



# Full wwPDB X-ray Structure Validation Report ⓘ

May 18, 2020 – 03:03 am BST

PDB ID : 2PMD  
Title : The structures of aIF2gamma subunit from the archaeon *Sulfolobus solfataricus* in the GDP-bound form.  
Authors : Nikonov, O.S.; Stolboushkina, E.A.; Nikulin, A.D.; Hasenohrl, D.; Blaes, U.; Manstein, D.J.; Fedorov, R.V.; Garber, M.B.; Nikonov, S.V.  
Deposited on : 2007-04-21  
Resolution : 2.65 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

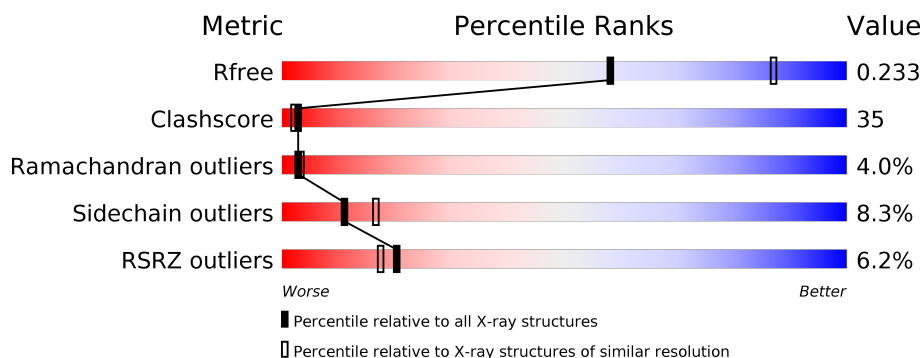
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.65 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	1332 (2.68-2.64)
Clashscore	141614	1374 (2.68-2.64)
Ramachandran outliers	138981	1349 (2.68-2.64)
Sidechain outliers	138945	1349 (2.68-2.64)
RSRZ outliers	127900	1318 (2.68-2.64)

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	415	<div> <div>6%</div> <div> <div></div> <div>48%</div> <div>42%</div> <div>8%</div> </div> </div>
1	B	415	<div> <div>6%</div> <div> <div></div> <div>45%</div> <div>47%</div> <div>7%</div> </div> </div>

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
4	PPV	A	419	-	-	-	X
4	PPV	A	420	-	-	-	X
4	PPV	B	418	-	-	-	X

## 2 Entry composition [i](#)

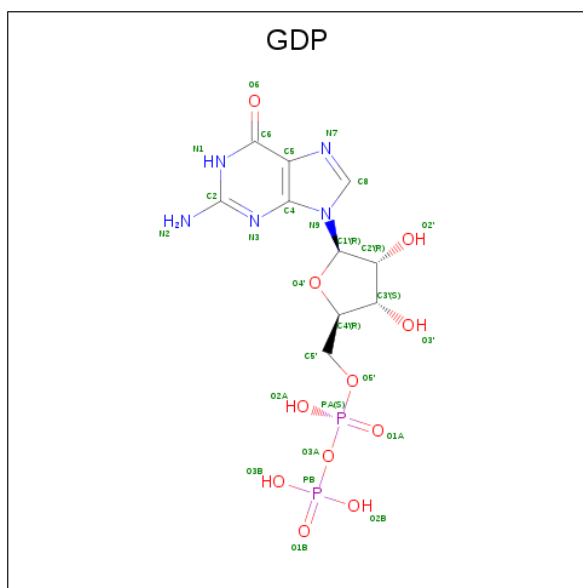
There are 5 unique types of molecules in this entry. The entry contains 6726 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Translation initiation factor 2 gamma subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	414	Total	C	N	O	S	0	0	0
			3212	2058	548	594	12			
1	B	414	Total	C	N	O	S	0	0	0
			3212	2058	548	594	12			

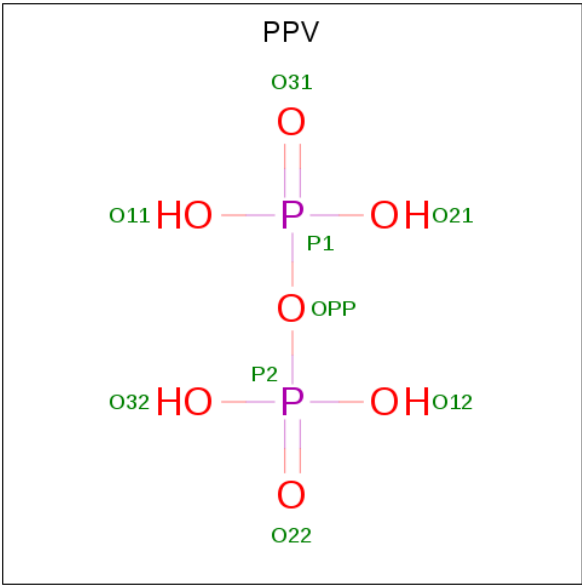
- Molecule 2 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula:  $C_{10}H_{15}N_5O_{11}P_2$ ).





Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			32	10	6	13	3		

- Molecule 4 is PYROPHOSPHATE (three-letter code: PPV) (formula:  $\text{H}_4\text{O}_7\text{P}_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	P	0	0
			9	7	2		
4	A	1	Total	O	P	0	0
			9	7	2		
4	A	1	Total	O	P	0	0
			9	7	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	O	P	0	0
			9	7	2		
4	B	1	Total	O	P	0	0
			9	7	2		
4	B	1	Total	O	P	0	0
			9	7	2		

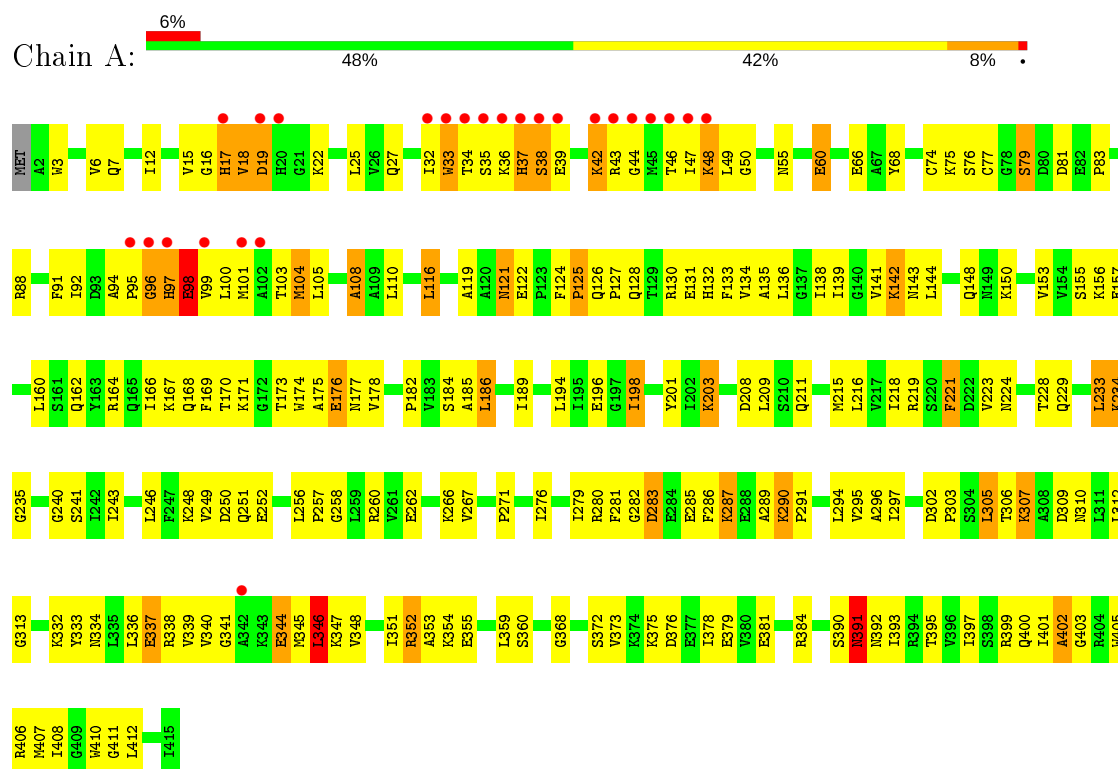
- Molecule 5 is water.

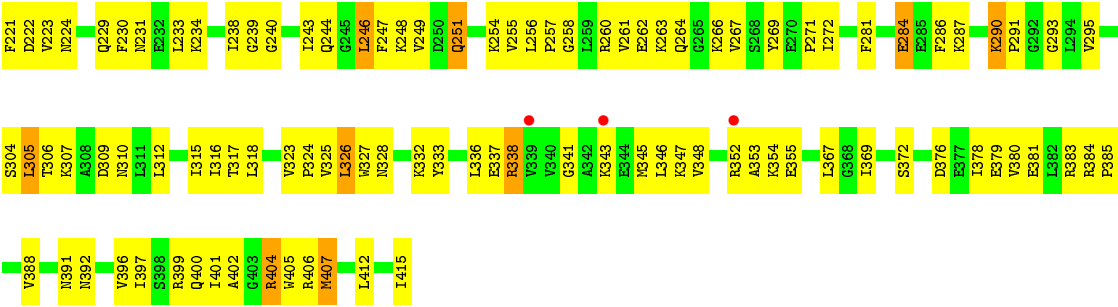
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	71	Total	O	0	0
			71	71		
5	B	89	Total	O	0	0
			89	89		

### 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: Translation initiation factor 2 gamma subunit







## 4 Data and refinement statistics

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	95.06 Å 95.06 Å 165.67 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.85 – 2.65 29.20 – 2.65	Depositor EDS
% Data completeness (in resolution range)	89.3 (19.85-2.65) 99.1 (29.20-2.65)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.62 (at 2.64 Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.220 , 0.275 0.231 , 0.233	Depositor DCC
$R_{free}$ test set	2426 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	51.2	Xtriage
Anisotropy	0.515	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 39.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.021 for -h,-k,l 0.469 for h,-h-k,-l 0.023 for -k,-h,-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	6726	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.82% 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: GDP, GNP, PPV

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	0.45	0/3271	0.76	4/4430 (0.1%)
1	B	0.45	0/3271	0.76	5/4430 (0.1%)
All	All	0.45	0/6542	0.76	9/8860 (0.1%)

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	37	HIS	N-CA-CB	-7.39	97.30	110.60
1	B	80	ASP	CB-CA-C	-6.88	96.64	110.40
1	A	403	GLY	N-CA-C	-6.44	97.01	113.10
1	A	37	HIS	N-CA-C	6.16	127.62	111.00
1	B	37	HIS	CB-CA-C	-5.68	99.04	110.40
1	B	37	HIS	CA-CB-CG	-5.21	104.75	113.60
1	B	80	ASP	C-N-CA	-5.20	108.71	121.70
1	B	37	HIS	N-CA-C	5.08	124.71	111.00
1	A	98	GLU	N-CA-C	5.06	124.66	111.00

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	3212	0	3332	234	0
1	B	3212	0	3332	236	0
2	A	28	0	12	6	0
2	B	28	0	12	2	0
3	A	32	0	13	4	0
4	A	27	0	0	1	0
4	B	27	0	0	0	0
5	A	71	0	0	10	0
5	B	89	0	0	4	0
All	All	6726	0	6701	467	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 35.

