



# Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2020 – 05:18 pm BST

PDB ID : 4HUK  
Title : MATE transporter NorM-NG in complex with TPP and monobody  
Authors : Lu, M.  
Deposited on : 2012-11-02  
Resolution : 3.59 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

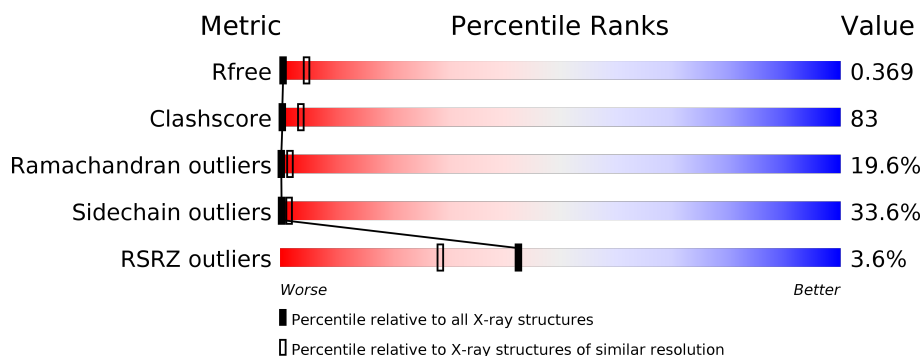
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.59 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	1257 (3.70-3.50)
Clashscore	141614	1353 (3.70-3.50)
Ramachandran outliers	138981	1307 (3.70-3.50)
Sidechain outliers	138945	1307 (3.70-3.50)
RSRZ outliers	127900	1161 (3.70-3.50)

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	459	
2	B	99	

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
3	P4P	A	501	-	-	X	-

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4240 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 Multidrug efflux protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	459	3508	2338	558	589	23	0	0	0

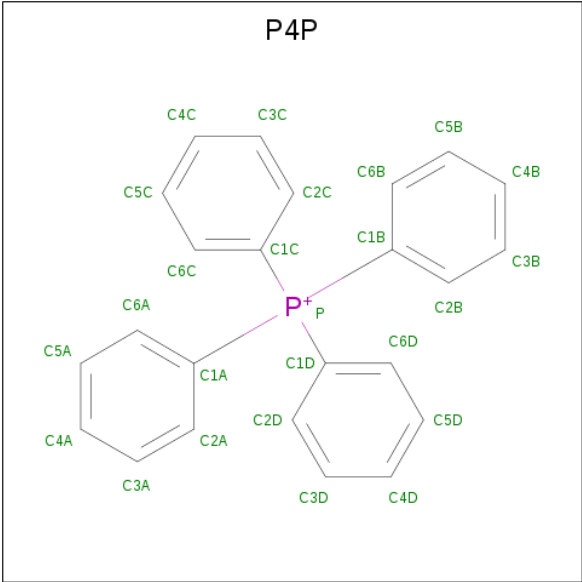
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	460	SER	-	EXPRESSION TAG	UNP E8SM44
A	461	SER	-	EXPRESSION TAG	UNP E8SM44
A	462	GLY	-	EXPRESSION TAG	UNP E8SM44
A	463	LEU	-	EXPRESSION TAG	UNP E8SM44

- Molecule 2 is a protein called Protein B.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	91	707	457	110	140	0	0	0

- Molecule 3 is TETRAPHENYLPHOSPHONIUM (three-letter code: P4P) (formula: C<sub>24</sub>H<sub>20</sub>P).

