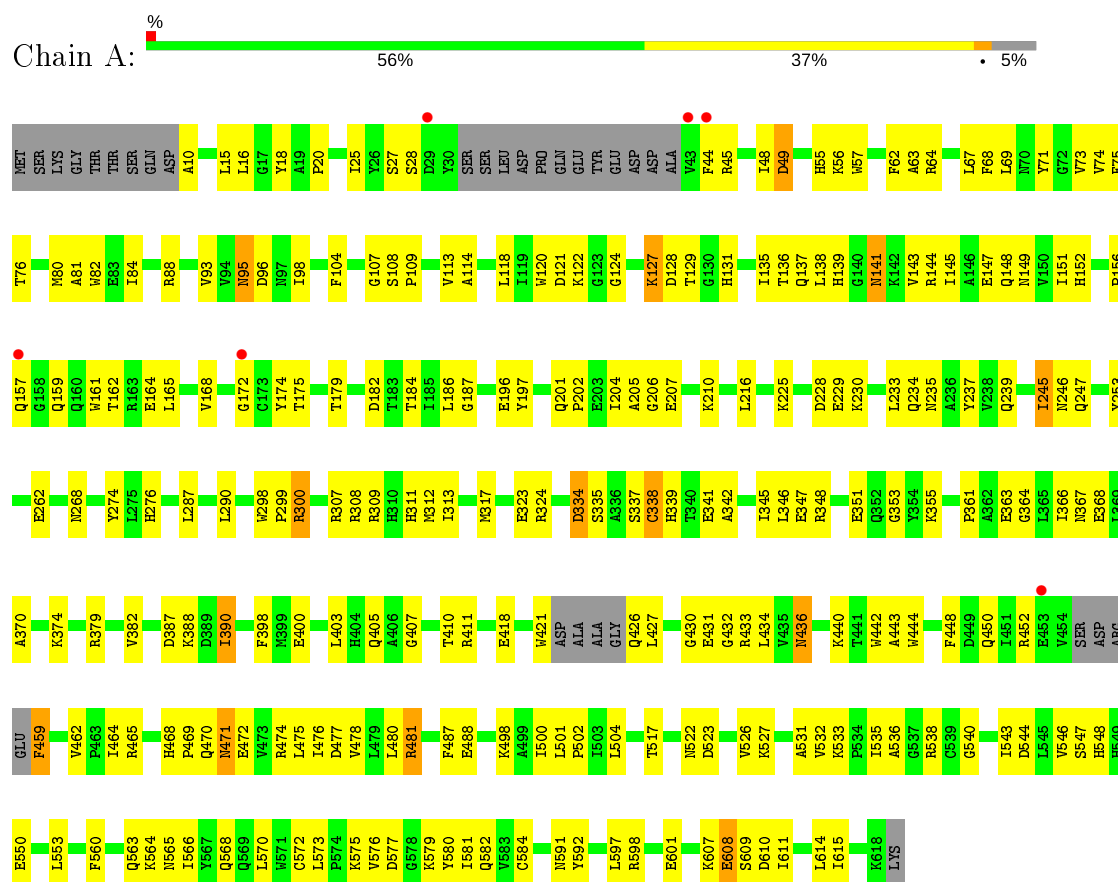
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	236	Total	O	0	0
			236	236		
5	B	221	Total	O	0	0
			221	221		

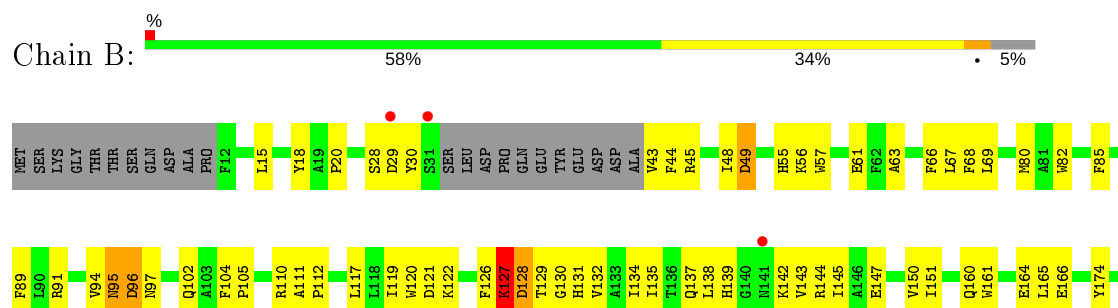
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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: Bifunctional glutathionylspermidine synthetase/amidase



- Molecule 1: Bifunctional glutathionylspermidine synthetase/amidase





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	60.03Å 75.29Å 84.66Å 70.09° 74.06° 77.55°	Depositor
Resolution (Å)	30.00 – 2.80 29.49 – 2.69	Depositor EDS
% Data completeness (in resolution range)	(Not available) (30.00-2.80) 93.6 (29.49-2.69)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	6.23 (at 2.68Å)	Xtriage
Refinement program	CNS, XTALVIEW	Depositor
R, $R_{free}$	0.173 , 0.243 0.178 , 0.246	Depositor DCC
$R_{free}$ test set	3491 reflections (9.91%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	32.8	Xtriage
Anisotropy	0.415	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 63.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	10089	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.63% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: MG, GGA, 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	0.43	0/4877	0.67	0/6621
1	B	0.43	0/4874	0.68	0/6615
All	All	0.43	0/9751	0.68	0/13236

There are no bond length outliers.

There are no bond angle outliers.

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	4755	0	4641	217	0
1	B	4753	0	4637	202	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	33	0	35	8	0
3	B	33	0	34	2	0
4	A	27	0	11	2	0
4	B	27	0	11	0	0
5	A	236	0	0	18	0
5	B	221	0	0	8	0
All	All	10089	0	9369	417	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 22.