All (467) 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:94:ALA:HB3	1:A:98:GLU:HA	1.25	1.13
1:B:230:PHE:HA	1:B:233:LEU:HD23	1.38	1.04
1:B:108:ALA:HB1	1:B:139:ILE:HD12	1.46	0.98
1:B:5:LYS:HE2	1:B:284:GLU:HB3	1.48	0.95
1:B:17:HIS:HB2	1:B:129:THR:HG23	1.50	0.93
1:B:36:LYS:HG3	1:B:37:HIS:H	1.35	0.91
1:A:94:ALA:CB	1:A:98:GLU:HA	2.02	0.89
1:B:94:ALA:HB2	1:B:99:VAL:HG13	1.50	0.89
1:A:97:HIS:O	1:A:98:GLU:CB	2.20	0.88
1:B:372:SER:HB3	1:B:379:GLU:HB2	1.58	0.86
1:A:46:THR:HG22	1:A:47:ILE:H	1.39	0.86
1:B:352:ARG:HH21	1:B:355:GLU:HA	1.39	0.85
1:A:46:THR:HA	1:A:219:ARG:HG3	1.59	0.84
1:A:337:GLU:CD	1:A:337:GLU:H	1.80	0.84
1:B:260:ARG:NH2	1:B:267:VAL:HG11	1.93	0.84
1:A:392:ASN:HB3	1:A:412:LEU:HD12	1.57	0.83
1:A:173:THR:HG23	1:A:175:ALA:H	1.43	0.82
1:A:219:ARG:HD3	1:A:309:ASP:OD1	1.80	0.82
1:B:338:ARG:HE	1:B:347:LYS:HE3	1.45	0.82
1:A:99:VAL:HG23	1:A:100:LEU:H	1.45	0.81
1:B:17:HIS:ND1	1:B:128:GLN:HB2	1.95	0.81
1:B:148:GLN:HE21	1:B:162:GLN:HE21	1.28	0.80
1:A:142:LYS:HB3	5:A:428:HOH:O	1.82	0.80
1:B:171:LYS:HA	1:B:171:LYS:HE2	1.61	0.80
1:B:47:ILE:HD13	1:B:219:ARG:HG3	1.65	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:230:PHE:HA	1:B:233:LEU:CD2	2.12	0.77
1:A:97:HIS:O	1:A:98:GLU:HB2	1.82	0.77
1:A:74:CYS:SG	1:A:83:PRO:HB3	2.25	0.76
1:B:367:LEU:HD23	1:B:383:ARG:HH21	1.49	0.76
1:A:312:LEU:HD12	1:A:313:GLY:N	2.02	0.75
1:A:340:VAL:HB	1:A:406:ARG:HH22	1.52	0.75
1:B:247:PHE:HA	1:B:251:GLN:HE22	1.52	0.74
1:A:6:VAL:HG22	1:A:7:GLN:N	2.04	0.73
1:B:168:GLN:O	1:B:171:LYS:HB2	1.88	0.73
1:B:384:ARG:HG2	1:B:385:PRO:HD2	1.71	0.73
1:B:248:LYS:H	1:B:251:GLN:NE2	1.86	0.73
1:B:48:LYS:NZ	1:B:103:THR:HG21	2.04	0.73
1:A:18:VAL:HG12	1:A:128:GLN:HE22	1.54	0.73
1:B:156:LYS:O	1:B:160:LEU:HG	1.88	0.72
1:A:7:GLN:HE22	1:A:290:LYS:H	1.36	0.72
1:B:333:TYR:CE2	1:B:378:ILE:HG23	2.24	0.72
1:B:219:ARG:HD3	1:B:309:ASP:OD2	1.90	0.71
1:B:74:CYS:SG	1:B:83:PRO:HB3	2.29	0.71
1:A:46:THR:HG21	1:A:49:LEU:HD11	1.72	0.71
1:A:6:VAL:HG22	1:A:7:GLN:H	1.55	0.71
1:A:136:LEU:HB3	1:A:141:VAL:HG11	1.74	0.70
1:A:18:VAL:O	1:A:19:ASP:HB2	1.91	0.70
1:B:338:ARG:HA	1:B:347:LYS:HA	1.73	0.70
1:A:144:LEU:HD23	1:A:178:VAL:HG21	1.74	0.70
1:B:209:LEU:H	1:B:209:LEU:HD12	1.56	0.70
1:B:338:ARG:NE	1:B:347:LYS:HE3	2.06	0.70
1:B:218:ILE:HG12	1:B:240:GLY:HA2	1.73	0.69
1:B:230:PHE:CA	1:B:233:LEU:HD23	2.18	0.69
1:B:263:LYS:HD2	1:B:264:GLN:HG2	1.74	0.69
1:A:131:GLU:HA	1:A:134:VAL:HG22	1.76	0.68
1:A:249:VAL:O	1:A:250:ASP:HB2	1.92	0.68
1:A:135:ALA:O	1:A:139:ILE:HG12	1.94	0.67
1:B:260:ARG:HD2	1:B:269:TYR:OH	1.93	0.67
1:B:36:LYS:HG3	1:B:37:HIS:N	2.07	0.67
1:A:119:ALA:HB3	1:A:122:GLU:HG3	1.75	0.67
1:B:384:ARG:HD2	1:B:385:PRO:O	1.94	0.67
1:B:23:THR:O	1:B:27:GLN:HG3	1.95	0.67
1:A:37:HIS:O	1:A:38:SER:HB3	1.93	0.67
1:B:209:LEU:HD12	1:B:209:LEU:N	2.10	0.67
1:B:260:ARG:HH21	1:B:267:VAL:HG11	1.60	0.67
1:B:126:GLN:HB3	1:B:127:PRO:HD2	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:150:LYS:O	1:A:153:VAL:HG22	1.95	0.67
1:A:340:VAL:HA	1:A:345:MET:CE	2.25	0.67
1:B:148:GLN:HE21	1:B:162:GLN:NE2	1.93	0.67
1:A:121:ASN:HD22	1:A:121:ASN:H	1.43	0.66
1:A:333:TYR:CE2	1:A:378:ILE:HG23	2.31	0.66
1:B:260:ARG:HB2	1:B:269:TYR:CE2	2.31	0.66
1:A:46:THR:HG22	1:A:47:ILE:N	2.09	0.66
1:A:110:LEU:HD22	1:A:241:SER:HB3	1.77	0.66
1:B:37:HIS:ND1	1:B:37:HIS:O	2.29	0.66
1:A:359:LEU:HD22	1:A:359:LEU:N	2.12	0.64
1:A:170:THR:HA	1:A:173:THR:HG22	1.80	0.64
1:A:266:LYS:NZ	1:A:266:LYS:HB2	2.12	0.64
1:A:400:GLN:HA	1:A:405:TRP:HA	1.78	0.64
1:A:401:ILE:HG23	1:A:402:ALA:N	2.13	0.63
1:B:392:ASN:HB3	1:B:412:LEU:HD13	1.79	0.63
1:B:99:VAL:HG11	1:B:104:MET:HG2	1.79	0.63
1:A:46:THR:C	1:A:219:ARG:HE	2.02	0.63
1:A:344:GLU:CD	1:A:345:MET:H	2.02	0.63
1:B:208:ASP:HB3	1:B:211:GLN:HG3	1.80	0.63
1:A:16:GLY:O	1:A:22:LYS:HD3	1.98	0.63
1:B:248:LYS:O	1:B:251:GLN:HB2	1.98	0.63
1:B:77:CYS:O	1:B:78:GLY:C	2.37	0.63
1:A:219:ARG:HD2	1:A:221:PHE:CE2	2.34	0.62
1:B:124:PHE:CE2	1:B:166:ILE:HA	2.35	0.62
1:A:173:THR:HG23	1:A:175:ALA:N	2.14	0.61
1:A:390:SER:H	1:A:393:ILE:HD11	1.64	0.61
1:B:48:LYS:HZ2	1:B:103:THR:HG21	1.62	0.61
1:A:124:PHE:CE2	1:A:166:ILE:HA	2.35	0.61
1:B:102:ALA:O	1:B:106:SER:HB3	2.00	0.61
1:B:262:GLU:HG2	1:B:267:VAL:HG12	1.82	0.61
1:B:105:LEU:N	1:B:105:LEU:CD2	2.64	0.61
1:B:246:LEU:C	1:B:246:LEU:HD12	2.21	0.61
1:B:148:GLN:HG3	1:B:162:GLN:NE2	2.15	0.61
1:B:171:LYS:HE2	1:B:171:LYS:CA	2.31	0.61
1:B:101:MET:CE	1:B:407:MET:SD	2.89	0.60
1:A:156:LYS:O	1:A:160:LEU:HD23	2.01	0.60
1:B:325:VAL:HG12	1:B:385:PRO:HB2	1.82	0.60
1:A:216:LEU:HG	1:A:243:ILE:HG12	1.83	0.60
1:A:395:THR:HG22	1:A:411:GLY:O	2.01	0.60
1:B:16:GLY:H	1:B:22:LYS:HD3	1.64	0.60
1:A:99:VAL:HG12	1:A:104:MET:HG3	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:105:LEU:HD12	1:B:396:VAL:HG21	1.83	0.60
1:B:17:HIS:HB2	1:B:129:THR:CG2	2.29	0.60
1:A:215:MET:HE1	1:A:297:ILE:HG13	1.82	0.60
1:B:144:LEU:HD23	1:B:178:VAL:HG21	1.84	0.59
1:A:373:VAL:HA	1:A:378:ILE:HG22	1.84	0.59
1:A:353:ALA:O	1:A:354:LYS:HB2	2.01	0.59
1:B:254:LYS:HA	1:B:272:ILE:O	2.02	0.59
1:B:94:ALA:CB	1:B:99:VAL:HG13	2.28	0.59