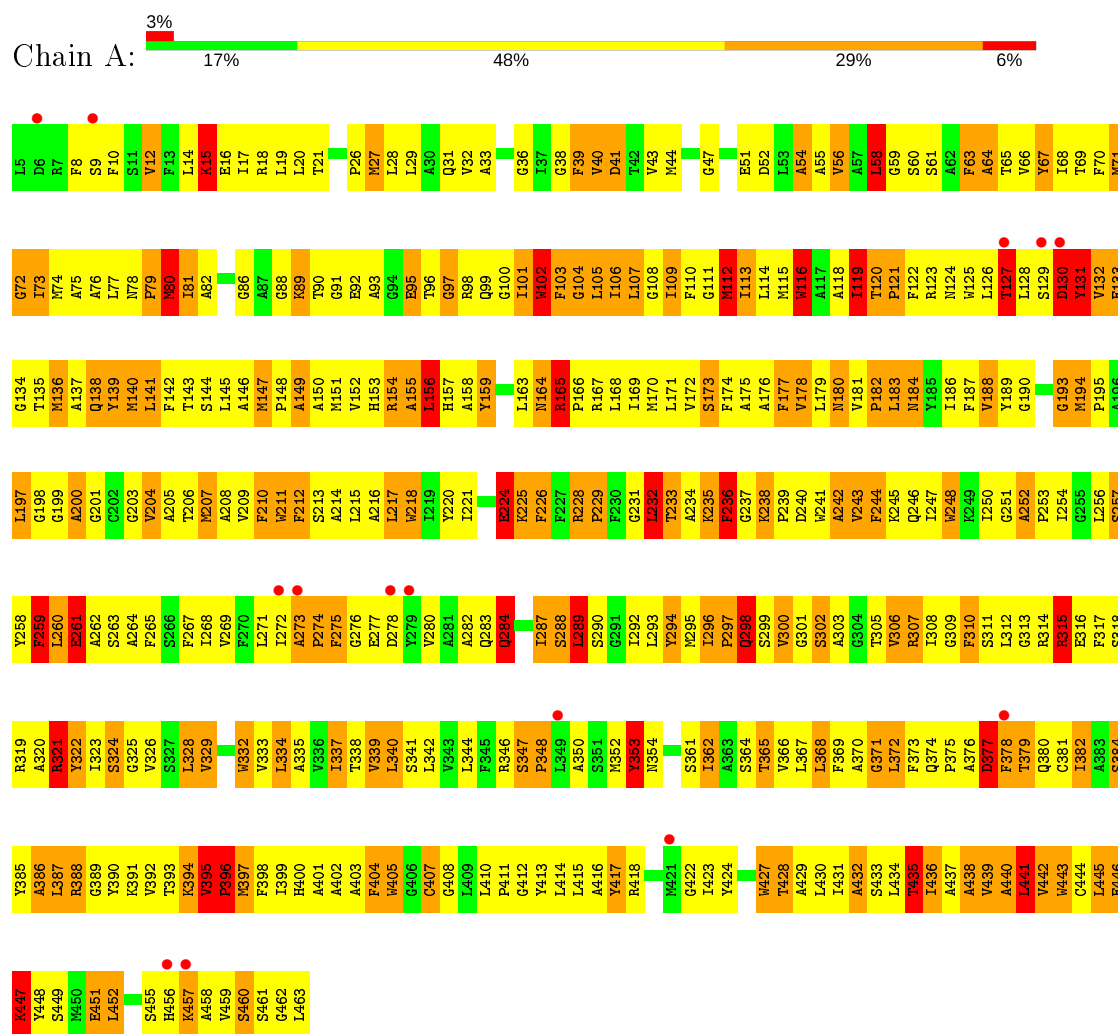


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	P	0	0
			25	24	1		

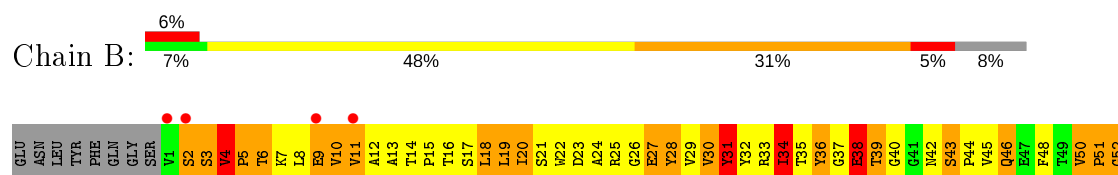
### 3 Residue-property plots

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: Multidrug efflux protein



#### • Molecule 2: Protein B





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	118.33Å 118.33Å 226.47Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 3.59 52.44 – 3.59	Depositor EDS
% Data completeness (in resolution range)	98.4 (20.00-3.59) 98.4 (52.44-3.59)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.77 (at 3.57Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, $R_{free}$	0.307 , 0.349 0.323 , 0.369	Depositor DCC
$R_{free}$ test set	1117 reflections (5.14%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	135.3	Xtriage
Anisotropy	0.475	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.21 , 151.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.39$ , $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	0.157 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.84	EDS
Total number of atoms	4240	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	200.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.45% 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: P4P

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	0.72	7/3605 (0.2%)	0.97	5/4898 (0.1%)
2	B	0.79	1/729 (0.1%)	1.08	2/1004 (0.2%)
All	All	0.74	8/4334 (0.2%)	0.99	7/5902 (0.1%)

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	15
2	B	1	2
All	All	1	17

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	211	TRP	CD2-CE2	5.59	1.48	1.41
1	A	116	TRP	CD2-CE2	5.58	1.48	1.41
1	A	443	TRP	CD2-CE2	5.41	1.47	1.41
1	A	102	TRP	CD2-CE2	5.39	1.47	1.41
1	A	125	TRP	CD2-CE2	5.31	1.47	1.41
1	A	427	TRP	CD2-CE2	5.04	1.47	1.41
1	A	405	TRP	CD2-CE2	5.03	1.47	1.41
2	B	81	TRP	CD2-CE2	5.01	1.47	1.41

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	321	ARG	NE-CZ-NH2	-5.71	117.44	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	441	LEU	CA-CB-CG	5.54	128.04	115.30
1	A	289	LEU	CB-CG-CD2	5.53	120.39	111.00
1	A	156	LEU	CA-CB-CG	5.43	127.79	115.30
2	B	33	ARG	N-CA-C	-5.27	96.77	111.00
1	A	372	LEU	CA-CB-CG	5.25	127.38	115.30
2	B	34	ILE	CB-CA-C	5.18	121.95	111.60

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	28	TYR	CA

All (17) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	138	GLN	Peptide
1	A	188	VAL	Peptide
1	A	194	MET	Peptide
1	A	220	TYR	Peptide
1	A	226	PHE	Peptide
1	A	273	ALA	Peptide
1	A	322	TYR	Peptide
1	A	337	ILE	Peptide
1	A	395	VAL	Peptide
1	A	396	PRO	Peptide
1	A	432	ALA	Peptide
1	A	435	THR	Peptide
1	A	446	GLU	Peptide
1	A	447	LYS	Peptide
1	A	54	ALA	Peptide
2	B	27	GLU	Peptide
2	B	4	VAL	Peptide

## 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	3508	0	3587	582	0
2	B	707	0	681	139	0
3	A	25	0	20	9	0
All	All	4240	0	4288	709	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 83.