All (417) 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:245:ILE:O	5:A:4192:HOH:O	1.73	1.03
1:A:210:LYS:HD3	1:A:323:GLU:HB3	1.40	1.02
1:A:64:ARG:HG3	1:A:74:VAL:HG23	1.43	0.96
1:A:311:HIS:ND1	5:A:4195:HOH:O	1.97	0.96
1:A:341:GLU:HG2	1:A:611:ILE:HG13	1.48	0.93
1:B:608:GLU:CD	1:B:608:GLU:H	1.79	0.87
1:B:268:ASN:HD21	1:B:592:TYR:H	1.24	0.83
1:A:311:HIS:CE1	5:A:4195:HOH:O	2.32	0.83
1:B:607:LYS:O	3:B:6002:GGA:H432	1.79	0.83
1:B:465:ARG:HG3	1:B:474:ARG:HH21	1.42	0.82
1:B:233:LEU:HD12	1:B:401:GLN:OE1	1.80	0.81
1:A:607:LYS:O	3:A:6001:GGA:H432	1.82	0.80
1:B:337:SER:O	1:B:338:CYS:HB2	1.81	0.80
1:A:121:ASP:HB2	1:A:186:LEU:HD21	1.62	0.80
1:A:28:SER:HB3	1:A:57:TRP:HB2	1.63	0.79
1:B:341:GLU:HG2	1:B:611:ILE:HG13	1.65	0.79
1:B:384:ILE:HG23	1:B:439:TRP:HE3	1.49	0.78
1:B:418:GLU:HG3	1:B:430:GLY:H	1.49	0.77
1:A:311:HIS:O	1:A:313:ILE:HD12	1.86	0.75
1:A:442:TRP:HE3	3:A:6001:GGA:O2	1.67	0.75
1:A:498:LYS:HB3	1:A:566:ILE:HD13	1.70	0.74
1:A:390:ILE:H	1:A:390:ILE:HD12	1.51	0.74
1:B:245:ILE:HG13	1:B:246:ASN:H	1.52	0.74
1:A:540:GLY:HA2	1:A:543:ILE:HD12	1.71	0.72
1:B:361:PRO:HG3	1:B:614:LEU:HD23	1.71	0.72
1:B:138:LEU:HD12	1:B:143:VAL:HG12	1.71	0.72
1:A:337:SER:O	1:A:338:CYS:HB2	1.88	0.72
1:A:138:LEU:HD12	1:A:143:VAL:HG12	1.71	0.72
1:A:137:GLN:HG2	1:A:144:ARG:HB2	1.72	0.71
1:A:421:TRP:H	1:A:471:ASN:HD21	1.38	0.71
1:A:442:TRP:CE3	3:A:6001:GGA:O2	2.44	0.71
1:B:204:ILE:HD13	1:B:205:ALA:N	2.05	0.71
1:A:151:ILE:HD12	1:A:162:THR:HB	1.72	0.70
1:B:301:LEU:HD13	1:B:494:ILE:HD11	1.73	0.70
1:A:48:ILE:HD13	1:A:69:LEU:HD21	1.74	0.69
1:A:96:ASP:CG	1:A:309:ARG:HH21	1.96	0.69
1:A:137:GLN:HE21	1:A:139:HIS:CE1	2.10	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:268:ASN:HD21	1:A:592:TYR:H	1.40	0.69
1:A:20:PRO:HG2	1:A:136:THR:HB	1.74	0.69
1:A:448:PHE:O	1:A:452:ARG:HG3	1.93	0.69
1:A:579:LYS:HD2	5:A:4086:HOH:O	1.92	0.68
1:A:201:GLN:HG3	1:A:202:PRO:HD2	1.73	0.68
1:A:157:GLN:CD	1:A:157:GLN:H	1.96	0.68
1:A:82:TRP:HD1	1:A:129:THR:O	1.77	0.68
1:B:413:LEU:HD23	1:B:418:GLU:OE1	1.94	0.68
1:B:532:VAL:HB	1:B:544:ASP:HB2	1.74	0.68
1:B:245:ILE:HG13	1:B:246:ASN:N	2.08	0.67
1:A:379:ARG:HH12	1:A:436:ASN:HB2	1.60	0.67
1:A:575:LYS:HD2	1:A:580:TYR:CZ	2.29	0.67
1:B:122:LYS:HB2	1:B:127:LYS:O	1.95	0.67
1:B:522:ASN:HD22	1:B:522:ASN:C	1.98	0.67
1:A:337:SER:OG	3:A:6001:GGA:H372	1.95	0.66
1:A:418:GLU:HG2	1:A:418:GLU:O	1.94	0.66
1:A:527:LYS:O	1:A:548:HIS:HB3	1.95	0.66
1:B:233:LEU:HD11	1:B:398:PHE:HA	1.79	0.65
1:B:418:GLU:CG	1:B:430:GLY:H	2.09	0.65
1:B:598:ARG:NH1	5:B:4308:HOH:O	2.28	0.65
1:A:540:GLY:HA2	1:A:543:ILE:CD1	2.27	0.65
1:A:535:ILE:HG22	1:A:566:ILE:HG23	1.79	0.65
1:A:135:ILE:HD13	1:A:145:ILE:HG22	1.78	0.65
1:B:522:ASN:HD21	1:B:525:LEU:H	1.43	0.65
1:A:341:GLU:CG	1:A:611:ILE:HG13	2.24	0.64
1:A:210:LYS:HD3	1:A:323:GLU:CB	2.22	0.64
1:A:95:ASN:HD22	1:A:95:ASN:N	1.94	0.64
1:B:227:LEU:HD23	1:B:348:ARG:HG2	1.78	0.64
1:A:64:ARG:CG	1:A:74:VAL:HG23	2.21	0.64
1:A:15:LEU:HD21	1:A:18:TYR:CZ	2.33	0.63
1:A:426:GLN:N	5:A:4229:HOH:O	2.30	0.63
1:B:102:GLN:NE2	1:B:195:THR:HG22	2.14	0.63
1:B:215:ARG:HD3	5:B:4401:HOH:O	1.98	0.63
1:B:303:LEU:HD13	1:B:307:ARG:NH2	2.14	0.63
1:B:384:ILE:HG23	1:B:439:TRP:CE3	2.34	0.63
1:A:411:ARG:NE	1:A:418:GLU:OE1	2.28	0.62
1:A:579:LYS:HE3	1:A:601:GLU:OE2	1.98	0.62
1:B:164:GLU:O	1:B:165:LEU:HD23	1.99	0.62
1:B:105:PRO:HD3	1:B:199:LEU:HG	1.79	0.62
1:A:210:LYS:NZ	1:A:323:GLU:HG2	2.13	0.62
1:B:298:TRP:HB2	1:B:299:PRO:HD3	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:137:GLN:CD	1:B:144:ARG:HD2	2.20	0.62
1:A:390:ILE:N	1:A:390:ILE:HD12	2.15	0.61
1:B:498:LYS:HB2	1:B:535:ILE:HA	1.80	0.61
1:A:124:GLY:HA3	1:A:182:ASP:O	2.00	0.61
1:B:418:GLU:HG3	1:B:430:GLY:N	2.14	0.61
1:A:144:ARG:HD3	1:A:161:TRP:CD1	2.35	0.61
1:B:204:ILE:HD13	1:B:205:ALA:H	1.63	0.61
1:A:462:VAL:HG12	1:A:464:ILE:HG23	1.81	0.61
1:A:400:GLU:HG3	1:A:410:THR:OG1	2.01	0.60
1:B:166:GLU:HB3	5:B:4283:HOH:O	2.00	0.60
1:A:121:ASP:HB2	1:A:186:LEU:CD2	2.32	0.60
1:A:390:ILE:H	1:A:390:ILE:CD1	2.12	0.60
1:B:246:ASN:HB2	5:B:4468:HOH:O	2.02	0.60
1:B:498:LYS:HB3	1:B:566:ILE:HD13	1.84	0.60
1:A:298:TRP:HB2	1:A:299:PRO:HD3	1.84	0.60
1:A:474:ARG:NH2	1:A:477:ASP:OD2	2.35	0.60
1:B:135:ILE:HA	1:B:145:ILE:HG22	1.82	0.60
1:B:465:ARG:HG3	1:B:474:ARG:NH2	2.16	0.59
1:B:522:ASN:O	1:B:526:VAL:HG23	2.02	0.59
1:A:137:GLN:CD	1:A:144:ARG:HD2	2.23	0.59
1:B:247:GLN:HG3	5:B:4468:HOH:O	2.03	0.59
1:A:120:TRP:HB2	1:A:131:HIS:HB3	1.84	0.58
1:A:104:PHE:O	1:A:187:GLY:HA3	2.02	0.58
1:A:341:GLU:HG2	1:A:611:ILE:CG1	2.29	0.58
1:A:573:LEU:HD22	1:A:581:ILE:O	2.04	0.58
1:B:382:VAL:HB	1:B:410:THR:HG22	1.84	0.58
1:B:238:VAL:O	1:B:242:GLY:N	2.32	0.58
1:B:82:TRP:HD1	1:B:129:THR:O	1.86	0.58
1:B:523:ASP:O	1:B:526:VAL:HB	2.04	0.58
1:B:102:GLN:CD	1:B:195:THR:HG22	2.24	0.58
1:B:251:HIS:HE1	1:B:577:ASP:OD2	1.86	0.58
1:A:95:ASN:N	1:A:95:ASN:ND2	2.52	0.57
1:B:48:ILE:O	1:B:49:ASP:HB2	2.04	0.57
1:A:137:GLN:HE21	1:A:139:HIS:HE1	1.50	0.57
1:A:235:ASN:O	1:A:239:GLN:HG2	2.04	0.57
1:A:361:PRO:HG3	1:A:614:LEU:HD23	1.86	0.57
1:A:387:ASP:OD1	1:A:388:LYS:N	2.36	0.57
1:A:121:ASP:CB	1:A:186:LEU:HD21	2.33	0.57
1:B:235:ASN:O	1:B:239:GLN:HG2	2.05	0.57
1:B:538:ARG:NH1	1:B:560:PHE:HZ	2.03	0.57
1:B:341:GLU:CG	1:B:611:ILE:HG13	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:403:LEU:HD13	1:A:410:THR:HG21	1.87	0.56
1:A:351:GLU:O	1:A:351:GLU:HG2	2.05	0.56
1:A:312:MET:HA	1:A:488:GLU:OE2	2.06	0.56
1:A:538:ARG:NH1	1:A:560:PHE:HZ	2.02	0.56
1:B:468:HIS:CG	1:B:469:PRO:HD2	2.40	0.56
1:B:282:LEU:HD21	1:B:494:ILE:CD1	2.35	0.56
1:A:164:GLU:O	1:A:165:LEU:HD23	2.05	0.56
1:B:322:ASP:OD2	1:B:324:ARG:HB2	2.05	0.56
1:B:94:VAL:HG13	5:B:4347:HOH:O	2.05	0.56
1:A:502:PRO:HG3	1:A:517:THR:HG22	1.88	0.56
1:B:303:LEU:HD13	1:B:307:ARG:HH21	1.70	0.56
1:B:522:ASN:ND2	1:B:525:LEU:H	2.02	0.56
1:A:131:HIS:HE1	1:A:147:GLU:OE2	1.89	0.55
1:A:347:GLU:OE2	1:A:363:GLU:HB3	2.06	0.55
1:A:335:SER:HB2	5:A:4005:HOH:O	2.05	0.55
1:B:44:PHE:HD2	1:B:55:HIS:HE1	1.54	0.55
1:A:151:ILE:CD1	1:A:162:THR:HB	2.35	0.55
1:A:225:LYS:HE2	1:A:229:GLU:OE2	2.07	0.55
1:A:80:MET:SD	1:A:129:THR:HG22	2.46	0.55
1:B:127:LYS:HB3	1:B:128:ASP:OD1	2.07	0.55