1:B:401:ILE:CG2	1:B:406:ARG:HD3	2.33	0.59
1:A:224:ASN:HD21	1:A:234:LYS:H	1.51	0.58
1:A:340:VAL:HA	1:A:345:MET:HE1	1.84	0.58
1:A:401:ILE:HG23	1:A:402:ALA:H	1.68	0.58
1:A:91:PHE:C	1:A:92:ILE:HD12	2.24	0.58
1:B:148:GLN:HG3	1:B:162:GLN:HE21	1.68	0.58
1:B:37:HIS:CG	1:B:37:HIS:O	2.52	0.58
1:A:42:LYS:HG3	5:A:453:HOH:O	2.03	0.58
1:B:354:LYS:HA	1:B:369:ILE:HD11	1.86	0.58
1:B:78:GLY:O	1:B:79:SER:CB	2.52	0.58
1:A:48:LYS:HE2	1:A:103:THR:OG1	2.03	0.58
1:B:27:GLN:HG2	1:B:32:ILE:O	2.04	0.58
1:B:399:ARG:O	1:B:405:TRP:HA	2.03	0.58
1:A:46:THR:HG22	1:A:47:ILE:HG22	1.86	0.57
1:B:337:GLU:N	1:B:337:GLU:CD	2.58	0.57
1:A:280:ARG:HB3	1:A:280:ARG:CZ	2.34	0.57
1:A:121:ASN:N	1:A:121:ASN:HD22	2.02	0.57
1:A:347:LYS:HB2	1:A:347:LYS:NZ	2.20	0.57
1:A:208:ASP:HB3	1:A:211:GLN:HG3	1.87	0.57
1:A:280:ARG:NH2	1:A:282:GLY:O	2.38	0.57
1:A:168:GLN:HA	1:A:171:LYS:HB2	1.87	0.56
1:A:6:VAL:CG2	1:A:7:GLN:H	2.17	0.56
1:A:97:HIS:O	1:A:98:GLU:HB3	2.02	0.56
1:B:138:ILE:CD1	1:B:407:MET:HB2	2.36	0.56
1:B:337:GLU:H	1:B:337:GLU:CD	2.09	0.56
1:B:397:ILE:HD12	1:B:397:ILE:N	2.21	0.56
1:B:8:PRO:HG2	1:B:293:GLY:HA3	1.86	0.56
1:A:68:TYR:CE1	1:A:196:GLU:HG3	2.40	0.56
1:B:133:PHE:O	1:B:174:TRP:HH2	1.89	0.56
1:A:141:VAL:HG13	1:A:141:VAL:O	2.05	0.56
1:B:148:GLN:NE2	1:B:162:GLN:HE21	2.01	0.56
1:B:120:ALA:HA	1:B:162:GLN:HE22	1.70	0.55
1:B:338:ARG:HG3	1:B:338:ARG:HH11	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:352:ARG:O	1:A:355:GLU:HG2	2.07	0.55
1:A:375:LYS:HG2	1:A:376:ASP:OD2	2.06	0.55
1:B:105:LEU:C	1:B:107:GLY:H	2.09	0.55
1:B:25:LEU:O	1:B:29:ILE:HG13	2.07	0.55
1:A:127:PRO:HA	1:A:130:ARG:HG3	1.89	0.55
1:A:167:LYS:HE2	5:A:486:HOH:O	2.06	0.55
1:A:312:LEU:HD12	1:A:313:GLY:H	1.68	0.55
1:A:95:PRO:O	1:A:97:HIS:N	2.40	0.54
1:A:260:ARG:HB3	4:A:418:PPV:O11	2.06	0.54
1:B:346:LEU:HD23	1:B:346:LEU:N	2.21	0.54
1:A:42:LYS:HA	5:A:453:HOH:O	2.08	0.54
1:B:153:VAL:O	1:B:153:VAL:HG12	2.07	0.54
1:B:224:ASN:HD21	1:B:234:LYS:H	1.53	0.54
1:B:263:LYS:CD	1:B:264:GLN:HE21	2.20	0.54
1:B:284:GLU:HB2	1:B:286:PHE:CE1	2.43	0.54
1:B:26:VAL:HG11	1:B:34:THR:HG21	1.90	0.54
1:A:352:ARG:HE	1:A:355:GLU:HB3	1.72	0.54
1:A:279:ILE:HG21	1:A:289:ALA:HB2	1.90	0.54
1:B:184:SER:HB3	1:B:189:ILE:HB	1.89	0.54
1:A:108:ALA:HB1	1:A:139:ILE:HG23	1.89	0.53
1:A:39:GLU:HG2	1:A:43:ARG:HB2	1.88	0.53
1:B:406:ARG:HG2	1:B:406:ARG:HH11	1.73	0.53
1:A:280:ARG:HH21	3:A:417:GNP:H2'	1.73	0.53
1:B:337:GLU:N	1:B:337:GLU:OE2	2.35	0.53
1:A:6:VAL:CG2	1:A:7:GLN:N	2.70	0.53
1:B:111:MET:CE	1:B:114:ALA:HB2	2.39	0.53
1:A:249:VAL:HG23	1:A:287:LYS:O	2.08	0.53
1:A:12:ILE:O	1:A:91:PHE:HA	2.08	0.53
1:A:194:LEU:O	1:A:198:ILE:HG23	2.08	0.53
1:A:338:ARG:HB2	1:A:346:LEU:O	2.08	0.53
1:A:209:LEU:HD22	1:A:246:LEU:HD23	1.91	0.53
1:B:345:MET:HG3	1:B:345:MET:O	2.08	0.53
1:A:138:ILE:HG21	1:A:407:MET:HE2	1.91	0.53
1:A:281:PHE:HB2	1:A:286:PHE:CE1	2.44	0.52
1:A:218:ILE:HA	1:A:312:LEU:HD13	1.91	0.52
1:A:340:VAL:HA	1:A:345:MET:HE2	1.90	0.52
1:B:108:ALA:HB1	1:B:139:ILE:CD1	2.27	0.52
1:A:280:ARG:HH12	1:A:283:ASP:C	2.13	0.52
1:A:39:GLU:CG	1:A:43:ARG:HB2	2.40	0.52
1:B:105:LEU:N	1:B:105:LEU:HD22	2.24	0.52
1:B:37:HIS:HD1	1:B:37:HIS:C	2.13	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:130:ARG:HB3	5:A:441:HOH:O	2.08	0.52
1:B:94:ALA:CB	1:B:99:VAL:HG22	2.40	0.52
1:A:160:LEU:O	1:A:164:ARG:HG2	2.10	0.52
1:A:42:LYS:O	1:A:42:LYS:HG2	2.10	0.52
1:B:63:LYS:O	1:B:66:GLU:HG2	2.10	0.52
1:A:136:LEU:HB3	1:A:141:VAL:CG1	2.40	0.52
1:A:246:LEU:HD12	1:A:246:LEU:C	2.30	0.52
1:A:391:ASN:HD22	1:A:391:ASN:C	2.14	0.52
1:A:79:SER:HB3	1:A:81:ASP:HB2	1.93	0.51
1:B:125:PRO:HG3	1:B:169:PHE:CE2	2.45	0.51
1:A:168:GLN:HG2	1:A:168:GLN:O	2.11	0.51
1:B:146:ILE:HG13	1:B:178:VAL:HG11	1.91	0.51
1:B:338:ARG:CA	1:B:347:LYS:HA	2.39	0.51
1:A:119:ALA:CB	1:A:122:GLU:HG3	2.39	0.51
1:A:260:ARG:HH22	1:A:267:VAL:CG1	2.24	0.51
1:A:88:ARG:HG3	1:A:88:ARG:NH1	2.25	0.51
1:B:317:THR:HG21	1:B:323:VAL:HG21	1.91	0.51
1:B:229:GLN:HG2	5:B:459:HOH:O	2.10	0.51
1:A:258:GLY:HA3	1:A:271:PRO:HA	1.93	0.51
1:B:324:PRO:HD2	1:B:388:VAL:O	2.11	0.51
1:B:88:ARG:HH11	1:B:88:ARG:HG3	1.76	0.51
1:A:235:GLY:HA2	1:B:230:PHE:CE1	2.46	0.51
1:A:3:TRP:CZ2	1:A:83:PRO:HG2	2.46	0.51
1:B:160:LEU:O	1:B:164:ARG:HG2	2.10	0.51
1:B:337:GLU:O	1:B:347:LYS:HB3	2.11	0.51
1:A:345:MET:HE2	1:A:345:MET:HA	1.92	0.51
1:B:116:LEU:HB2	1:B:144:LEU:HD11	1.93	0.51
1:B:130:ARG:O	1:B:134:VAL:HG23	2.11	0.51
1:A:397:ILE:HD12	1:A:410:TRP:HA	1.93	0.50
1:A:229:GLN:HG2	5:A:474:HOH:O	2.12	0.50
1:A:101:MET:O	1:A:105:LEU:CD1	2.59	0.50
1:B:48:LYS:HZ3	1:B:103:THR:HG21	1.76	0.50
1:B:216:LEU:CD1	1:B:243:ILE:HD11	2.42	0.50
1:A:18:VAL:HG13	1:A:18:VAL:O	2.11	0.50
1:B:16:GLY:N	1:B:22:LYS:HD3	2.25	0.50
1:B:388:VAL:HG11	1:B:415:ILE:HG21	1.94	0.50
1:B:263:LYS:HD3	1:B:264:GLN:HE21	1.77	0.49
1:A:98:GLU:HG2	1:A:132:HIS:NE2	2.27	0.49
1:A:228:THR:HG21	1:A:233:LEU:HB3	1.94	0.49
1:B:404:ARG:HG2	1:B:404:ARG:HH11	1.76	0.49
1:A:127:PRO:O	1:A:130:ARG:HG3	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:406:ARG:HH11	1:A:406:ARG:HG2	1.76	0.49
1:A:99:VAL:HG23	1:A:100:LEU:N	2.21	0.49
1:B:218:ILE:O	1:B:312:LEU:HD13	2.12	0.49