All (709) 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:447:LYS:HD2	1:A:448:TYR:CE1	1.47	1.48
1:A:447:LYS:CD	1:A:448:TYR:HE1	1.45	1.29
1:A:44:MET:HE1	1:A:180:ASN:ND2	1.51	1.26
1:A:164:ASN:O	1:A:166:PRO:HD3	1.32	1.23
1:A:411:PRO:HB3	1:A:428:THR:HG23	1.18	1.17
1:A:447:LYS:CD	1:A:448:TYR:CE1	2.22	1.17
2:B:4:VAL:HG22	2:B:6:THR:HG23	1.21	1.17
1:A:439:VAL:HG23	1:A:440:ALA:H	1.09	1.16
1:A:78:ASN:HA	1:A:163:LEU:CD1	1.75	1.15
1:A:44:MET:CE	1:A:180:ASN:HD21	1.59	1.15
1:A:365:THR:HB	1:A:423:ILE:HG21	1.31	1.11
1:A:144:SER:CB	1:A:204:VAL:HG12	1.80	1.10
1:A:78:ASN:HA	1:A:163:LEU:HD13	1.19	1.10
1:A:224:GLU:HG2	1:A:225:LYS:H	1.03	1.08
1:A:339:VAL:HG21	1:A:375:PRO:HD3	1.07	1.05
1:A:242:ALA:HA	1:A:245:LYS:H	1.21	1.05
1:A:418:ARG:HG2	1:A:422:GLY:HA3	1.10	1.05
1:A:259:PHE:HA	1:A:262:ALA:HB3	1.35	1.05
1:A:317:PHE:HB3	1:A:452:LEU:HB3	1.40	1.02
1:A:141:LEU:CD2	1:A:203:GLY:HA3	1.90	1.01
1:A:44:MET:HE1	1:A:180:ASN:HD21	0.84	1.01
1:A:56:VAL:HA	1:A:138:GLN:HE22	1.26	1.00
3:A:501:P4P:H2B	3:A:501:P4P:C6C	1.92	0.99
2:B:76:SER:HB3	2:B:82:TYR:CD2	1.97	0.99
1:A:183:LEU:HA	1:A:186:ILE:HD12	1.38	0.99
1:A:144:SER:HB3	1:A:204:VAL:CG1	1.92	0.98
1:A:218:TRP:HA	1:A:218:TRP:CE3	1.98	0.98
1:A:418:ARG:HG2	1:A:422:GLY:CA	1.92	0.98
1:A:321:ARG:HH22	1:A:391:LYS:HB2	1.23	0.98
1:A:387:LEU:HD11	1:A:444:CYS:O	1.61	0.98
1:A:439:VAL:CG2	1:A:440:ALA:H	1.75	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:411:PRO:HB3	1:A:428:THR:CG2	1.94	0.98
1:A:148:PRO:HG3	1:A:207:MET:HB2	1.42	0.98
1:A:248:TRP:HZ3	1:A:252:ALA:HB2	1.29	0.97
1:A:297:PRO:HB3	1:A:378:PHE:CE2	2.01	0.96
1:A:439:VAL:HG23	1:A:440:ALA:N	1.81	0.96
1:A:144:SER:O	1:A:207:MET:HG2	1.67	0.95
1:A:248:TRP:CZ3	1:A:252:ALA:HB2	2.01	0.94
1:A:460:SER:O	2:B:8:LEU:HD12	1.66	0.94
1:A:224:GLU:HG2	1:A:225:LYS:N	1.83	0.93
1:A:188:VAL:HA	1:A:198:GLY:HA2	1.49	0.93
1:A:315:ARG:HG3	1:A:317:PHE:CE1	2.04	0.93
1:A:66:VAL:HA	1:A:69:THR:HG22	1.49	0.93
1:A:429:ALA:O	1:A:433:SER:CB	2.18	0.91
1:A:447:LYS:HD3	1:A:448:TYR:HE1	1.36	0.91
1:A:429:ALA:O	1:A:433:SER:HB2	1.71	0.91
1:A:318:SER:C	1:A:320:ALA:H	1.74	0.91
1:A:136:MET:O	1:A:139:TYR:HB2	1.71	0.90
1:A:224:GLU:CG	1:A:225:LYS:H	1.84	0.89
1:A:259:PHE:HA	1:A:262:ALA:CB	2.03	0.89
2:B:27:GLU:O	2:B:28:TYR:CD2	2.26	0.89
1:A:144:SER:HB3	1:A:204:VAL:HG12	0.95	0.89
1:A:460:SER:O	2:B:8:LEU:CD1	2.21	0.89
1:A:102:TRP:O	1:A:106:ILE:HB	1.71	0.88
1:A:102:TRP:CD1	1:A:233:THR:OG1	2.25	0.88
1:A:235:LYS:HB2	1:A:241:TRP:HB3	1.55	0.88
1:A:142:PHE:O	1:A:146:ALA:HB3	1.74	0.87
2:B:27:GLU:O	2:B:28:TYR:HD2	1.57	0.87
2:B:4:VAL:HG22	2:B:6:THR:CG2	2.04	0.87
1:A:145:LEU:HD12	1:A:207:MET:HB3	1.57	0.87
1:A:321:ARG:NH2	1:A:391:LYS:HB2	1.90	0.87
1:A:89:LYS:HD3	1:A:89:LYS:H	1.36	0.87
2:B:24:ALA:O	2:B:53:SER:OG	1.92	0.86
1:A:387:LEU:CD2	1:A:445:LEU:HD13	2.07	0.85
1:A:99:GLN:NE2	1:A:234:ALA:O	2.09	0.85
2:B:31:TYR:CD1	2:B:75:ARG:NH1	2.44	0.85
1:A:154:ARG:HH21	1:A:215:LEU:CD2	1.89	0.85
1:A:218:TRP:HE3	1:A:218:TRP:HA	1.37	0.85
1:A:408:GLY:HA2	1:A:411:PRO:HG2	1.56	0.85
1:A:183:LEU:CD2	1:A:209:VAL:HG23	2.07	0.85
1:A:254:ILE:HB	1:A:394:LYS:NZ	1.92	0.85