1:B:112:PRO:HB3	1:B:188:TRP:CD2	2.41	0.55
1:A:307:ARG:HD3	1:B:49:ASP:OD2	2.07	0.55
1:B:63:ALA:O	1:B:67:LEU:HG	2.07	0.55
1:A:107:GLY:HA2	1:A:174:TYR:O	2.07	0.55
1:A:465:ARG:NH2	1:A:472:GLU:O	2.38	0.55
1:A:137:GLN:NE2	1:A:144:ARG:HD2	2.22	0.54
1:A:426:GLN:HG3	5:A:4381:HOH:O	2.06	0.54
1:A:114:ALA:HB1	1:B:460:ALA:HB2	1.88	0.54
1:A:44:PHE:HB3	1:A:55:HIS:CE1	2.42	0.54
1:A:597:LEU:HD11	1:A:614:LEU:HD13	1.89	0.54
1:B:481:ARG:NH1	1:B:483:GLU:OE1	2.39	0.54
1:A:113:VAL:HG22	1:A:114:ALA:N	2.22	0.54
1:B:572:CYS:HB3	1:B:603:LEU:HD22	1.90	0.54
1:B:80:MET:SD	1:B:129:THR:HG22	2.47	0.54
1:B:89:PHE:CE2	1:B:269:GLU:HG3	2.42	0.54
1:B:301:LEU:HD23	1:B:490:LEU:HG	1.89	0.54
1:A:345:ILE:N	1:A:345:ILE:HD12	2.23	0.54
1:A:427:LEU:HD21	1:A:478:VAL:HG22	1.90	0.54
1:A:335:SER:OG	3:A:6001:GGA:H223	2.07	0.54
1:A:433:ARG:HG2	1:A:434:LEU:N	2.23	0.54
1:A:48:ILE:O	1:A:49:ASP:HB2	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:71:TYR:HB2	1:A:73:VAL:HG22	1.89	0.53
1:A:546:VAL:O	1:A:570:LEU:HD22	2.08	0.53
1:A:540:GLY:CA	1:A:543:ILE:HD12	2.36	0.53
1:A:450:GLN:OE1	1:A:475:LEU:HB3	2.09	0.53
1:A:96:ASP:OD1	1:A:309:ARG:NH2	2.38	0.53
1:B:254:THR:HA	1:B:615:ILE:O	2.08	0.53
1:B:45:ARG:NH2	5:B:4203:HOH:O	2.33	0.53
1:B:311:HIS:N	1:B:311:HIS:CD2	2.76	0.53
1:A:342:ALA:HA	1:A:346:LEU:HD12	1.91	0.52
1:A:532:VAL:HB	1:A:544:ASP:HB2	1.89	0.52
1:A:207:GLU:OE2	1:A:207:GLU:HA	2.09	0.52
1:A:45:ARG:O	1:A:56:LYS:HE3	2.10	0.52
1:B:268:ASN:ND2	1:B:592:TYR:H	2.01	0.52
1:A:81:ALA:O	1:A:84:ILE:HG13	2.09	0.52
1:A:96:ASP:OD1	1:A:309:ARG:NE	2.40	0.52
1:B:44:PHE:HD2	1:B:55:HIS:CE1	2.26	0.52
1:B:236:ALA:CB	1:B:397:GLN:HE22	2.22	0.52
1:B:533:LYS:NZ	1:B:568:GLN:HE22	2.08	0.52
1:A:122:LYS:HB2	1:A:127:LYS:O	2.09	0.52
1:A:98:ILE:N	1:A:98:ILE:HD12	2.25	0.52
1:B:527:LYS:HE2	1:B:528:THR:HG22	1.92	0.52
1:A:95:ASN:HD22	1:A:95:ASN:H	1.56	0.52
1:A:196:GLU:O	1:A:197:TYR:HB2	2.10	0.52
1:B:339:HIS:H	1:B:339:HIS:CD2	2.27	0.52
1:A:57:TRP:HB3	1:A:148:GLN:NE2	2.24	0.52
1:B:254:THR:HG22	1:B:615:ILE:HG22	1.91	0.51
1:A:210:LYS:HZ2	1:A:323:GLU:HG2	1.73	0.51
1:B:139:HIS:HB2	1:B:142:LYS:O	2.10	0.51
1:B:342:ALA:HA	1:B:346:LEU:HD12	1.92	0.51
1:B:57:TRP:HZ3	1:B:61:GLU:OE1	1.93	0.51
1:B:126:PHE:O	1:B:127:LYS:O	2.28	0.51
1:B:341:GLU:CB	1:B:611:ILE:HG13	2.41	0.51
1:B:144:ARG:HD3	1:B:161:TRP:CD1	2.45	0.51
1:B:534:PRO:HB2	1:B:563:GLN:NE2	2.26	0.51
1:A:370:ALA:O	1:A:374:LYS:HG3	2.11	0.51
1:B:328:VAL:HG12	1:B:513:TYR:O	2.11	0.51
1:A:118:LEU:HD22	1:A:135:ILE:HD11	1.91	0.51
1:A:337:SER:HG	3:A:6001:GGA:H372	1.76	0.51
1:A:564:LYS:HG2	1:A:565:ASN:N	2.26	0.51
1:B:15:LEU:HD21	1:B:18:TYR:OH	2.10	0.51
1:A:113:VAL:CG2	1:A:114:ALA:N	2.74	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:538:ARG:HG3	1:A:538:ARG:HH11	1.77	0.50
1:B:43:VAL:N	5:B:4183:HOH:O	2.43	0.50
1:B:527:LYS:HE2	1:B:528:THR:CG2	2.41	0.50
1:A:228:ASP:OD2	1:A:230:LYS:N	2.45	0.50
1:A:614:LEU:O	1:A:615:ILE:HD12	2.12	0.50
1:B:112:PRO:HB2	1:B:135:ILE:HD13	1.93	0.50
1:B:240:ALA:CB	1:B:390:ILE:HG13	2.41	0.50
1:B:131:HIS:HE1	1:B:147:GLU:OE1	1.95	0.49
1:B:137:GLN:HG2	1:B:144:ARG:HB2	1.93	0.49
1:B:137:GLN:CG	1:B:144:ARG:HB2	2.42	0.49
5:A:4487:HOH:O	1:B:160:GLN:HG2	2.12	0.49
1:B:236:ALA:HB2	1:B:397:GLN:HE22	1.78	0.49
1:B:313:ILE:HD13	1:B:487:PHE:HD2	1.77	0.49
1:B:48:ILE:HD13	1:B:69:LEU:HD21	1.93	0.49
1:A:233:LEU:HD21	1:A:398:PHE:HD1	1.77	0.49
1:A:443:ALA:HB3	3:A:6001:GGA:O4	2.12	0.49
1:A:246:ASN:HB2	5:A:4392:HOH:O	2.12	0.49
1:B:468:HIS:HE1	1:B:470:GLN:HB2	1.76	0.49
1:B:327:LYS:HG3	1:B:515:LEU:HD21	1.93	0.49
1:B:341:GLU:HB3	1:B:611:ILE:HG13	1.94	0.49
1:A:459:PHE:HD1	1:A:459:PHE:O	1.96	0.49
1:B:601:GLU:H	1:B:601:GLU:CD	2.16	0.49
1:A:608:GLU:H	1:A:608:GLU:CD	2.15	0.49
1:A:364:GLY:C	5:A:4456:HOH:O	2.51	0.49
1:A:608:GLU:O	1:A:609:SER:C	2.51	0.49
1:B:104:PHE:O	1:B:187:GLY:HA3	2.11	0.49
1:B:233:LEU:HD13	1:B:344:LEU:HD22	1.95	0.49
1:B:215:ARG:HH11	1:B:215:ARG:HG3	1.77	0.49
1:A:82:TRP:CD1	1:A:129:THR:O	2.63	0.48
1:B:120:TRP:NE1	1:B:185:ILE:HD11	2.28	0.48
1:A:311:HIS:CG	5:A:4195:HOH:O	2.58	0.48
1:A:436:ASN:HD22	1:A:436:ASN:C	2.15	0.48
1:A:598:ARG:HD2	1:A:611:ILE:HD13	1.94	0.48
1:B:533:LYS:NZ	1:B:568:GLN:NE2	2.60	0.48
1:A:137:GLN:NE2	1:A:144:ARG:NH1	2.61	0.48
1:A:366:ILE:HG23	1:A:367:ASN:N	2.27	0.48
1:B:43:VAL:HG12	1:B:43:VAL:O	2.12	0.48
1:A:109:PRO:HB2	1:A:197:TYR:CE1	2.48	0.48
1:A:474:ARG:NH1	1:A:476:ILE:HD11	2.29	0.48
1:B:44:PHE:HB3	1:B:55:HIS:CE1	2.49	0.48
1:B:533:LYS:HZ3	1:B:568:GLN:HE22	1.60	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:568:GLN:HG2	4:A:3001:ADP:HN61	1.78	0.48
1:B:418:GLU:HG3	1:B:430:GLY:CA	2.43	0.48
1:A:247:GLN:HG2	5:A:4392:HOH:O	2.13	0.48
1:A:364:GLY:O	1:A:368:GLU:HB2	2.14	0.48
1:B:524:GLU:O	1:B:527:LYS:HG3	2.13	0.48
1:B:127:LYS:HB3	1:B:128:ASP:H	1.46	0.48
1:B:262:GLU:OE1	1:B:262:GLU:HA	2.14	0.47
1:A:165:LEU:CD2	1:A:179:THR:HG23	2.44	0.47
1:A:287:LEU:HA	1:A:290:LEU:HD12	1.96	0.47
1:B:196:GLU:O	1:B:197:TYR:HB2	2.13	0.47
1:B:150:VAL:HG12	1:B:151:ILE:HD12	1.96	0.47
1:B:581:ILE:CG2	1:B:597:LEU:HD22	2.44	0.47
1:B:150:VAL:C	1:B:151:ILE:HD12	2.34	0.47
1:A:538:ARG:HH11	1:A:538:ARG:CG	2.28	0.47
1:B:427:LEU:HD21	1:B:478:VAL:HG22	1.97	0.47
1:B:274:TYR:CE1	1:B:504:LEU:HD11	2.49	0.47
1:B:95:ASN:O	1:B:97:ASN:N	2.48	0.47
1:A:522:ASN:O	1:A:526:VAL:HG23	2.14	0.47
1:B:547:SER:OG	1:B:551:GLU:HG2	2.15	0.47
1:A:274:TYR:CZ	1:A:504:LEU:HD11	2.50	0.46
1:A:575:LYS:HE2	5:A:4254:HOH:O	2.15	0.46
1:B:316:ARG:HD2	1:B:584:CYS:HB3	1.97	0.46
1:B:400:GLU:HG3	1:B:410:THR:OG1	2.15	0.46
1:A:98:ILE:HD13	1:A:276:HIS:CD2	2.50	0.46
1:B:104:PHE:CE2	1:B:110:ARG:HG2	2.49	0.46
1:B:347:GLU:HA	1:B:347:GLU:OE1	2.15	0.46
1:B:85:PHE:HA	1:B:189:MET:CE	2.45	0.46
1:A:137:GLN:HE22	1:A:144:ARG:NH1	2.13	0.46
1:B:121:ASP:O	1:B:130:GLY:HA2	2.16	0.46
1:B:339:HIS:N	1:B:339:HIS:CD2	2.84	0.46
1:A:421:TRP:HE3	1:A:471:ASN:HD22	1.64	0.46
1:B:131:HIS:CG	1:B:132:VAL:N	2.83	0.46
1:A:547:SER:HB3	1:A:553:LEU:HD11	1.97	0.46
1:B:240:ALA:HB2	1:B:390:ILE:HG13	1.98	0.46
1:B:48:ILE:CG2	1:B:68:PHE:HE2	2.29	0.46
1:B:117:LEU:O	1:B:188:TRP:HA	2.16	0.46
1:B:221:GLN:OE1	1:B:250:TYR:HE2	1.99	0.46
1:B:418:GLU:HG3	1:B:430:GLY:HA3	1.98	0.46