1:B:217:VAL:HG13	1:B:238:ILE:HG23	1.95	0.49
1:B:37:HIS:ND1	1:B:37:HIS:C	2.65	0.49
1:B:258:GLY:HA3	1:B:271:PRO:HA	1.94	0.49
1:A:125:PRO:HG3	1:A:169:PHE:CE2	2.48	0.49
1:A:22:LYS:HB2	1:A:22:LYS:NZ	2.28	0.49
1:A:260:ARG:HH22	1:A:267:VAL:HG11	1.77	0.49
1:B:188:LYS:HD2	1:B:188:LYS:N	2.28	0.49
1:A:198:ILE:HG13	1:A:198:ILE:O	2.12	0.49
1:A:266:LYS:HB2	1:A:266:LYS:HZ2	1.77	0.49
1:A:170:THR:CA	1:A:173:THR:HG22	2.43	0.48
1:A:44:GLY:HA2	3:A:417:GNP:O3'	2.12	0.48
1:B:352:ARG:HG2	1:B:353:ALA:N	2.28	0.48
1:B:105:LEU:HD11	1:B:396:VAL:HG11	1.95	0.48
1:B:18:VAL:HG21	1:B:97:HIS:CG	2.47	0.48
1:B:127:PRO:HA	5:B:467:HOH:O	2.12	0.48
1:A:184:SER:HB3	1:A:189:ILE:HB	1.95	0.48
1:A:12:ILE:CD1	1:A:198:ILE:HD12	2.43	0.48
1:A:347:LYS:HB2	1:A:347:LYS:HZ3	1.78	0.48
1:B:338:ARG:HB2	1:B:346:LEU:O	2.12	0.48
1:A:121:ASN:H	1:A:121:ASN:ND2	2.09	0.48
1:B:10:VAL:HG23	1:B:112:ASP:HB2	1.94	0.48
1:B:157:GLU:HG2	1:B:158:GLU:N	2.29	0.48
1:A:27:GLN:HA	1:A:32:ILE:O	2.14	0.48
1:B:260:ARG:HH12	1:B:262:GLU:CD	2.17	0.48
1:A:34:THR:HB	1:A:50:GLY:HA3	1.94	0.48
1:B:352:ARG:HE	1:B:355:GLU:HB2	1.78	0.48
1:B:401:ILE:O	1:B:401:ILE:HG23	2.14	0.48
1:A:136:LEU:O	1:A:141:VAL:HG12	2.13	0.47
1:B:262:GLU:HG2	1:B:267:VAL:CG1	2.44	0.47
1:B:96:GLY:O	1:B:97:HIS:CB	2.62	0.47
1:A:148:GLN:NE2	1:A:162:GLN:HB3	2.28	0.47
1:B:132:HIS:O	1:B:136:LEU:HG	2.14	0.47
1:A:256:LEU:HA	1:A:257:PRO:C	2.34	0.47
1:B:18:VAL:HG12	1:B:128:GLN:HE22	1.79	0.47
1:B:407:MET:H	1:B:407:MET:HG2	1.38	0.47
1:A:185:ALA:N	2:A:416:GDP:O6	2.45	0.47
1:A:46:THR:CG2	1:A:47:ILE:H	2.19	0.47
1:B:14:VAL:HB	1:B:93:ASP:HB3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:334:ASN:ND2	5:A:478:HOH:O	2.47	0.47
1:A:341:GLY:HA3	1:A:345:MET:O	2.14	0.47
1:B:209:LEU:H	1:B:209:LEU:CD1	2.14	0.47
1:B:3:TRP:CZ2	1:B:83:PRO:HG2	2.49	0.47
1:B:88:ARG:HG3	1:B:88:ARG:NH1	2.30	0.47
1:A:15:VAL:HG23	1:A:116:LEU:HD23	1.96	0.47
1:B:326:LEU:O	1:B:385:PRO:HA	2.15	0.47
1:B:12:ILE:HD13	1:B:89:ILE:HD12	1.95	0.47
1:B:5:LYS:CE	1:B:284:GLU:HB3	2.33	0.47
1:B:138:ILE:HD12	1:B:407:MET:HE2	1.97	0.47
1:A:224:ASN:HD22	1:A:228:THR:HG21	1.80	0.47
1:A:175:ALA:HA	1:A:178:VAL:HG23	1.97	0.46
1:B:22:LYS:HB2	2:B:416:GDP:O1B	2.15	0.46
1:A:88:ARG:HG3	1:A:88:ARG:HH11	1.79	0.46
1:B:94:ALA:HB1	1:B:99:VAL:HG22	1.98	0.46
1:A:46:THR:CA	1:A:219:ARG:HG3	2.37	0.46
1:A:224:ASN:ND2	1:A:228:THR:HG21	2.30	0.46
1:A:295:VAL:HG22	1:A:296:ALA:N	2.29	0.46
1:A:305:LEU:O	1:A:310:ASN:HB3	2.16	0.46
1:B:120:ALA:HA	1:B:162:GLN:NE2	2.28	0.46
1:B:75:LYS:O	1:B:77:CYS:O	2.32	0.46
1:B:95:PRO:O	1:B:97:HIS:N	2.48	0.46
1:A:175:ALA:O	1:A:176:GLU:C	2.54	0.46
1:A:203:LYS:HB3	1:A:203:LYS:HZ2	1.80	0.46
1:A:341:GLY:H	1:A:345:MET:HA	1.80	0.46
1:A:194:LEU:O	1:A:198:ILE:CG2	2.63	0.46
1:A:218:ILE:HG12	1:A:240:GLY:HA2	1.97	0.46
1:B:11:ASN:OD1	1:B:293:GLY:N	2.37	0.46
1:A:302:ASP:OD1	1:B:222:ASP:OD2	2.34	0.46
1:B:400:GLN:OE1	1:B:400:GLN:HA	2.15	0.46
1:A:290:LYS:HB3	1:A:291:PRO:CD	2.46	0.46
1:A:280:ARG:HH21	3:A:417:GNP:C2'	2.29	0.46
1:B:328:ASN:HA	1:B:380:VAL:O	2.16	0.46
1:A:32:ILE:CG2	1:A:37:HIS:CE1	2.99	0.46
1:B:105:LEU:CD1	1:B:396:VAL:HG11	2.46	0.46
1:B:105:LEU:HD23	1:B:105:LEU:H	1.81	0.46
1:A:17:HIS:C	1:A:17:HIS:CD2	2.89	0.46
1:A:336:LEU:O	1:A:348:VAL:HG21	2.16	0.46
1:B:284:GLU:HB2	1:B:286:PHE:HE1	1.79	0.46
1:B:281:PHE:O	1:B:284:GLU:HG3	2.16	0.45
1:A:27:GLN:CD	1:A:33:TRP:HD1	2.20	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:179:PRO:HG3	1:B:201:TYR:CD2	2.51	0.45
1:B:196:GLU:O	1:B:200:GLU:HG3	2.17	0.45
1:B:336:LEU:O	1:B:348:VAL:HB	2.15	0.45
1:A:248:LYS:O	1:A:251:GLN:HG3	2.16	0.45
1:A:75:LYS:O	1:A:77:CYS:N	2.50	0.45
1:A:280:ARG:HH12	1:A:283:ASP:CA	2.28	0.45
1:B:210:SER:O	1:B:211:GLN:C	2.55	0.45
1:B:255:VAL:HG22	1:B:316:ILE:HD13	1.98	0.45
1:B:338:ARG:CB	1:B:347:LYS:HA	2.47	0.45
1:B:105:LEU:CD2	1:B:105:LEU:H	2.30	0.45
1:A:306:THR:O	1:A:307:LYS:C	2.54	0.45
1:A:223:VAL:N	5:A:472:HOH:O	2.48	0.45
1:A:399:ARG:HB2	1:A:408:ILE:HD13	1.98	0.45
1:B:37:HIS:O	1:B:41:LEU:HD12	2.16	0.45
1:B:101:MET:HE1	1:B:407:MET:HG2	1.98	0.45
1:A:170:THR:HB	1:A:175:ALA:HB3	1.98	0.45
1:A:332:LYS:HA	1:A:376:ASP:O	2.16	0.45
1:A:12:ILE:HD13	1:A:198:ILE:HD12	1.98	0.45
1:B:105:LEU:CD1	1:B:396:VAL:HG21	2.47	0.45
1:B:260:ARG:HD2	1:B:269:TYR:CZ	2.52	0.44
1:B:369:ILE:HG23	1:B:381:GLU:HB3	1.98	0.44
1:B:43:ARG:HA	1:B:43:ARG:NE	2.32	0.44
1:B:224:ASN:HA	5:B:501:HOH:O	2.17	0.44
1:B:144:LEU:HG	1:B:145:ILE:N	2.32	0.44
1:B:255:VAL:HG22	1:B:316:ILE:CD1	2.47	0.44
1:B:186:LEU:HB2	2:B:416:GDP:C5	2.52	0.44
1:B:266:LYS:HD2	1:B:266:LYS:H	1.83	0.44
1:B:306:THR:O	1:B:307:LYS:C	2.56	0.44
1:B:346:LEU:H	1:B:346:LEU:HD23	1.83	0.44
1:B:108:ALA:CB	1:B:139:ILE:HD12	2.31	0.44
1:B:261:VAL:HG23	1:B:261:VAL:O	2.18	0.44
1:A:406:ARG:NH1	1:A:406:ARG:HG2	2.32	0.44
1:A:74:CYS:HB2	1:A:79:SER:HB2	2.00	0.44
1:A:92:ILE:HD12	1:A:92:ILE:N	2.32	0.44
1:A:99:VAL:O	1:A:103:THR:HB	2.18	0.44
1:B:16:GLY:O	1:B:17:HIS:C	2.55	0.44
1:A:203:LYS:NZ	1:A:203:LYS:HB3	2.33	0.44
1:A:105:LEU:HD13	1:A:360:SER:OG	2.18	0.44
1:B:266:LYS:HD2	1:B:266:LYS:N	2.32	0.44
1:B:290:LYS:HB3	1:B:291:PRO:CD	2.47	0.44