1:A:321:ARG:HH21	1:A:390:TYR:HB3	1.42	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:193:GLY:O	1:A:195:PRO:HD3	1.77	0.83
1:A:404:PHE:HA	1:A:433:SER:OG	1.77	0.83
1:A:102:TRP:CZ3	1:A:235:LYS:HG2	2.12	0.83
1:A:154:ARG:HH21	1:A:215:LEU:HD22	1.41	0.83
1:A:346:ARG:HD2	1:A:367:LEU:HD11	1.58	0.83
1:A:394:LYS:HA	1:A:397:MET:HB2	1.61	0.83
1:A:393:THR:HG1	1:A:448:TYR:HE2	1.26	0.82
1:A:329:VAL:HA	1:A:332:TRP:HB3	1.61	0.82
1:A:418:ARG:CG	1:A:422:GLY:HA3	2.03	0.82
1:A:78:ASN:CA	1:A:163:LEU:HD13	2.07	0.82
1:A:154:ARG:NH2	1:A:215:LEU:CD2	2.43	0.82
1:A:408:GLY:HA3	1:A:430:LEU:HG	1.60	0.82
1:A:102:TRP:HZ3	1:A:235:LYS:HG2	1.44	0.82
1:A:73:ILE:O	1:A:76:ALA:HB3	1.80	0.81
1:A:251:GLY:O	1:A:254:ILE:HG22	1.80	0.81
2:B:36:TYR:HA	2:B:70:ILE:HD11	1.62	0.81
1:A:397:MET:O	1:A:400:HIS:ND1	2.14	0.81
1:A:225:LYS:HD3	1:A:226:PHE:CD2	2.15	0.81
1:A:388:ARG:HB3	1:A:394:LYS:HB3	1.63	0.81
1:A:448:TYR:HA	1:A:451:GLU:HG2	1.64	0.80
3:A:501:P4P:H2B	3:A:501:P4P:H6C	1.64	0.80
1:A:308:ILE:CD1	1:A:386:ALA:HA	2.12	0.79
1:A:387:LEU:HD23	1:A:445:LEU:HD13	1.62	0.79
1:A:432:ALA:O	1:A:436:ILE:HG23	1.82	0.79
1:A:184:ASN:HA	1:A:205:ALA:HB1	1.63	0.79
1:A:181:VAL:HB	1:A:182:PRO:CD	2.12	0.79
1:A:154:ARG:NH2	1:A:215:LEU:HD21	1.97	0.79
1:A:56:VAL:HA	1:A:138:GLN:NE2	1.97	0.79
1:A:387:LEU:CD2	1:A:445:LEU:CD1	2.61	0.79
1:A:151:MET:SD	1:A:211:TRP:CE3	2.76	0.78
1:A:172:VAL:HG21	1:A:216:ALA:CB	2.13	0.78
2:B:32:TYR:HB2	2:B:50:VAL:HG23	1.65	0.78
1:A:141:LEU:HD22	1:A:203:GLY:HA3	1.65	0.78
1:A:96:THR:O	1:A:99:GLN:N	2.17	0.77
2:B:73:TYR:CD2	2:B:84:PRO:HB3	2.19	0.77
2:B:73:TYR:CE2	2:B:84:PRO:HB3	2.19	0.77
1:A:164:ASN:O	1:A:166:PRO:CD	2.26	0.77
1:A:148:PRO:HG3	1:A:207:MET:CB	2.15	0.76
2:B:17:SER:OG	2:B:59:ILE:O	2.01	0.76
2:B:9:GLU:O	2:B:22:TRP:NE1	2.17	0.76
2:B:69:THR:HA	2:B:88:ASN:HA	1.68	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:458:ALA:HB1	2:B:8:LEU:HB2	1.68	0.76
1:A:290:SER:O	1:A:294:TYR:HB3	1.85	0.76
2:B:38:GLU:HA	2:B:68:TYR:HA	1.68	0.76
1:A:184:ASN:HA	1:A:205:ALA:CB	2.16	0.75
1:A:373:PHE:HB2	1:A:434:LEU:HD22	1.68	0.75
1:A:375:PRO:HA	1:A:378:PHE:HB2	1.68	0.75
2:B:19:LEU:HA	2:B:58:THR:HG22	1.69	0.75
1:A:78:ASN:HA	1:A:163:LEU:HD11	1.68	0.75
2:B:76:SER:HB3	2:B:82:TYR:CE2	2.20	0.75
2:B:10:VAL:HG12	2:B:18:LEU:HD22	1.69	0.75
1:A:329:VAL:HA	1:A:332:TRP:CB	2.17	0.74
1:A:424:TYR:HA	1:A:427:TRP:CD1	2.23	0.74
1:A:189:TYR:HA	1:A:195:PRO:O	1.87	0.74
1:A:252:ALA:HB3	1:A:253:PRO:HD3	1.68	0.74
2:B:4:VAL:HG21	2:B:85:ILE:HB	1.69	0.74
1:A:399:ILE:HG23	1:A:402:ALA:HB3	1.70	0.74
1:A:115:MET:O	1:A:118:ALA:HB3	1.88	0.73
1:A:148:PRO:CG	1:A:207:MET:HB2	2.16	0.73
2:B:10:VAL:HG12	2:B:18:LEU:CD2	2.18	0.73
1:A:289:LEU:HA	1:A:292:ILE:HG12	1.70	0.73
1:A:214:ALA:C	1:A:215:LEU:HD23	2.09	0.73
1:A:333:VAL:HG12	1:A:334:LEU:HD13	1.69	0.73
1:A:92:GLU:HA	1:A:95:GLU:HG2	1.70	0.73
1:A:89:LYS:HG2	1:A:92:GLU:HB3	1.71	0.72
1:A:372:LEU:HB3	1:A:431:ILE:HD13	1.70	0.72
2:B:67:ASP:HA	2:B:90:ARG:HG2	1.70	0.72
1:A:116:TRP:HH2	1:A:147:MET:HA	1.52	0.72
1:A:373:PHE:HB3	1:A:431:ILE:HG22	1.72	0.72
1:A:181:VAL:HB	1:A:182:PRO:HD2	1.71	0.71