1:B:379:ARG:HE	1:B:485:LEU:HB2	1.81	0.46
1:B:552:VAL:HG11	1:B:555:LYS:HE3	1.98	0.46
1:A:138:LEU:HD12	1:A:143:VAL:CG1	2.42	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:85:PHE:HA	1:B:189:MET:SD	2.56	0.46
1:B:96:ASP:CG	1:B:309:ARG:HH21	2.18	0.46
1:B:66:PHE:CE2	1:B:134:ILE:HG21	2.51	0.46
1:A:268:ASN:ND2	1:A:592:TYR:H	2.11	0.45
1:B:324:ARG:NH2	1:B:572:CYS:O	2.45	0.45
1:B:348:ARG:NH1	1:B:351:GLU:OE2	2.48	0.45
1:A:313:ILE:HD13	1:A:487:PHE:HD2	1.81	0.45
1:B:459:PHE:CD2	1:B:459:PHE:N	2.82	0.45
1:A:174:TYR:CD1	1:A:174:TYR:N	2.84	0.45
1:A:548:HIS:C	1:A:550:GLU:H	2.19	0.45
1:A:498:LYS:HB2	1:A:535:ILE:HA	1.99	0.45
1:B:303:LEU:O	1:B:307:ARG:HG2	2.17	0.45
1:B:379:ARG:H	1:B:379:ARG:HD3	1.82	0.45
1:B:449:ASP:OD1	1:B:452:ARG:NH2	2.40	0.45
1:A:379:ARG:NH1	1:A:436:ASN:HB2	2.29	0.45
1:B:608:GLU:O	1:B:609:SER:C	2.54	0.45
1:B:386:GLN:NE2	1:B:387:ASP:O	2.50	0.44
3:A:6001:GGA:H491	5:A:4176:HOH:O	2.17	0.44
1:B:120:TRP:NE1	1:B:185:ILE:CD1	2.80	0.44
1:A:204:ILE:HG21	1:A:262:GLU:HG2	1.99	0.44
1:B:112:PRO:HB2	1:B:135:ILE:CD1	2.48	0.44
1:B:138:LEU:HD12	1:B:143:VAL:CG1	2.43	0.44
1:A:56:LYS:HA	1:A:57:TRP:HA	1.61	0.44
1:B:28:SER:HB2	1:B:57:TRP:O	2.17	0.44
1:B:444:TRP:HB2	1:B:493:VAL:HG12	1.99	0.44
1:A:300:ARG:NH1	5:A:4196:HOH:O	2.50	0.44
1:A:533:LYS:NZ	1:A:568:GLN:NE2	2.66	0.44
1:A:25:ILE:HG12	1:A:62:PHE:CE1	2.52	0.44
1:B:387:ASP:HB2	3:B:6002:GGA:HN81	1.81	0.44
1:A:346:LEU:HD23	1:A:346:LEU:HA	1.80	0.44
1:A:63:ALA:O	1:A:67:LEU:HG	2.18	0.44
1:B:468:HIS:HE1	1:B:470:GLN:HE21	1.66	0.44
1:A:430:GLY:O	1:A:432:GLY:N	2.49	0.44
1:B:584:CYS:HB2	1:B:596:CYS:SG	2.58	0.44
1:A:10:ALA:N	5:A:4348:HOH:O	2.50	0.44
1:B:360:ASN:OD1	1:B:361:PRO:HD2	2.18	0.44
1:A:151:ILE:HD12	1:A:162:THR:CB	2.44	0.44
1:B:311:HIS:O	1:B:313:ILE:HD12	2.18	0.44
1:B:56:LYS:HA	1:B:57:TRP:HA	1.66	0.44
1:A:137:GLN:CG	1:A:144:ARG:HB2	2.46	0.43
1:A:421:TRP:HE3	1:A:471:ASN:ND2	2.16	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:421:TRP:HA	1:A:426:GLN:O	2.18	0.43
1:A:430:GLY:C	1:A:432:GLY:H	2.21	0.43
1:A:68:PHE:HE1	1:A:93:VAL:HG11	1.82	0.43
1:A:109:PRO:HA	1:A:172:GLY:O	2.17	0.43
1:B:535:ILE:HG23	1:B:564:LYS:O	2.18	0.43
1:B:521:VAL:HG22	1:B:567:TYR:CD1	2.53	0.43
1:A:109:PRO:HB2	1:A:197:TYR:CD1	2.53	0.43
1:A:411:ARG:HA	5:A:4313:HOH:O	2.19	0.43
1:B:120:TRP:HB2	1:B:131:HIS:HB3	1.99	0.43
1:B:20:PRO:HD3	1:B:160:GLN:O	2.17	0.43
1:A:308:ARG:HH11	1:A:308:ARG:HG3	1.83	0.43
1:B:512:ARG:HH11	1:B:512:ARG:HG2	1.82	0.43
1:B:444:TRP:CB	1:B:493:VAL:HG12	2.49	0.43
1:A:205:ALA:O	1:A:207:GLU:N	2.52	0.43
1:A:74:VAL:HG22	1:A:75:PHE:N	2.34	0.43
1:B:48:ILE:O	1:B:49:ASP:CB	2.66	0.43
1:A:10:ALA:N	1:A:152:HIS:O	2.52	0.43
1:A:15:LEU:HD21	1:A:18:TYR:CE1	2.53	0.43
1:A:201:GLN:CG	1:A:202:PRO:HD2	2.47	0.43
1:A:348:ARG:HD2	1:A:351:GLU:OE1	2.19	0.43
1:B:131:HIS:CE1	1:B:150:VAL:HG21	2.54	0.43
1:B:337:SER:O	1:B:338:CYS:CB	2.58	0.43
1:B:490:LEU:O	1:B:493:VAL:HG13	2.18	0.43
1:B:314:THR:HA	1:B:587:THR:O	2.18	0.43
1:A:234:GLN:O	1:A:237:TYR:HB3	2.19	0.42
1:A:468:HIS:HA	1:A:469:PRO:HD2	1.85	0.42
1:A:481:ARG:NH2	5:A:4229:HOH:O	2.52	0.42
1:B:503:ILE:O	1:B:506:SER:HB3	2.19	0.42
1:B:45:ARG:O	1:B:56:LYS:HE3	2.19	0.42
1:A:107:GLY:CA	1:A:174:TYR:O	2.66	0.42
1:A:62:PHE:HB2	1:A:148:GLN:HB2	2.01	0.42
1:B:522:ASN:C	1:B:522:ASN:ND2	2.68	0.42
1:B:44:PHE:O	1:B:56:LYS:HG3	2.20	0.42
1:A:337:SER:O	1:A:338:CYS:CB	2.60	0.42
1:A:245:ILE:HG23	1:A:345:ILE:HG21	2.01	0.42
1:B:533:LYS:HZ3	1:B:568:GLN:NE2	2.16	0.42
1:A:141:ASN:HD22	1:A:141:ASN:H	1.67	0.42
1:A:168:VAL:CG2	1:A:175:THR:HB	2.49	0.42
1:A:536:ALA:H	1:A:563:GLN:NE2	2.18	0.42
1:A:317:MET:O	1:A:584:CYS:HA	2.19	0.42
1:A:88:ARG:HG3	1:A:201:GLN:HB2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:431:GLU:HA	1:B:431:GLU:OE2	2.19	0.42
1:A:334:ASP:OD2	1:A:444:TRP:HB2	2.20	0.42
1:B:111:ALA:HB2	1:B:174:TYR:CZ	2.55	0.42
1:A:582:GLN:NE2	4:A:3001:ADP:O3'	2.53	0.42
1:A:501:LEU:HD23	1:A:504:LEU:HD12	2.01	0.42
1:B:532:VAL:HG22	1:B:567:TYR:CD1	2.55	0.42
1:A:339:HIS:HB3	1:A:398:PHE:CE2	2.55	0.42
1:B:219:LYS:HE3	1:B:219:LYS:HB3	1.89	0.42
1:B:601:GLU:N	1:B:601:GLU:CD	2.73	0.42
1:A:108:SER:HA	1:A:109:PRO:HD3	1.93	0.42
1:A:465:ARG:HD3	1:A:474:ARG:NH2	2.34	0.42
1:A:137:GLN:CG	1:A:144:ARG:HD2	2.50	0.41
1:A:16:LEU:HD21	1:A:27:SER:HB2	2.02	0.41
1:B:151:ILE:N	1:B:151:ILE:HD12	2.35	0.41
1:A:382:VAL:HB	1:A:410:THR:HG22	2.00	0.41
1:A:324:ARG:NH2	1:A:572:CYS:O	2.49	0.41
1:A:576:VAL:HG12	1:A:577:ASP:OD1	2.20	0.41
1:B:244:VAL:CG1	1:B:245:ILE:N	2.83	0.41
1:B:276:HIS:CE1	1:B:280:LYS:HE2	2.55	0.41
1:B:381:PHE:CD1	1:B:409:GLU:HB2	2.56	0.41
1:A:379:ARG:HH11	1:A:379:ARG:HG3	1.85	0.41
1:A:440:LYS:HE2	1:A:444:TRP:CD1	2.55	0.41
1:B:131:HIS:CG	1:B:132:VAL:H	2.39	0.41
1:B:231:ASP:CB	1:B:234:GLN:HE21	2.33	0.41
1:B:245:ILE:HG13	1:B:246:ASN:OD1	2.20	0.41
1:B:29:ASP:O	1:B:30:TYR:CG	2.73	0.41
1:B:418:GLU:CG	1:B:418:GLU:O	2.68	0.41
1:B:515:LEU:HD12	1:B:568:GLN:OE1	2.21	0.41
1:A:268:ASN:ND2	1:A:591:ASN:HA	2.36	0.41
1:B:119:ILE:HD12	1:B:119:ILE:N	2.36	0.41
1:A:18:TYR:CG	1:B:466:THR:HG21	2.56	0.41
1:A:237:TYR:CE2	1:A:345:ILE:HG12	2.55	0.41
1:A:598:ARG:HA	1:A:610:ASP:O	2.21	0.41
1:A:498:LYS:C	1:A:500:ILE:H	2.24	0.41
1:A:253:TYR:CZ	1:A:581:ILE:HD11	2.56	0.41
1:B:204:ILE:HD11	1:B:208:LEU:HD12	2.03	0.41
1:A:405:GLN:C	1:A:407:GLY:H	2.24	0.41
1:B:196:GLU:HG2	1:B:197:TYR:CD1	2.55	0.41
1:B:470:GLN:HE21	1:B:470:GLN:HB2	1.71	0.41
1:A:313:ILE:HD13	1:A:487:PHE:CD2	2.56	0.41
1:B:312:MET:HA	1:B:488:GLU:OE2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:216:LEU:HD13	1:A:353:GLY:O	2.21	0.40
1:A:527:LYS:O	1:A:548:HIS:CB	2.66	0.40
1:B:144:ARG:HD3	1:B:161:TRP:CG	2.56	0.40
1:A:15:LEU:HD21	1:A:18:TYR:OH	2.20	0.40
1:A:462:VAL:HG11	1:A:480:LEU:HD12	2.03	0.40
1:B:564:LYS:HG2	1:B:565:ASN:N	2.36	0.40
1:A:531:ALA:HA	1:A:544:ASP:O	2.21	0.40
1:B:560:PHE:N	1:B:560:PHE:CD1	2.89	0.40
1:A:156:PRO:O	1:A:159:GLN:HB2	2.21	0.40
1:B:322:ASP:OD2	1:B:322:ASP:C	2.60	0.40
1:B:597:LEU:HD11	1:B:614:LEU:HD13	2.03	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	581/619 (94%)	534 (92%)	40 (7%)	7 (1%)	13	39
1	B	581/619 (94%)	526 (90%)	47 (8%)	8 (1%)	11	34
All	All	1162/1238 (94%)	1060 (91%)	87 (8%)	15 (1%)	12	36