1:A:216:LEU:HG	1:A:243:ILE:CG1	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:130:ARG:O	1:A:133:PHE:HB3	2.18	0.43
1:A:218:ILE:HD11	1:A:294:LEU:HD22	2.00	0.43
1:A:18:VAL:O	1:A:19:ASP:CB	2.62	0.43
1:A:110:LEU:CD2	1:A:241:SER:HB3	2.47	0.43
1:A:55:ASN:HA	1:A:88:ARG:HA	2.00	0.43
1:B:171:LYS:O	1:B:176:GLU:HG3	2.18	0.43
1:B:60:GLU:OE2	1:B:84:LYS:HE3	2.18	0.43
1:A:16:GLY:O	1:A:17:HIS:C	2.55	0.43
1:B:11:ASN:HB3	1:B:92:ILE:HD11	1.99	0.43
1:B:401:ILE:O	1:B:401:ILE:CG2	2.66	0.43
1:B:94:ALA:HB2	1:B:99:VAL:CG1	2.35	0.43
1:B:346:LEU:H	1:B:346:LEU:CD2	2.30	0.43
1:A:260:ARG:NH2	1:A:267:VAL:HG12	2.34	0.43
1:A:186:LEU:HB2	2:A:416:GDP:C5	2.52	0.43
1:B:224:ASN:HD21	1:B:234:LYS:N	2.16	0.43
1:A:32:ILE:HG23	1:A:37:HIS:NE2	2.34	0.43
1:B:231:ASN:ND2	5:B:444:HOH:O	2.52	0.43
1:B:399:ARG:HG2	1:B:400:GLN:N	2.33	0.43
1:A:333:TYR:HE2	1:A:378:ILE:HG23	1.77	0.43
1:B:146:ILE:HG13	1:B:178:VAL:CG1	2.49	0.43
1:B:327:TRP:CH2	1:B:385:PRO:HD3	2.54	0.43
1:A:48:LYS:CE	1:A:103:THR:OG1	2.67	0.43
1:B:286:PHE:CD1	1:B:286:PHE:N	2.87	0.43
1:B:305:LEU:O	1:B:310:ASN:HB3	2.19	0.43
1:A:126:GLN:HB3	1:A:127:PRO:HD2	2.01	0.43
1:A:143:ASN:HB3	1:A:201:TYR:O	2.19	0.43
1:A:124:PHE:CZ	1:A:166:ILE:HA	2.53	0.43
1:A:351:ILE:O	1:A:373:VAL:HG21	2.19	0.43
1:A:359:LEU:HD22	1:A:359:LEU:H	1.80	0.43
1:A:372:SER:HB3	1:A:379:GLU:HG3	2.00	0.43
1:A:60:GLU:OE1	1:A:60:GLU:HA	2.18	0.43
1:A:303:PRO:HB2	1:B:304:SER:OG	2.19	0.43
1:B:213:PRO:HG2	1:B:318:LEU:HD11	2.01	0.43
1:B:98:GLU:HB3	1:B:99:VAL:H	1.76	0.43
1:B:332:LYS:HA	1:B:376:ASP:O	2.19	0.42
1:A:39:GLU:OE2	1:A:43:ARG:HB2	2.20	0.42
1:A:96:GLY:HA2	2:A:416:GDP:O3B	2.19	0.42
1:B:18:VAL:O	1:B:19:ASP:HB2	2.19	0.42
1:B:89:ILE:HD11	1:B:91:PHE:CZ	2.54	0.42
1:A:401:ILE:CG2	1:A:402:ALA:N	2.80	0.42
1:A:142:LYS:HG2	1:A:143:ASN:N	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:392:ASN:HB3	1:A:412:LEU:CD1	2.40	0.42
1:A:42:LYS:HE2	1:A:280:ARG:NH1	2.35	0.42
1:B:246:LEU:HD12	1:B:247:PHE:N	2.34	0.42
1:B:343:LYS:O	1:B:343:LYS:HG2	2.19	0.42
1:B:341:GLY:HA3	1:B:346:LEU:HD21	2.01	0.42
1:B:40:GLU:HA	1:B:40:GLU:OE1	2.18	0.42
1:A:18:VAL:HA	2:A:416:GDP:O2B	2.19	0.42
1:A:224:ASN:HD21	1:A:233:LEU:HA	1.83	0.42
1:B:367:LEU:HD23	1:B:383:ARG:NH2	2.26	0.42
1:A:280:ARG:HH12	1:A:283:ASP:HA	1.85	0.42
1:A:170:THR:HA	1:A:173:THR:CG2	2.46	0.42
1:A:339:VAL:HG12	1:A:346:LEU:HB3	2.01	0.42
1:A:99:VAL:HA	1:A:104:MET:HG3	2.01	0.42
1:B:353:ALA:O	1:B:354:LYS:HB2	2.19	0.42
1:A:110:LEU:HD22	1:A:241:SER:CB	2.48	0.42
1:A:280:ARG:HG2	1:A:285:GLU:HG2	2.00	0.42
1:A:46:THR:HG21	1:A:49:LEU:CD1	2.44	0.42
1:B:212:LYS:HG2	1:B:244:GLN:NE2	2.35	0.42
1:A:186:LEU:HA	1:A:186:LEU:HD23	1.81	0.42
1:A:305:LEU:HA	1:A:305:LEU:HD12	1.80	0.42
1:A:49:LEU:HD13	1:A:92:ILE:HG23	2.01	0.42
1:B:47:ILE:HG22	1:B:49:LEU:H	1.84	0.42
1:A:160:LEU:HA	1:A:160:LEU:HD13	1.93	0.41
1:A:399:ARG:HB3	1:A:408:ILE:HG21	2.01	0.41
1:B:158:GLU:O	1:B:161:SER:HB3	2.20	0.41
1:A:384:ARG:HD3	5:A:483:HOH:O	2.20	0.41
1:B:98:GLU:HG3	1:B:100:LEU:CD1	2.49	0.41
1:B:3:TRP:CZ2	1:B:57:GLY:HA3	2.56	0.41
1:A:276:ILE:HG23	1:A:297:ILE:HG23	2.02	0.41
1:A:302:ASP:C	1:A:302:ASP:OD2	2.57	0.41
1:B:166:ILE:O	1:B:170:THR:HG23	2.20	0.41
1:B:249:VAL:HG23	1:B:287:LYS:O	2.21	0.41
1:A:148:GLN:O	1:A:182:PRO:HA	2.19	0.41
1:B:125:PRO:HG3	1:B:169:PHE:CD2	2.56	0.41
1:B:170:THR:O	1:B:176:GLU:HA	2.21	0.41
1:B:215:MET:HG2	1:B:216:LEU:N	2.36	0.41
1:B:101:MET:HE3	1:B:407:MET:SD	2.60	0.41
1:A:175:ALA:O	1:A:177:ASN:N	2.53	0.41
1:A:22:LYS:HE3	2:A:416:GDP:O2B	2.20	0.41
1:B:164:ARG:HH11	1:B:164:ARG:HG3	1.86	0.41
1:B:18:VAL:HG23	1:B:97:HIS:HB2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:352:ARG:NH2	1:B:355:GLU:HA	2.19	0.41
1:A:243:ILE:HA	1:A:243:ILE:HD13	1.86	0.41
1:A:368:GLY:CA	1:A:381:GLU:O	2.69	0.41
1:A:186:LEU:HG	2:A:416:GDP:H2'	2.03	0.41
1:B:18:VAL:HG12	1:B:128:GLN:NE2	2.36	0.41
1:A:401:ILE:CG2	1:A:402:ALA:H	2.32	0.41
1:B:108:ALA:CB	1:B:139:ILE:CD1	2.97	0.41
1:B:256:LEU:HA	1:B:257:PRO:C	2.41	0.41
1:B:346:LEU:CD2	1:B:346:LEU:N	2.83	0.41
1:B:124:PHE:CE1	1:B:125:PRO:HB3	2.56	0.41
1:B:168:GLN:OE1	1:B:168:GLN:HA	2.20	0.41
1:A:296:ALA:O	3:A:417:GNP:N2	2.51	0.41
1:B:98:GLU:HG3	1:B:100:LEU:HD13	2.02	0.41
1:B:239:GLY:HA2	1:B:295:VAL:O	2.21	0.40
1:A:25:LEU:HA	1:A:185:ALA:HB1	2.03	0.40
1:A:348:VAL:HA	5:A:424:HOH:O	2.21	0.40
1:A:32:ILE:CG2	1:A:37:HIS:NE2	2.84	0.40
1:A:75:LYS:C	1:A:77:CYS:H	2.25	0.40
1:B:338:ARG:HG3	1:B:338:ARG:NH1	2.36	0.40
1:A:155:SER:OG	1:A:157:GLU:HG2	2.22	0.40
1:A:221:PHE:CD1	1:A:221:PHE:N	2.87	0.40
1:A:336:LEU:O	1:A:348:VAL:CG2	2.70	0.40
1:B:105:LEU:HD11	1:B:407:MET:SD	2.62	0.40
1:B:20:HIS:ND1	1:B:118:VAL:HA	2.36	0.40
1:B:18:VAL:CG1	1:B:128:GLN:HE22	2.35	0.40
1:B:43:ARG:CA	1:B:43:ARG:NE	2.85	0.40
1:A:68:TYR:HE1	1:A:196:GLU:HG3	1.84	0.40
1:A:75:LYS:C	1:A:77:CYS:N	2.75	0.40
1:B:172:GLY:HA2	1:B:176:GLU:CD	2.42	0.40
1:B:315:ILE:HG13	1:B:315:ILE:O	2.21	0.40
1:B:323:VAL:HA	1:B:324:PRO:HD3	1.77	0.40
1:B:352:ARG:HH21	1:B:355:GLU:CA	2.22	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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