1:A:396:PRO:HB3	1:A:399:ILE:HG13	1.72	0.71
1:A:441:LEU:C	1:A:443:TRP:H	1.93	0.71
1:A:318:SER:HA	1:A:321:ARG:H	1.56	0.71
1:A:332:TRP:HA	1:A:335:ALA:CB	2.20	0.71
1:A:308:ILE:HB	1:A:390:TYR:CD1	2.25	0.71
1:A:308:ILE:HD11	1:A:386:ALA:HA	1.71	0.71
1:A:334:LEU:H	1:A:334:LEU:HD22	1.55	0.71
1:A:283:GLN:HG2	1:A:283:GLN:O	1.89	0.71
1:A:108:GLY:HA2	1:A:153:HIS:HD2	1.56	0.71
1:A:339:VAL:HG11	1:A:375:PRO:HG3	1.71	0.70
1:A:89:LYS:CG	1:A:92:GLU:HB3	2.21	0.70
1:A:315:ARG:HH21	2:B:11:VAL:HG11	1.56	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:372:LEU:HD11	1:A:424:TYR:HD1	1.56	0.70
1:A:447:LYS:HB3	1:A:448:TYR:CD1	2.26	0.70
1:A:164:ASN:O	1:A:165:ARG:HD3	1.91	0.70
1:A:100:GLY:O	1:A:104:GLY:N	2.23	0.70
1:A:28:LEU:O	1:A:32:VAL:HG23	1.92	0.70
2:B:68:TYR:H	2:B:90:ARG:HB3	1.56	0.69
1:A:77:LEU:HA	1:A:80:MET:HG3	1.74	0.69
1:A:164:ASN:C	1:A:166:PRO:HD3	2.11	0.69
1:A:31:GLN:HE22	1:A:300:VAL:HG23	1.58	0.69
1:A:193:GLY:O	1:A:195:PRO:CD	2.40	0.69
2:B:5:PRO:HD3	2:B:74:ALA:HB2	1.75	0.69
1:A:183:LEU:HD12	1:A:187:PHE:HE1	1.56	0.69
1:A:318:SER:C	1:A:320:ALA:N	2.47	0.69
1:A:365:THR:HA	1:A:368:LEU:HD11	1.73	0.69
3:A:501:P4P:C2B	3:A:501:P4P:C6C	2.71	0.69
2:B:22:TRP:HZ3	2:B:85:ILE:HG23	1.58	0.69
1:A:332:TRP:CE3	1:A:332:TRP:O	2.46	0.68
1:A:447:LYS:HD2	1:A:448:TYR:CD1	2.22	0.68
1:A:86:GLY:HA3	1:A:313:GLY:HA3	1.76	0.68
2:B:35:THR:O	2:B:70:ILE:HG12	1.94	0.68
1:A:218:TRP:CE3	1:A:221:ILE:HD11	2.29	0.68
1:A:288:SER:O	1:A:292:ILE:HG23	1.93	0.68
1:A:441:LEU:O	1:A:443:TRP:N	2.27	0.68
1:A:238:LYS:HB2	1:A:239:PRO:HD2	1.75	0.67
1:A:296:ILE:HG22	1:A:297:PRO:HD3	1.75	0.67
2:B:78:TYR:C	2:B:80:GLY:H	1.96	0.67
1:A:391:LYS:NZ	1:A:451:GLU:HG3	2.09	0.67
1:A:436:ILE:HD12	1:A:436:ILE:O	1.94	0.67
1:A:82:ALA:HB1	1:A:310:PHE:HB2	1.76	0.67
1:A:429:ALA:O	1:A:433:SER:HB3	1.94	0.67
2:B:20:ILE:HD11	2:B:59:ILE:HG23	1.76	0.67
1:A:455:SER:O	2:B:11:VAL:HA	1.95	0.67
1:A:16:GLU:HA	1:A:19:LEU:HD12	1.76	0.67
2:B:8:LEU:O	2:B:9:GLU:HB2	1.92	0.67
1:A:373:PHE:O	1:A:377:ASP:HB3	1.94	0.67
1:A:447:LYS:C	1:A:448:TYR:HD1	1.98	0.67
2:B:65:GLY:HA2	2:B:91:THR:HB	1.75	0.67
1:A:215:LEU:N	1:A:215:LEU:HD23	2.09	0.66
1:A:149:ALA:HA	1:A:152:VAL:CG2	2.24	0.66
1:A:60:SER:HB3	1:A:141:LEU:CD1	2.26	0.66
2:B:67:ASP:HA	2:B:90:ARG:CG	2.25	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:172:VAL:O	1:A:174:PHE:N	2.25	0.66
1:A:183:LEU:HD12	1:A:187:PHE:CE1	2.31	0.66
1:A:332:TRP:HA	1:A:335:ALA:HB2	1.77	0.66
1:A:439:VAL:CG2	1:A:440:ALA:N	2.48	0.66
1:A:444:CYS:C	1:A:448:TYR:HB2	2.17	0.65
1:A:306:VAL:O	1:A:308:ILE:N	2.29	0.65
1:A:403:ALA:O	1:A:407:CYS:N	2.26	0.65
1:A:400:HIS:HD2	1:A:404:PHE:HE1	1.42	0.65
1:A:441:LEU:O	1:A:444:CYS:N	2.29	0.65
3:A:501:P4P:H6C	3:A:501:P4P:C2B	2.27	0.65
1:A:315:ARG:HG3	1:A:317:PHE:HE1	1.57	0.65
1:A:332:TRP:O	1:A:332:TRP:HE3	1.79	0.65
2:B:30:VAL:O	2:B:31:TYR:HB2	1.96	0.65
1:A:318:SER:HA	1:A:321:ARG:N	2.12	0.65
1:A:339:VAL:HG21	1:A:375:PRO:CD	2.03	0.65
1:A:95:GLU:HA	1:A:98:ARG:HG2	1.79	0.64
1:A:73:ILE:HA	1:A:251:GLY:HA2	1.79	0.64
2:B:29:VAL:O	2:B:30:VAL:HG12	1.96	0.64
1:A:183:LEU:HD23	1:A:209:VAL:HG23	1.78	0.64