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	76	THR
1	A	127	LYS
1	A	334	ASP
1	B	96	ASP
1	B	127	LYS
1	B	334	ASP
1	A	431	GLU

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Mol	Chain	Res	Type
1	B	49	ASP
1	B	338	CYS
1	A	49	ASP
1	A	338	CYS
1	B	95	ASN
1	B	365	LEU
1	B	522	ASN
1	A	206	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	505/530 (95%)	489 (97%)	16 (3%)	39	73
1	B	505/530 (95%)	481 (95%)	24 (5%)	25	58
All	All	1010/1060 (95%)	970 (96%)	40 (4%)	31	65

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	95	ASN
1	A	128	ASP
1	A	141	ASN
1	A	149	ASN
1	A	184	THR
1	A	245	ILE
1	A	300	ARG
1	A	355	LYS
1	A	390	ILE
1	A	436	ASN
1	A	459	PHE
1	A	470	GLN
1	A	471	ASN
1	A	481	ARG
1	A	523	ASP

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Mol	Chain	Res	Type
1	A	608	GLU
1	B	91	ARG
1	B	127	LYS
1	B	128	ASP
1	B	201	GLN
1	B	204	ILE
1	B	233	LEU
1	B	247	GLN
1	B	261	GLN
1	B	352	GLN
1	B	377	ARG
1	B	379	ARG
1	B	386	GLN
1	B	389	ASP
1	B	421	TRP
1	B	426	GLN
1	B	459	PHE
1	B	466	THR
1	B	470	GLN
1	B	471	ASN
1	B	522	ASN
1	B	524	GLU
1	B	527	LYS
1	B	560	PHE
1	B	615	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (44) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	55	HIS
1	A	70	ASN
1	A	95	ASN
1	A	131	HIS
1	A	137	GLN
1	A	139	HIS
1	A	141	ASN
1	A	149	ASN
1	A	152	HIS
1	A	268	ASN
1	A	310	HIS
1	A	339	HIS
1	A	352	GLN