of similar resolution.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	412/415 (99%)	351 (85%)	44 (11%)	17 (4%)	3	3
1	B	412/415 (99%)	356 (86%)	40 (10%)	16 (4%)	3	3
All	All	824/830 (99%)	707 (86%)	84 (10%)	33 (4%)	3	3

All (33) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	19	ASP
1	A	38	SER
1	A	48	LYS
1	A	98	GLU
1	B	78	GLY
1	B	80	ASP
1	B	96	GLY
1	B	97	HIS
1	B	101	MET
1	B	402	ALA
1	A	42	LYS
1	A	96	GLY
1	A	142	LYS
1	A	176	GLU
1	A	391	ASN
1	B	22	LYS
1	B	35	SER
1	B	45	MET
1	B	171	LYS
1	A	76	SER
1	A	108	ALA
1	A	307	LYS
1	B	100	LEU
1	B	211	GLN
1	A	97	HIS
1	B	143	ASN
1	B	62	CYS
1	A	35	SER
1	A	346	LEU
1	A	402	ALA
1	B	79	SER

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Mol	Chain	Res	Type
1	B	391	ASN
1	A	18	VAL

### 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	356/357 (100%)	327 (92%)	29 (8%)	11	17
1	B	356/357 (100%)	326 (92%)	30 (8%)	11	16
All	All	712/714 (100%)	653 (92%)	59 (8%)	11	16

All (59) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	HIS
1	A	33	TRP
1	A	36	LYS
1	A	60	GLU
1	A	66	GLU
1	A	79	SER
1	A	98	GLU
1	A	104	MET
1	A	116	LEU
1	A	121	ASN
1	A	125	PRO
1	A	174	TRP
1	A	186	LEU
1	A	198	ILE
1	A	203	LYS
1	A	221	PHE
1	A	233	LEU
1	A	234	LYS
1	A	252	GLU
1	A	262	GLU
1	A	283	ASP

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Mol	Chain	Res	Type
1	A	287	LYS
1	A	290	LYS
1	A	305	LEU
1	A	337	GLU
1	A	344	GLU
1	A	346	LEU
1	A	352	ARG
1	A	391	ASN
1	B	25	LEU
1	B	36	LYS
1	B	37	HIS
1	B	38	SER
1	B	39	GLU
1	B	53	GLU
1	B	66	GLU
1	B	79	SER
1	B	99	VAL
1	B	101	MET
1	B	104	MET
1	B	105	LEU
1	B	110	LEU
1	B	116	LEU
1	B	118	VAL
1	B	171	LYS
1	B	174	TRP
1	B	186	LEU
1	B	209	LEU
1	B	221	PHE
1	B	223	VAL
1	B	246	LEU
1	B	251	GLN
1	B	284	GLU
1	B	290	LYS
1	B	305	LEU
1	B	326	LEU
1	B	338	ARG
1	B	404	ARG
1	B	407	MET

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	7	GLN
1	A	17	HIS
1	A	27	GLN
1	A	121	ASN
1	A	128	GLN
1	A	224	ASN
1	A	391	ASN
1	B	128	GLN
1	B	162	GLN
1	B	224	ASN
1	B	231	ASN
1	B	251	GLN
1	B	264	GLN
1	B	310	ASN
1	B	334	ASN

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

9 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	PPV	B	419	-	6,8,8	2.37	2 (33%)	13,13,13	1.99	1 (7%)
4	PPV	A	419	-	6,8,8	2.40	2 (33%)	13,13,13	1.97	1 (7%)
3	GNP	A	417	-	28,34,34	4.20	12 (42%)	30,54,54	1.60	3 (10%)
4	PPV	A	420	-	6,8,8	2.38	2 (33%)	13,13,13	2.00	1 (7%)
2	GDP	B	416	-	24,30,30	1.46	3 (12%)	31,47,47	2.26	8 (25%)
4	PPV	B	418	-	6,8,8	2.44	2 (33%)	13,13,13	1.96	1 (7%)
4	PPV	A	418	-	6,8,8	2.40	2 (33%)	13,13,13	2.00	1 (7%)
2	GDP	A	416	-	24,30,30	1.47	3 (12%)	31,47,47	2.24	8 (25%)
4	PPV	B	417	-	6,8,8	2.38	2 (33%)	13,13,13	2.00	1 (7%)

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
4	PPV	B	419	-	-	0/6/6/6	-
4	PPV	A	419	-	-	0/6/6/6	-
3	GNP	A	417	-	-	6/17/38/38	0/3/3/3
4	PPV	A	420	-	-	0/6/6/6	-
2	GDP	B	416	-	-	0/12/32/32	0/3/3/3
4	PPV	B	418	-	-	0/6/6/6	-
4	PPV	A	418	-	-	0/6/6/6	-
2	GDP	A	416	-	-	0/12/32/32	0/3/3/3
4	PPV	B	417	-	-	0/6/6/6	-

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	417	GNP	PB-O3A	10.21	1.71	1.59
3	A	417	GNP	PB-O1B	9.70	1.61	1.46
3	A	417	GNP	PG-O1G	7.84	1.58	1.46
3	A	417	GNP	C4-N9	-7.27	1.38	1.47
3	A	417	GNP	C5-C6	-5.72	1.43	1.52
3	A	417	GNP	PG-O2G	5.66	1.72	1.56
3	A	417	GNP	PG-O3G	5.57	1.71	1.56
3	A	417	GNP	PB-O2B	5.43	1.71	1.56
3	A	417	GNP	PG-N3B	4.15	1.74	1.63
3	A	417	GNP	PB-N3B	3.93	1.73	1.63
2	A	416	GDP	O4'-C1'	3.89	1.46	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	416	GDP	O4'-C1'	3.77	1.46	1.41
4	B	418	PPV	P1-O31	3.45	1.61	1.50
4	B	418	PPV	P2-O22	3.45	1.61	1.50
4	A	419	PPV	P2-O22	3.43	1.61	1.50
4	A	418	PPV	P2-O22	3.40	1.61	1.50
4	A	419	PPV	P1-O31	3.39	1.61	1.50
4	B	419	PPV	P2-O22	3.38	1.61	1.50
4	A	420	PPV	P1-O31	3.36	1.61	1.50
4	B	417	PPV	P1-O31	3.36	1.61	1.50
4	B	419	PPV	P1-O31	3.33	1.61	1.50
4	A	418	PPV	P1-O31	3.30	1.61	1.50
4	A	420	PPV	P2-O22	3.27	1.61	1.50
4	B	417	PPV	P2-O22	3.26	1.61	1.50
2	B	416	GDP	C6-N1	2.77	1.37	1.33
3	A	417	GNP	C6-N1	2.62	1.37	1.33
2	A	416	GDP	C6-N1	2.55	1.37	1.33
3	A	417	GNP	C8-N9	-2.16	1.38	1.45
2	A	416	GDP	C8-N7	-2.12	1.30	1.34
2	B	416	GDP	C8-N7	-2.02	1.31	1.34

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	418	PPV	P2-OPP-P1	-6.51	110.50	132.83
4	B	417	PPV	P2-OPP-P1	-6.48	110.58	132.83
4	B	419	PPV	P2-OPP-P1	-6.46	110.67	132.83
4	A	420	PPV	P2-OPP-P1	-6.45	110.68	132.83
4	A	419	PPV	P2-OPP-P1	-6.38	110.92	132.83
4	B	418	PPV	P2-OPP-P1	-6.38	110.93	132.83
2	A	416	GDP	PA-O3A-PB	-6.28	111.27	132.83
2	B	416	GDP	PA-O3A-PB	-6.28	111.29	132.83
2	B	416	GDP	C2-N3-C4	5.48	121.62	115.36
2	A	416	GDP	C2-N3-C4	5.34	121.46	115.36
3	A	417	GNP	PA-O3A-PB	-4.55	116.58	132.62
2	B	416	GDP	N3-C2-N1	-4.48	121.24	127.22
2	A	416	GDP	N3-C2-N1	-4.43	121.31	127.22
3	A	417	GNP	C4-C5-N7	3.97	107.73	102.46
2	A	416	GDP	C3'-C2'-C1'	3.83	106.75	100.98
2	B	416	GDP	C3'-C2'-C1'	3.43	106.14	100.98
2	B	416	GDP	C6-C5-C4	-3.27	117.68	120.80
2	B	416	GDP	C5-C6-N1	-3.24	119.01	123.43
2	A	416	GDP	C5-C6-N1	-3.22	119.03	123.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	416	GDP	C6-N1-C2	2.97	120.65	115.93
2	A	416	GDP	C6-N1-C2	2.92	120.58	115.93
2	A	416	GDP	C6-C5-C4	-2.91	118.02	120.80
3	A	417	GNP	O1G-PG-N3B	-2.34	108.33	111.77
2	B	416	GDP	PA-O5'-C5'	-2.32	108.08	121.68
2	A	416	GDP	PA-O5'-C5'	-2.07	109.52	121.68

There are no chirality outliers.