1:A:261:GLU:HA	1:A:264:ALA:HB3	1.80	0.64
1:A:141:LEU:CD2	1:A:203:GLY:CA	2.73	0.64
1:A:254:ILE:HG13	1:A:258:TYR:CE1	2.32	0.64
1:A:254:ILE:HB	1:A:394:LYS:HZ1	1.62	0.64
2:B:4:VAL:CG2	2:B:6:THR:HG23	2.15	0.64
1:A:458:ALA:HB3	2:B:9:GLU:N	2.13	0.63
1:A:457:LYS:HD3	2:B:10:VAL:HB	1.80	0.63
1:A:287:ILE:O	3:A:501:P4P:H4C	1.99	0.63
1:A:145:LEU:CD1	1:A:206:THR:HB	2.29	0.63
1:A:429:ALA:HA	1:A:432:ALA:HB3	1.79	0.63
2:B:13:ALA:HB1	2:B:17:SER:O	1.98	0.63
1:A:232:LEU:C	1:A:234:ALA:H	2.01	0.62
1:A:321:ARG:HA	1:A:324:SER:HB3	1.81	0.62
1:A:382:ILE:HA	1:A:385:TYR:CD2	2.34	0.62
2:B:26:GLY:O	2:B:53:SER:HA	1.99	0.62
1:A:411:PRO:HG3	1:A:429:ALA:HB3	1.81	0.62
1:A:148:PRO:O	1:A:150:ALA:N	2.32	0.62
2:B:7:LYS:CB	2:B:23:ASP:HB2	2.29	0.62
1:A:174:PHE:C	1:A:176:ALA:H	2.02	0.62
1:A:119:ILE:HG12	1:A:142:PHE:CD2	2.34	0.62
1:A:339:VAL:HG23	1:A:342:LEU:HD12	1.81	0.62
2:B:12:ALA:O	2:B:18:LEU:HD23	1.98	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:333:VAL:O	1:A:337:ILE:HG12	1.99	0.62
1:A:458:ALA:CB	2:B:8:LEU:HB2	2.29	0.62
1:A:259:PHE:CA	1:A:262:ALA:HB3	2.20	0.62
1:A:377:ASP:HA	1:A:380:GLN:HB2	1.81	0.62
1:A:63:PHE:C	1:A:65:THR:H	2.03	0.61
1:A:81:ILE:CG1	1:A:163:LEU:HD12	2.30	0.61
1:A:31:GLN:O	1:A:296:ILE:HG13	2.00	0.61
2:B:36:TYR:HA	2:B:70:ILE:CD1	2.31	0.61
1:A:151:MET:SD	1:A:211:TRP:CD2	2.93	0.61
1:A:105:LEU:O	1:A:109:ILE:HG23	1.99	0.61
1:A:371:GLY:O	1:A:375:PRO:HD2	2.01	0.61
1:A:172:VAL:C	1:A:174:PHE:H	2.03	0.61
1:A:272:ILE:HG22	1:A:280:VAL:O	2.00	0.61
1:A:329:VAL:CA	1:A:332:TRP:HB3	2.30	0.61
1:A:372:LEU:HB3	1:A:431:ILE:HG21	1.82	0.61
1:A:400:HIS:HD2	1:A:404:PHE:CE1	2.18	0.61
2:B:31:TYR:HB3	2:B:75:ARG:HB3	1.82	0.61
1:A:101:ILE:HD11	1:A:217:LEU:HD22	1.83	0.61
1:A:328:LEU:O	1:A:332:TRP:HB2	2.01	0.61
1:A:33:ALA:HB2	1:A:170:MET:HA	1.83	0.61
1:A:116:TRP:HH2	1:A:147:MET:CA	2.14	0.61
1:A:148:PRO:O	1:A:152:VAL:HG13	2.01	0.61
1:A:74:MET:C	1:A:76:ALA:H	2.05	0.61
1:A:81:ILE:HG13	1:A:163:LEU:HD12	1.83	0.60
1:A:442:VAL:HA	1:A:445:LEU:HB3	1.83	0.60
1:A:388:ARG:O	1:A:391:LYS:O	2.19	0.60
1:A:40:VAL:O	1:A:43:VAL:HG12	2.00	0.60
1:A:79:PRO:O	1:A:80:MET:C	2.39	0.60
2:B:7:LYS:HB2	2:B:23:ASP:HB2	1.83	0.60
1:A:322:TYR:HE1	1:A:449:SER:HB2	1.66	0.60
1:A:415:LEU:HG	1:A:422:GLY:O	2.01	0.60
1:A:372:LEU:HD11	1:A:424:TYR:CD1	2.36	0.60
1:A:458:ALA:HB1	2:B:8:LEU:CB	2.32	0.60
1:A:254:ILE:HB	1:A:394:LYS:CE	2.32	0.60
1:A:27:MET:HG3	1:A:303:ALA:O	2.01	0.60
1:A:130:ASP:O	1:A:131:TYR:HB3	2.02	0.60
1:A:81:ILE:HG13	1:A:163:LEU:HB2	1.84	0.60
1:A:256:LEU:HB3	1:A:398:PHE:HE1	1.67	0.60
1:A:145:LEU:HD13	1:A:203:GLY:O	2.02	0.59
1:A:271:LEU:O	1:A:280:VAL:HG12	2.02	0.59
2:B:37:GLY:N	2:B:70:ILE:HD11	2.17	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:340:LEU:O	1:A:344:LEU:HB2	2.01	0.59
1:A:391:LYS:HB3	1:A:393:THR:H	1.68	0.59
1:A:396:PRO:HB3	1:A:399:ILE:CG1	2.31	0.59
1:A:238:LYS:HB2	1:A:239:PRO:CD	2.32	0.59
1:A:274:PRO:C	1:A:276:GLY:H	2.04	0.59
1:A:141:LEU:HD21	1:A:203:GLY:HA3	1.84	0.59
1:A:458:ALA:HB3	2:B:8:LEU:C	2.23	0.59
1:A:149:ALA:HA	1:A:152:VAL:HG21	1.84	0.59
1:A:457:LYS:NZ	2:B:89:TYR:HB3	2.18	0.59
2:B:63:SER:HB3	2:B:64:PRO:HD2	1.84	0.59