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Mol	Chain	Res	Type
1	A	395	HIS
1	A	405	GLN
1	A	436	ASN
1	A	470	GLN
1	A	471	ASN
1	A	563	GLN
1	A	568	GLN
1	B	55	HIS
1	B	102	GLN
1	B	131	HIS
1	B	157	GLN
1	B	201	GLN
1	B	234	GLN
1	B	247	GLN
1	B	251	HIS
1	B	268	ASN
1	B	286	ASN
1	B	310	HIS
1	B	339	HIS
1	B	357	ASN
1	B	367	ASN
1	B	375	HIS
1	B	395	HIS
1	B	397	GLN
1	B	468	HIS
1	B	470	GLN
1	B	471	ASN
1	B	522	ASN
1	B	563	GLN
1	B	568	GLN
1	B	582	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates 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
3	GGA	A	6001	2	23,32,32	2.26	3 (13%)	26,42,42	1.67	7 (26%)
4	ADP	A	3001	2	24,29,29	1.84	2 (8%)	29,45,45	1.55	5 (17%)
3	GGA	B	6002	2	23,32,32	2.35	3 (13%)	26,42,42	1.84	7 (26%)
4	ADP	B	3002	2	24,29,29	1.93	3 (12%)	29,45,45	1.55	5 (17%)

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	GGA	A	6001	2	-	5/32/40/40	-
4	ADP	A	3001	2	-	2/12/32/32	0/3/3/3
3	GGA	B	6002	2	-	6/32/40/40	-
4	ADP	B	3002	2	-	2/12/32/32	0/3/3/3

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	6002	GGA	P34-O56	-9.13	1.32	1.49
3	A	6001	GGA	P34-O56	-8.64	1.33	1.49
4	B	3002	ADP	O3'-C3'	-7.91	1.24	1.43
4	A	3001	ADP	O3'-C3'	-7.73	1.24	1.43
3	B	6002	GGA	P60-O64	-5.18	1.34	1.54
3	A	6001	GGA	P60-O64	-5.11	1.35	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	3002	ADP	C2-N1	3.26	1.40	1.33
4	A	3001	ADP	C2-N1	3.16	1.39	1.33
3	B	6002	GGA	C14-N18	2.90	1.40	1.34
3	A	6001	GGA	C14-N18	2.34	1.39	1.34
4	B	3002	ADP	O4'-C1'	2.02	1.43	1.41

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	6002	GGA	C20-N18-C14	4.23	127.69	121.34
3	B	6002	GGA	C22-C20-N18	4.14	118.15	110.38
3	A	6001	GGA	C22-C20-N18	4.10	118.08	110.38
4	A	3001	ADP	C5-C6-N6	3.62	125.85	120.35
3	B	6002	GGA	O26-C24-C20	-3.48	112.81	120.52
3	A	6001	GGA	C20-N18-C14	3.44	126.50	121.34
4	B	3002	ADP	N3-C2-N1	-3.35	123.44	128.68
4	B	3002	ADP	C5-C6-N6	3.25	125.30	120.35
4	A	3001	ADP	N3-C2-N1	-3.18	123.71	128.68
3	A	6001	GGA	O26-C24-C20	-3.09	113.67	120.52
3	B	6002	GGA	C20-C24-N30	3.04	122.75	116.45
4	B	3002	ADP	C5-C6-N1	-2.85	113.89	120.35
4	A	3001	ADP	C5-C6-N1	-2.84	113.90	120.35
4	A	3001	ADP	C3'-C2'-C1'	2.81	105.20	100.98
3	A	6001	GGA	C37-C39-N44	-2.58	105.18	112.14
4	A	3001	ADP	C2-N1-C6	2.56	123.14	118.75
4	B	3002	ADP	C2-N1-C6	2.54	123.09	118.75
3	B	6002	GGA	C37-C39-N44	-2.41	105.63	112.14
3	B	6002	GGA	O62-P60-O58	2.32	112.41	104.64
3	A	6001	GGA	C20-C24-N30	2.25	121.11	116.45
3	A	6001	GGA	O62-P60-O58	2.21	112.05	104.64
4	B	3002	ADP	C3'-C2'-C1'	2.18	104.26	100.98
3	B	6002	GGA	C12-C10-C6	-2.16	108.81	113.84
3	A	6001	GGA	O64-P60-O58	2.15	111.85	104.64

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	6001	GGA	C22-C20-C24-O26
3	A	6001	GGA	N30-C29-P34-C33
4	A	3001	ADP	PA-O3A-PB-O3B
3	B	6002	GGA	C12-C10-C6-C1

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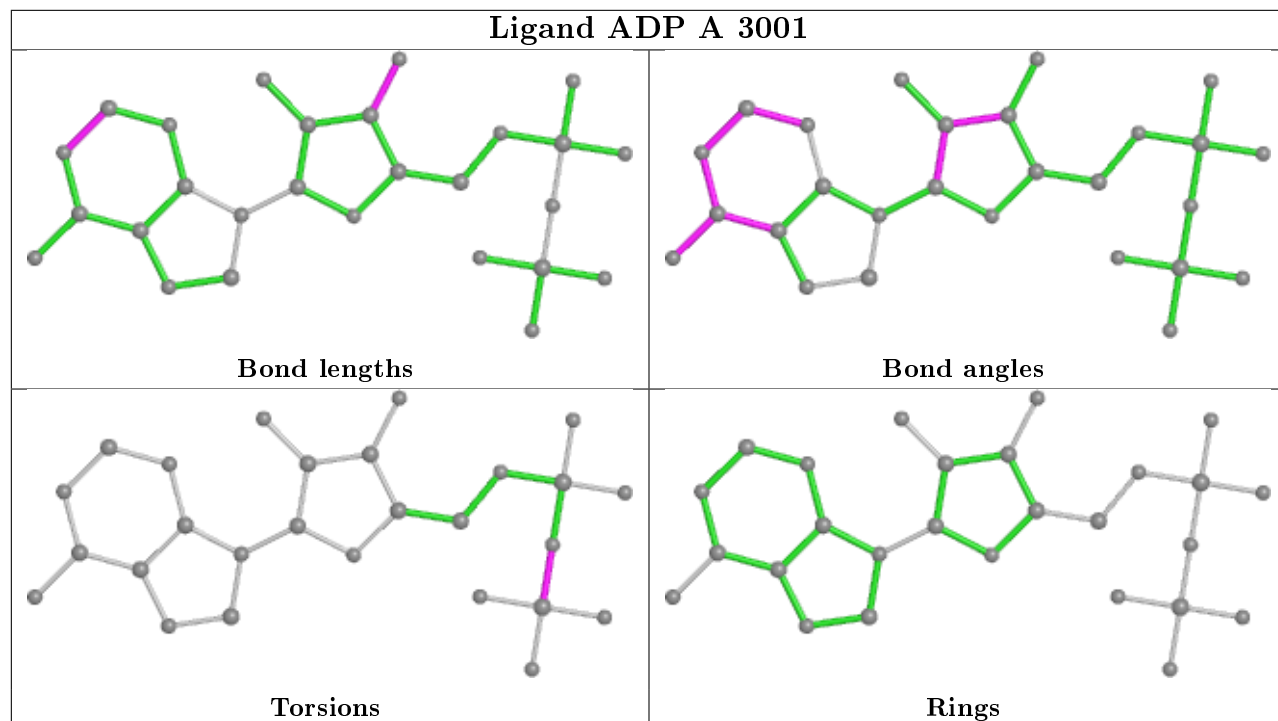
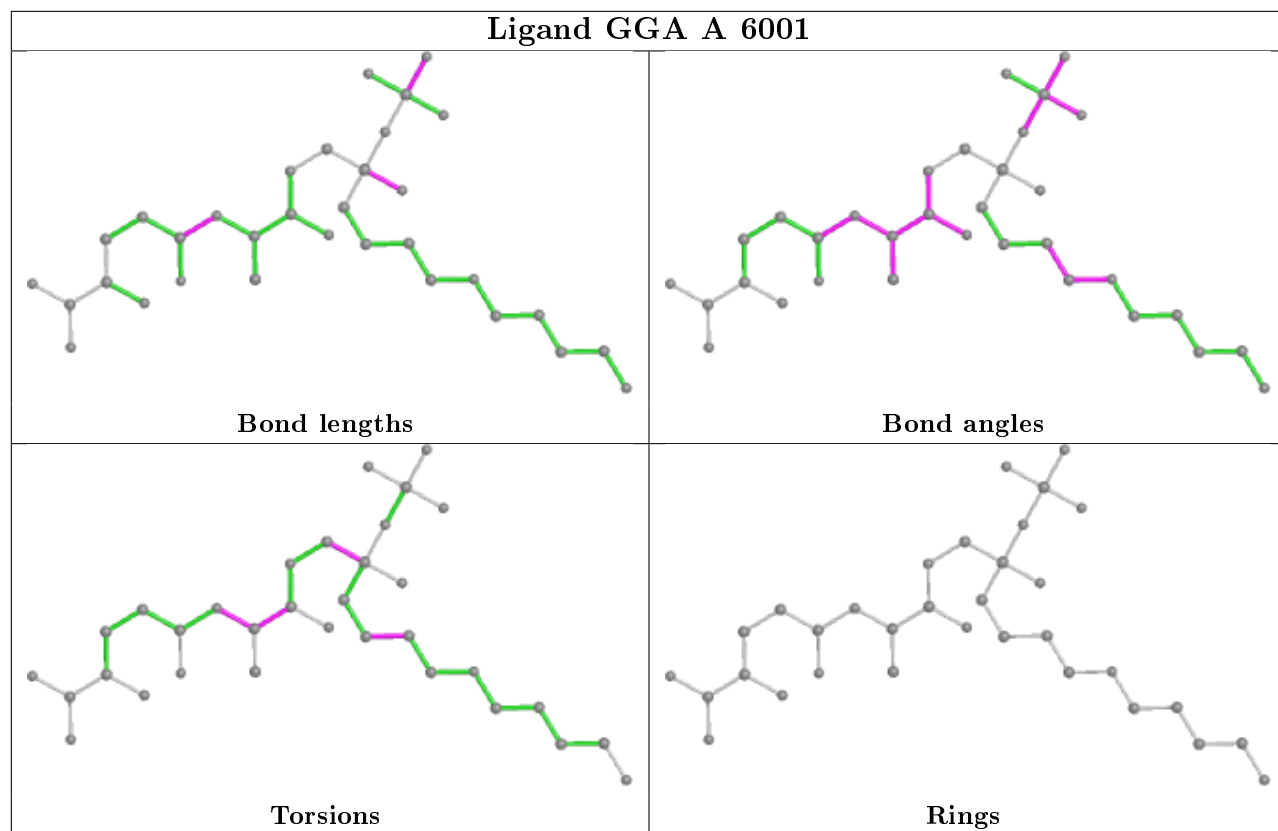
Mol	Chain	Res	Type	Atoms
3	B	6002	GGA	C22-C20-C24-O26
3	B	6002	GGA	N30-C29-P34-C33
4	B	3002	ADP	PA-O3A-PB-O3B
3	A	6001	GGA	C22-C20-C24-N30
3	B	6002	GGA	C22-C20-C24-N30
3	B	6002	GGA	C22-C20-N18-C14
3	A	6001	GGA	C22-C20-N18-C14
3	A	6001	GGA	C33-C35-C37-C39
3	B	6002	GGA	C33-C35-C37-C39
4	A	3001	ADP	PA-O3A-PB-O2B
4	B	3002	ADP	PA-O3A-PB-O2B