All (6) torsion outliers are listed below:

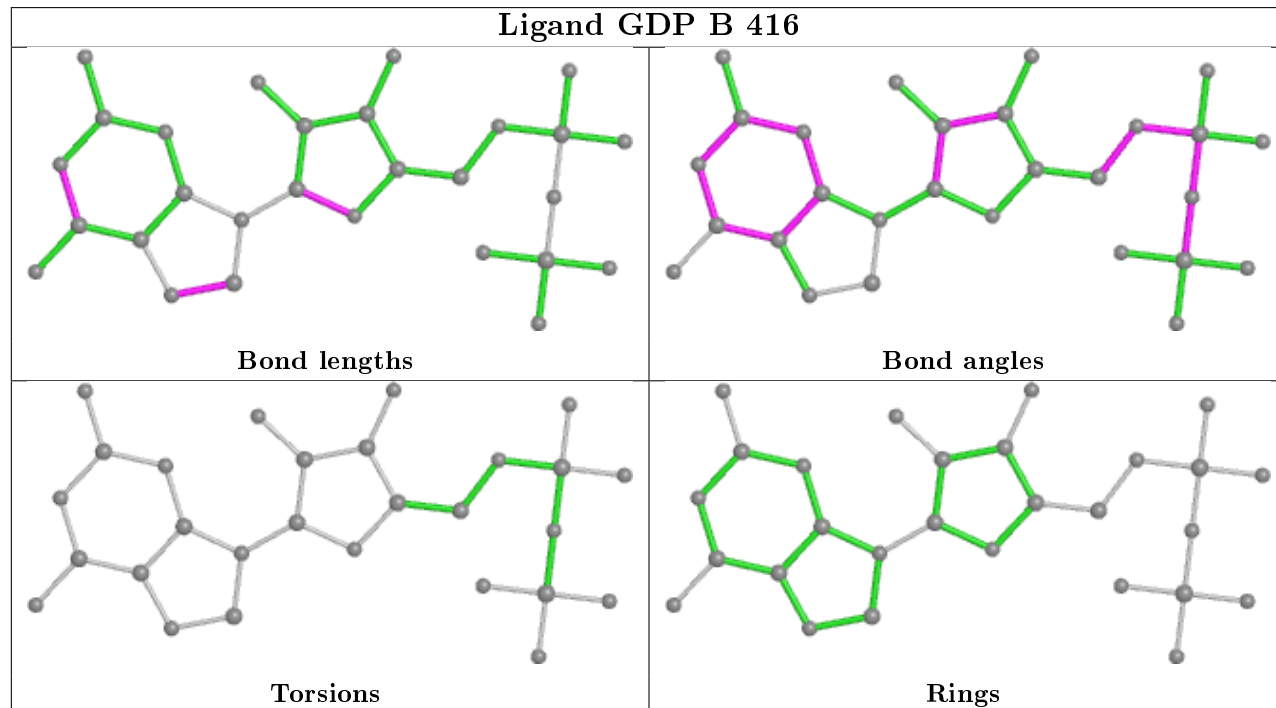
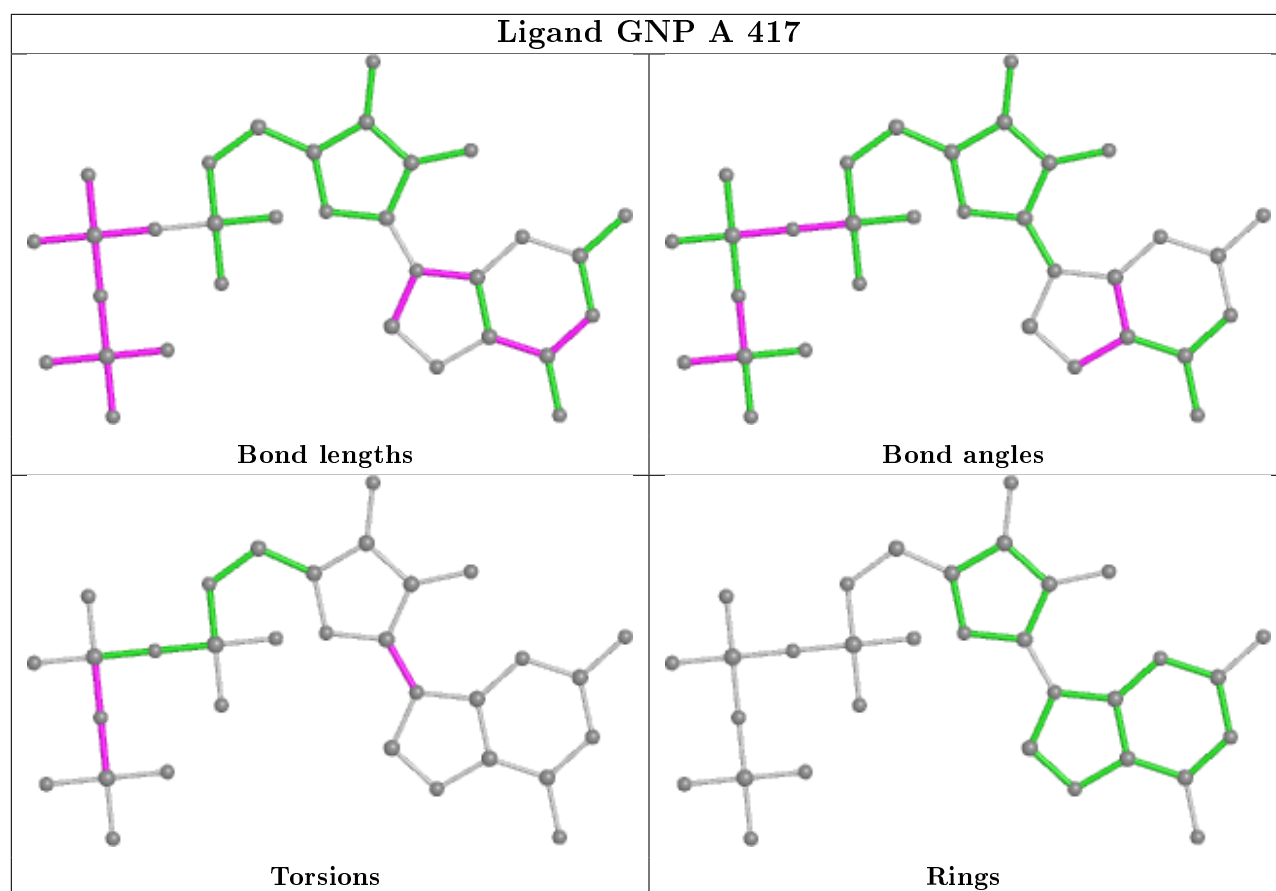
Mol	Chain	Res	Type	Atoms
3	A	417	GNP	PB-N3B-PG-O1G
3	A	417	GNP	PG-N3B-PB-O1B
3	A	417	GNP	PG-N3B-PB-O3A
3	A	417	GNP	O4'-C1'-N9-C4
3	A	417	GNP	C2'-C1'-N9-C8
3	A	417	GNP	C2'-C1'-N9-C4

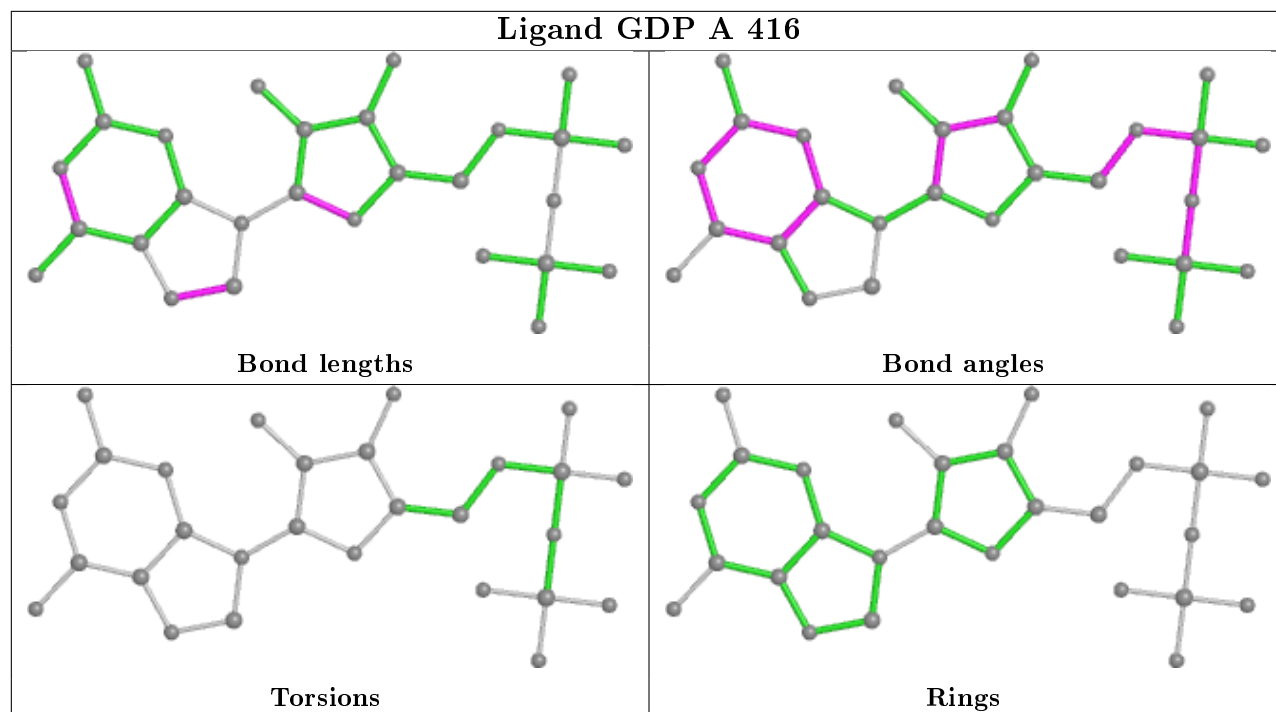
There are no ring outliers.