1:A:218:TRP:CA	1:A:218:TRP:CE3	2.83	0.59
1:A:265:PHE:CZ	3:A:501:P4P:H4A	2.38	0.58
2:B:38:GLU:HA	2:B:68:TYR:HD1	1.67	0.58
2:B:8:LEU:HD13	2:B:87:ILE:HD11	1.85	0.58
1:A:373:PHE:HB2	1:A:434:LEU:CD2	2.32	0.58
1:A:394:LYS:HA	1:A:397:MET:CB	2.30	0.58
1:A:451:GLU:HA	1:A:451:GLU:OE1	2.02	0.58
1:A:51:GLU:HB3	1:A:54:ALA:HB3	1.86	0.58
2:B:30:VAL:O	2:B:30:VAL:HG13	2.04	0.58
1:A:60:SER:HB3	1:A:141:LEU:HD12	1.86	0.58
1:A:369:PHE:HB3	1:A:372:LEU:HD12	1.86	0.58
1:A:322:TYR:HE1	1:A:449:SER:CB	2.17	0.58
1:A:329:VAL:O	1:A:329:VAL:HG13	2.03	0.57
1:A:332:TRP:HD1	1:A:379:THR:HG21	1.69	0.57
1:A:441:LEU:C	1:A:443:TRP:N	2.58	0.57
1:A:68:ILE:HA	1:A:71:MET:CB	2.34	0.57
1:A:387:LEU:HD21	1:A:445:LEU:HB2	1.86	0.57
1:A:145:LEU:HD13	1:A:206:THR:HB	1.86	0.57
1:A:141:LEU:HD13	1:A:145:LEU:HD23	1.86	0.57
1:A:377:ASP:O	1:A:380:GLN:N	2.38	0.57
1:A:89:LYS:O	1:A:89:LYS:HG2	2.05	0.57
1:A:218:TRP:CZ3	1:A:221:ILE:HD11	2.39	0.57
1:A:253:PRO:O	1:A:257:SER:HB2	2.04	0.57
1:A:393:THR:OG1	1:A:448:TYR:HE2	1.87	0.57
1:A:95:GLU:HB2	1:A:98:ARG:HE	1.70	0.56
1:A:242:ALA:HA	1:A:245:LYS:N	2.06	0.56
2:B:8:LEU:HD13	2:B:87:ILE:CG1	2.36	0.56
2:B:22:TRP:CZ3	2:B:85:ILE:HG23	2.39	0.56
1:A:183:LEU:HD23	1:A:209:VAL:CG2	2.35	0.56
1:A:387:LEU:CD2	1:A:445:LEU:HD12	2.35	0.56
1:A:132:VAL:O	1:A:133:GLU:O	2.24	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:15:LYS:HG2	1:A:322:TYR:HA	1.88	0.56
1:A:332:TRP:HA	1:A:335:ALA:HB3	1.88	0.56
1:A:44:MET:SD	1:A:206:THR:OG1	2.63	0.56
1:A:411:PRO:HA	1:A:414:LEU:HB2	1.87	0.56
2:B:5:PRO:CD	2:B:74:ALA:HB2	2.36	0.56
2:B:9:GLU:O	2:B:22:TRP:CD1	2.58	0.55
1:A:447:LYS:HD3	1:A:448:TYR:CE1	2.20	0.55
1:A:120:THR:C	1:A:122:PHE:H	2.08	0.55
1:A:364:SER:C	1:A:366:VAL:H	2.09	0.55
1:A:89:LYS:HG3	1:A:92:GLU:CB	2.37	0.55
1:A:302:SER:HA	1:A:385:TYR:HB3	1.88	0.55
1:A:158:ALA:HB2	1:A:217:LEU:HG	1.88	0.55
2:B:65:GLY:HA2	2:B:91:THR:CB	2.36	0.55
1:A:410:LEU:O	1:A:414:LEU:HD13	2.06	0.55
2:B:36:TYR:HB2	2:B:46:GLN:O	2.07	0.55
1:A:381:CYS:O	1:A:384:SER:N	2.35	0.55
1:A:154:ARG:HG2	1:A:155:ALA:N	2.21	0.55
1:A:99:GLN:OE1	1:A:241:TRP:CD1	2.60	0.55
1:A:19:LEU:C	1:A:21:THR:H	2.11	0.54
1:A:242:ALA:C	1:A:244:PHE:N	2.61	0.54
1:A:394:LYS:CA	1:A:397:MET:HB2	2.35	0.54
2:B:67:ASP:HA	2:B:90:ARG:HB3	1.88	0.54
1:A:399:ILE:HG23	1:A:402:ALA:CB	2.37	0.54
1:A:440:ALA:O	1:A:443:TRP:HB3	2.08	0.54
1:A:317:PHE:HD2	1:A:455:SER:HB2	1.71	0.54
1:A:254:ILE:HD13	1:A:388:ARG:HD2	1.90	0.54
3:A:501:P4P:H6A	3:A:501:P4P:C6C	2.36	0.54
2:B:37:GLY:H	2:B:70:ILE:HD11	1.71	0.54
1:A:146:ALA:N	1:A:148:PRO:HD2	2.23	0.54
1:A:323:ILE:C	1:A:325:GLY:H	2.10	0.54
2:B:78:TYR:C	2:B:80:GLY:N	2.61	0.54
2:B:32:TYR:HA	2:B:73:TYR:O	2.07	0.54
1:A:168:LEU:HA	1:A:171:LEU:HD13	1.90	0.54
1:A:180:ASN:O	1:A:184:ASN:N	2.23	0.54
1:A:318:SER:O	1:A:322:TYR:HB2	2.08	0.54
1:A:151:MET:HB2	1:A:211:TRP:CE2	2.43	0.54
1:A:284:GLN:O	1:A:288:SER:HB2	2.07	0.54
1:A:242:ALA:HB2	1:A:245:LYS:HB3	1.88	0.53
1:A:55:ALA:HB1	1:A:58:LEU:HD21	1.90	0.53
2:B:4:VAL:CG2	2:B:85:ILE:HB	2.37	0.53
1:A:128:LEU:HD12	1:A:129:SER:H	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:250:ILE:HA	1:A:394:LYS:HD2	1.90	0.53