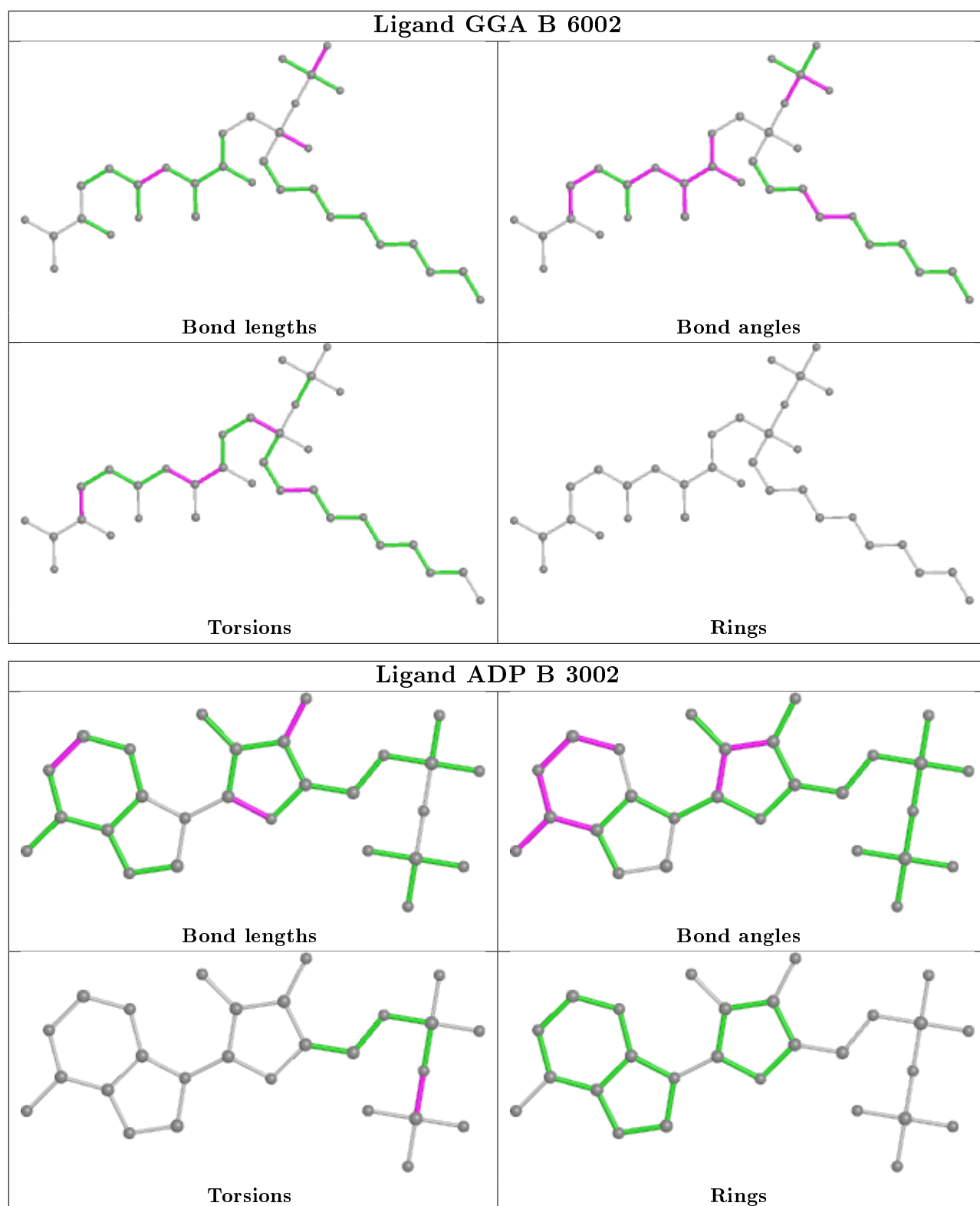
There are no ring outliers.

3 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	6001	GGA	8	0
4	A	3001	ADP	2	0
3	B	6002	GGA	2	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 ⓘ

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 [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	589/619 (95%)	-0.42	6 (1%) 82 77	7, 27, 48, 63	0
1	B	589/619 (95%)	-0.37	4 (0%) 87 84	8, 29, 48, 67	0
All	All	1178/1238 (95%)	-0.39	10 (0%) 86 81	7, 28, 48, 67	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	43	VAL	3.2
1	A	172	GLY	3.1
1	A	44	PHE	2.9
1	B	562	GLU	2.8
1	B	31	SER	2.7
1	A	453	GLU	2.5
1	A	29	ASP	2.2
1	B	29	ASP	2.2
1	B	141	ASN	2.1
1	A	157	GLN	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](#)

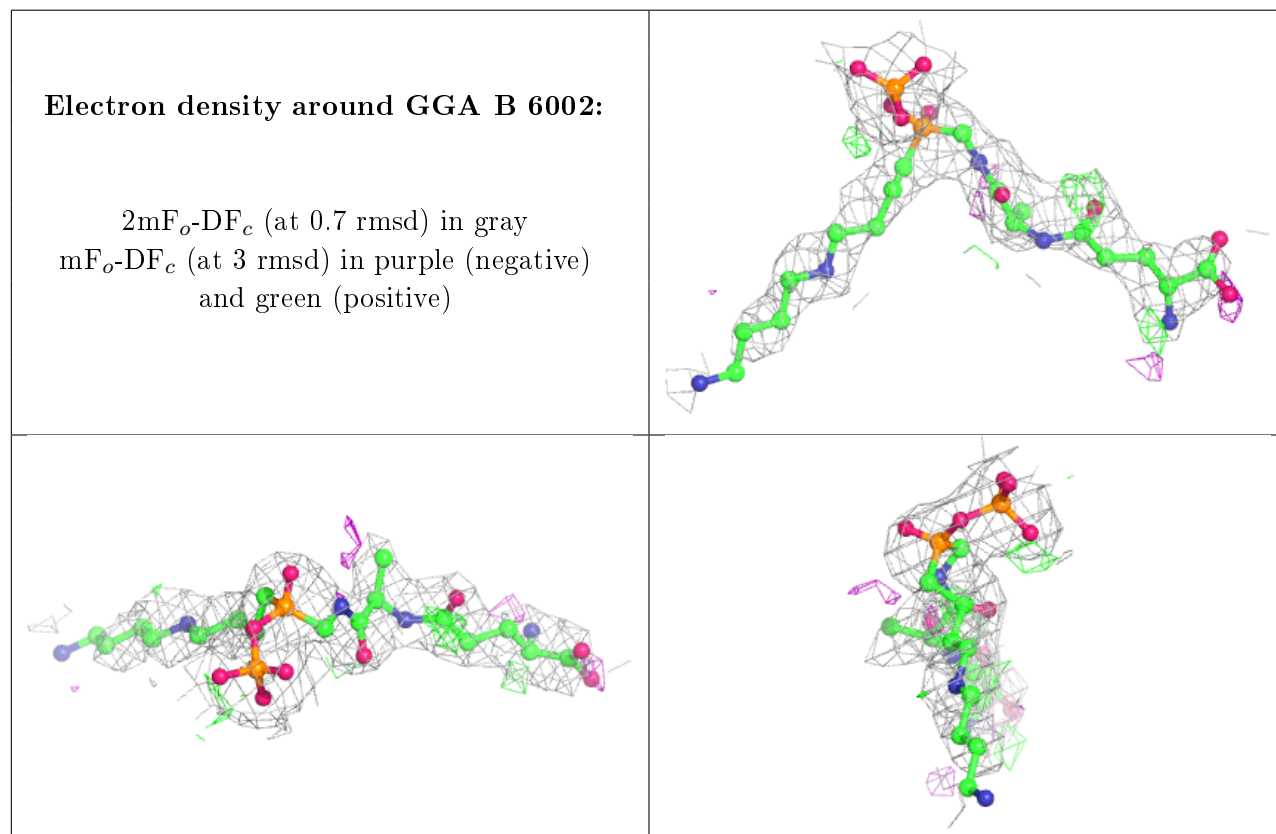
There are no carbohydrates in this entry.