4 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	417	GNP	4	0
2	B	416	GDP	2	0
4	A	418	PPV	1	0
2	A	416	GDP	6	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 ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	414/415 (99%)	0.32	25 (6%)	21 18	31, 53, 122, 162	0
1	B	414/415 (99%)	0.36	26 (6%)	20 17	31, 54, 121, 165	0
All	All	828/830 (99%)	0.34	51 (6%)	20 17	31, 54, 122, 165	0

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	45	MET	6.3
1	B	37	HIS	6.2
1	B	44	GLY	5.9
1	A	46	THR	5.3
1	B	34	THR	5.0
1	B	38	SER	4.8
1	B	47	ILE	4.7
1	B	46	THR	4.7
1	A	43	ARG	4.7
1	B	41	LEU	4.6
1	A	99	VAL	4.3
1	B	97	HIS	4.0
1	B	101	MET	3.9
1	A	35	SER	3.7
1	A	44	GLY	3.7
1	B	48	LYS	3.7
1	A	33	TRP	3.6
1	B	20	HIS	3.6
1	A	20	HIS	3.3
1	A	37	HIS	3.2
1	A	95	PRO	3.2
1	A	47	ILE	3.1
1	A	42	LYS	3.1
1	B	36	LYS	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	343	LYS	3.0
1	A	97	HIS	2.9
1	A	96	GLY	2.8
1	A	34	THR	2.8
1	A	17	HIS	2.8
1	B	43	ARG	2.8
1	B	352	ARG	2.7
1	B	42	LYS	2.5
1	B	40	GLU	2.5
1	B	105	LEU	2.4
1	B	45	MET	2.4
1	A	102	ALA	2.4
1	B	96	GLY	2.4
1	A	38	SER	2.4
1	B	17	HIS	2.3
1	A	32	ILE	2.3
1	B	19	ASP	2.3
1	B	32	ILE	2.3
1	A	101	MET	2.2
1	B	102	ALA	2.2
1	A	39	GLU	2.1
1	B	35	SER	2.1
1	B	339	VAL	2.1
1	A	36	LYS	2.1
1	A	19	ASP	2.1
1	A	48	LYS	2.0
1	A	342	ALA	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.

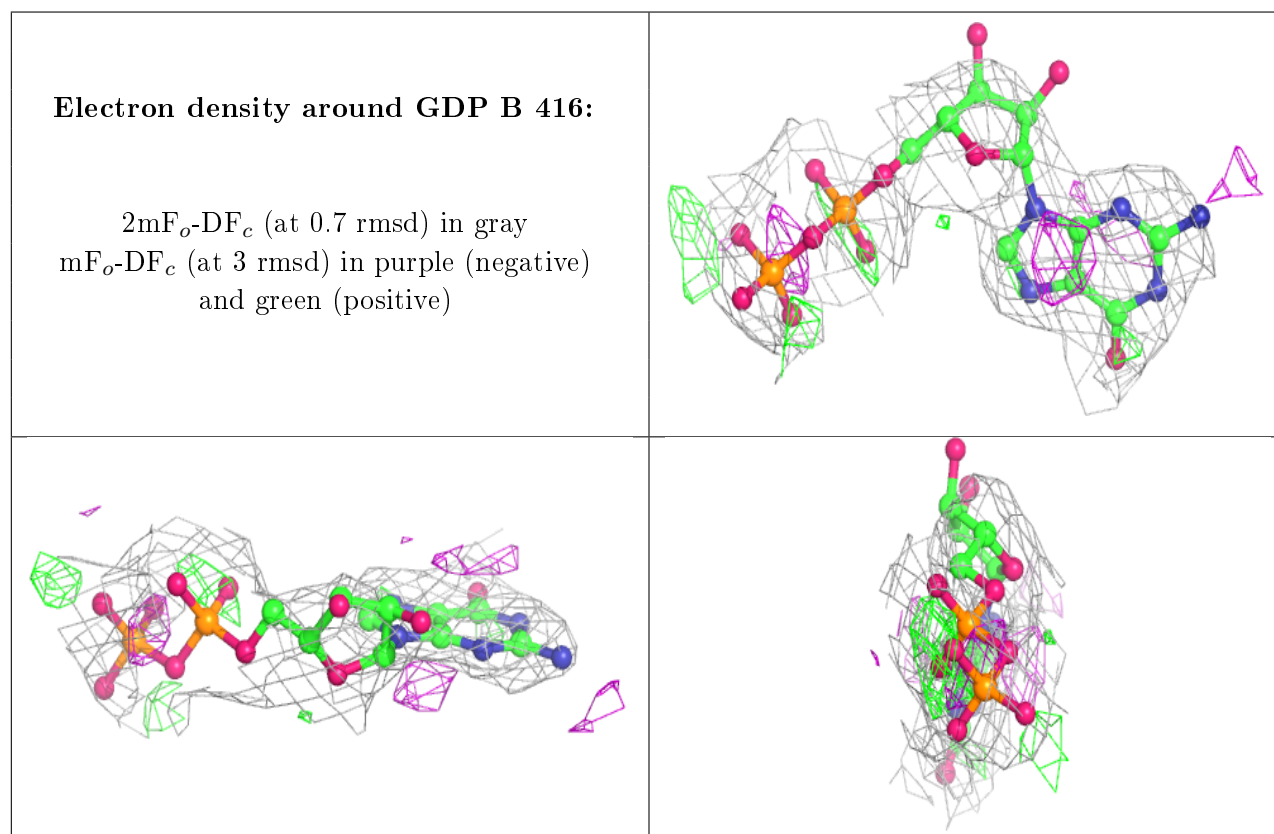
## 6.4 Ligands [i](#)

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, 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.

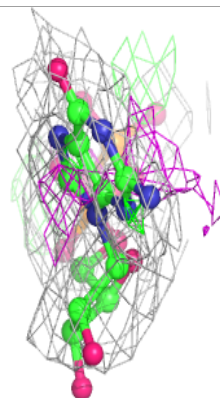
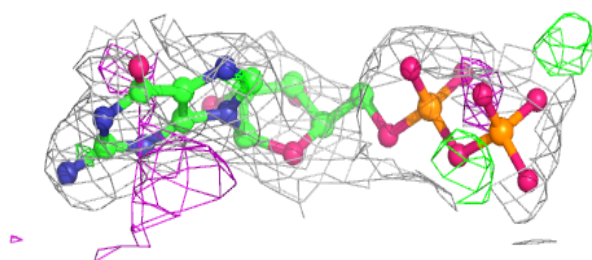
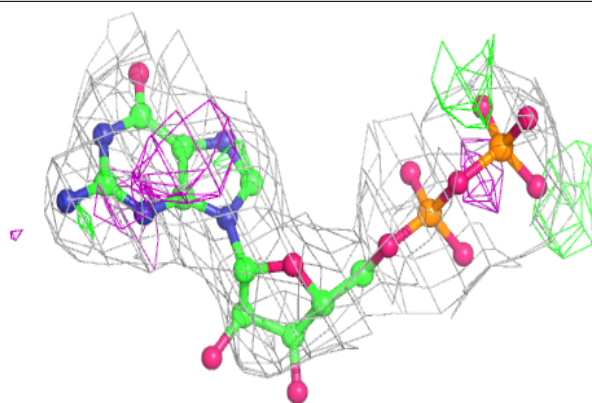
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
4	PPV	B	418	9/9	0.59	0.70	197,198,198,198	0
4	PPV	A	419	9/9	0.61	0.64	197,197,198,198	0
4	PPV	B	419	9/9	0.74	0.39	173,174,175,175	0
2	GDP	B	416	28/28	0.78	0.25	127,136,145,146	0
4	PPV	A	420	9/9	0.79	0.41	166,167,168,168	0
2	GDP	A	416	28/28	0.82	0.23	118,131,142,143	0
4	PPV	A	418	9/9	0.85	0.44	183,184,184,184	0
4	PPV	B	417	9/9	0.88	0.38	182,183,186,186	0
3	GNP	A	417	32/32	0.95	0.22	16,156,168,168	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.

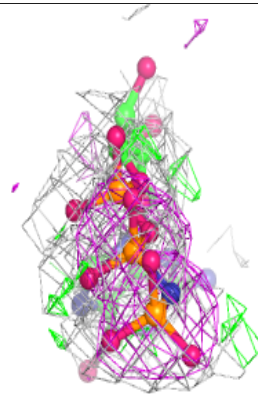
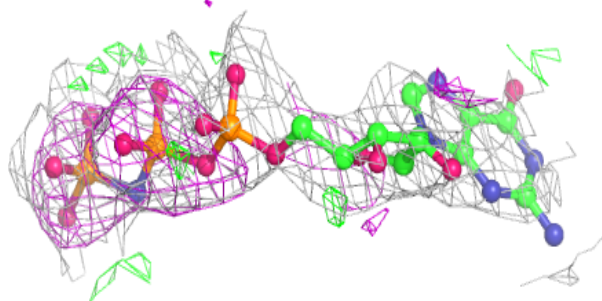
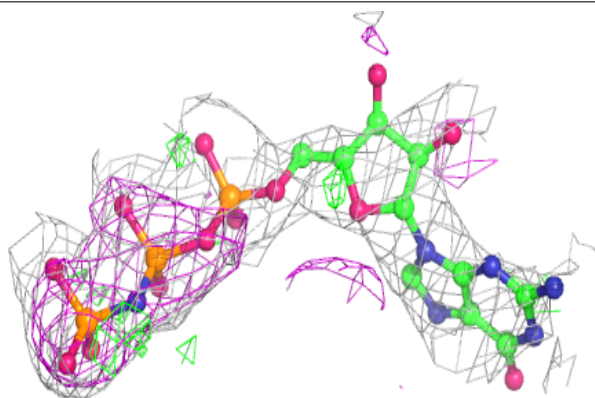


**Electron density around GDP A 416:**

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

**Electron density around GNP A 417:**

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



## 6.5 Other polymers

There are no such residues in this entry.