## 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, 95<sup>th</sup> 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.

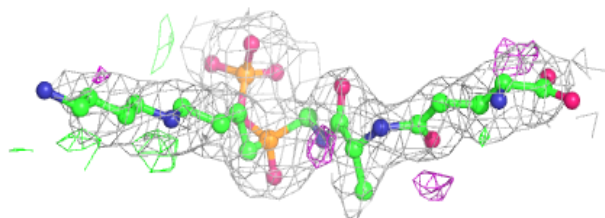
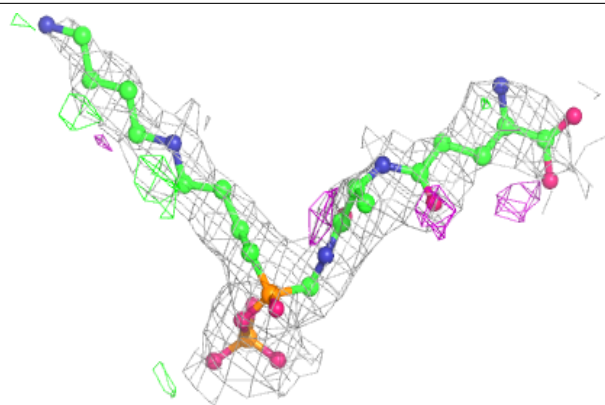
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	GGA	B	6002	33/33	0.93	0.20	22,37,54,56	0
3	GGA	A	6001	33/33	0.94	0.21	22,31,45,49	0
2	MG	A	5001	1/1	0.94	0.16	8,8,8,8	0
2	MG	A	5002	1/1	0.95	0.14	8,8,8,8	0
2	MG	B	5004	1/1	0.98	0.12	12,12,12,12	0
4	ADP	A	3001	27/27	0.98	0.12	1,18,21,23	0
2	MG	B	5003	1/1	0.99	0.11	10,10,10,10	0
4	ADP	B	3002	27/27	0.99	0.14	6,18,20,21	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.

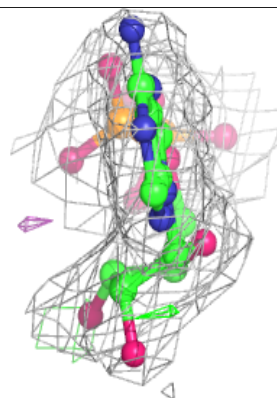
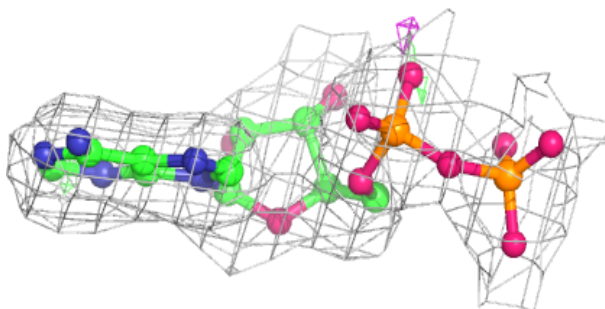
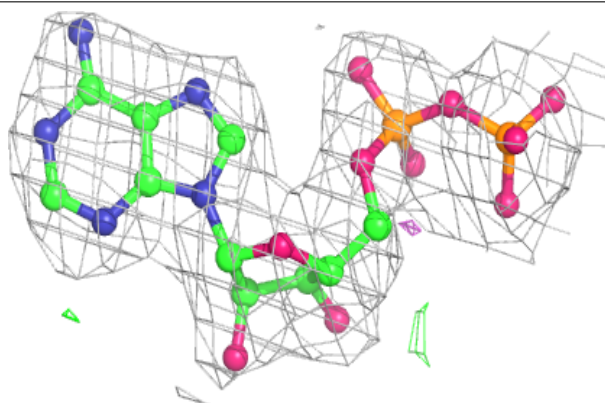


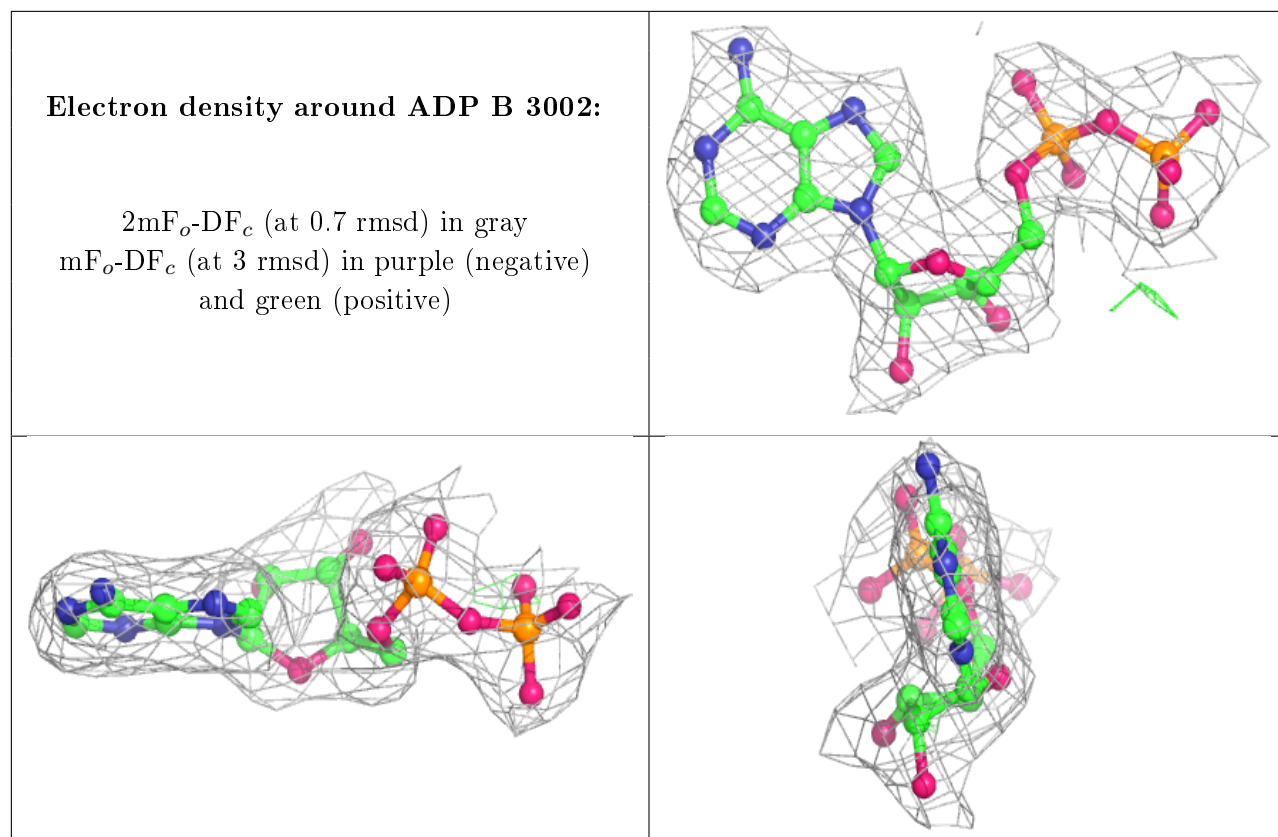
**Electron density around GGA A 6001:**

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

**Electron density around ADP A 3001:**

$2mF_o - DF_c$  (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.