2:B:42:ASN:HD22	2:B:43:SER:H	1.56	0.53
2:B:78:TYR:O	2:B:80:GLY:N	2.41	0.53
2:B:68:TYR:N	2:B:90:ARG:HB3	2.23	0.53
1:A:89:LYS:CG	1:A:92:GLU:CB	2.87	0.53
1:A:107:LEU:HD23	1:A:108:GLY:N	2.23	0.53
1:A:90:THR:HA	1:A:93:ALA:HB3	1.90	0.53
2:B:4:VAL:HG23	2:B:5:PRO:C	2.29	0.53
1:A:316:GLU:HB3	1:A:319:ARG:HB2	1.91	0.53
1:A:254:ILE:HB	1:A:394:LYS:HE2	1.91	0.53
2:B:67:ASP:HA	2:B:90:ARG:CB	2.39	0.53
2:B:76:SER:CB	2:B:82:TYR:CD2	2.82	0.53
1:A:457:LYS:HZ2	2:B:89:TYR:HB3	1.73	0.53
1:A:261:GLU:HG2	1:A:264:ALA:HB3	1.89	0.53
1:A:415:LEU:HD11	1:A:423:ILE:HD12	1.90	0.53
1:A:457:LYS:HE3	2:B:89:TYR:O	2.09	0.53
1:A:137:ALA:O	1:A:199:GLY:O	2.27	0.53
2:B:16:THR:O	2:B:61:GLY:O	2.27	0.53
2:B:7:LYS:O	2:B:8:LEU:HD23	2.09	0.53
1:A:396:PRO:HB3	1:A:399:ILE:CD1	2.38	0.53
1:A:128:LEU:O	1:A:129:SER:HB3	2.08	0.52
1:A:263:SER:C	1:A:265:PHE:H	2.12	0.52
1:A:380:GLN:HB3	1:A:437:ALA:HB1	1.90	0.52
1:A:18:ARG:O	1:A:18:ARG:HD3	2.09	0.52
1:A:141:LEU:HD21	1:A:203:GLY:CA	2.39	0.52
1:A:348:PRO:HD2	1:A:350:ALA:HB3	1.91	0.52
1:A:73:ILE:H	1:A:73:ILE:HD12	1.74	0.52
2:B:20:ILE:CD1	2:B:59:ILE:HG23	2.38	0.52
1:A:63:PHE:CD2	1:A:64:ALA:N	2.78	0.52
1:A:323:ILE:C	1:A:325:GLY:N	2.62	0.52
1:A:292:ILE:HG13	1:A:293:LEU:H	1.74	0.52
1:A:387:LEU:HD12	1:A:393:THR:CG2	2.39	0.52
1:A:120:THR:H	1:A:121:PRO:CD	2.22	0.52
2:B:36:TYR:CA	2:B:70:ILE:HD11	2.38	0.52
1:A:264:ALA:HA	1:A:267:PHE:HB2	1.90	0.52
1:A:116:TRP:CH2	1:A:147:MET:HA	2.39	0.52
1:A:248:TRP:CE3	1:A:252:ALA:HB2	2.44	0.52
1:A:375:PRO:C	1:A:377:ASP:H	2.13	0.52
1:A:395:VAL:HG22	1:A:396:PRO:HD3	1.91	0.52
2:B:68:TYR:O	2:B:88:ASN:O	2.28	0.52
1:A:107:LEU:HD23	1:A:108:GLY:H	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:397:MET:O	1:A:400:HIS:N	2.35	0.52
1:A:225:LYS:HE2	1:A:226:PHE:CE2	2.45	0.51
1:A:260:LEU:C	1:A:262:ALA:H	2.13	0.51
1:A:238:LYS:CB	1:A:239:PRO:CD	2.87	0.51
1:A:329:VAL:C	1:A:332:TRP:HB3	2.30	0.51
1:A:55:ALA:O	1:A:138:GLN:NE2	2.43	0.51
1:A:89:LYS:HG3	1:A:92:GLU:HB2	1.93	0.51
2:B:27:GLU:HG3	2:B:52:GLY:C	2.31	0.51
1:A:108:GLY:O	1:A:112:MET:HB2	2.11	0.51
1:A:149:ALA:HA	1:A:152:VAL:HG22	1.91	0.51
1:A:183:LEU:CD1	1:A:187:PHE:HE1	2.22	0.51
1:A:31:GLN:HG3	1:A:296:ILE:HA	1.92	0.51
1:A:169:ILE:HA	1:A:172:VAL:HG12	1.91	0.51
1:A:457:LYS:CD	2:B:10:VAL:HB	2.41	0.51
1:A:110:PHE:O	1:A:114:LEU:HG	2.10	0.51
1:A:55:ALA:CB	1:A:58:LEU:HD21	2.40	0.51
1:A:147:MET:N	1:A:148:PRO:HD2	2.26	0.51
1:A:141:LEU:HD23	1:A:200:ALA:HA	1.92	0.51
1:A:250:ILE:HA	1:A:394:LYS:CD	2.41	0.51
1:A:60:SER:HB3	1:A:141:LEU:HD11	1.92	0.51
1:A:308:ILE:HG13	1:A:309:GLY:H	1.76	0.51
1:A:257:SER:OG	1:A:398:PHE:HA	2.10	0.51
1:A:60:SER:CB	1:A:141:LEU:CD1	2.89	0.51
2:B:38:GLU:HB2	2:B:40:GLY:H	1.76	0.51
1:A:268:ILE:HD13	1:A:287:ILE:HD11	1.92	0.51
1:A:66:VAL:HA	1:A:69:THR:CG2	2.32	0.51
1:A:118:ALA:O	1:A:120:THR:N	2.44	0.50
1:A:156:LEU:HD12	1:A:159:TYR:CE1	2.47	0.50
2:B:38:GLU:CD	2:B:38:GLU:H	2.14	0.50
1:A:31:GLN:HE22	1:A:300:VAL:HA	1.76	0.50
1:A:65:THR:CG2	1:A:66:VAL:N	2.74	0.50
2:B:27:GLU:HG2	2:B:30:VAL:HG23	1.92	0.50
1:A:400:HIS:CD2	1:A:404:PHE:HE1	2.28	0.50
1:A:441:LEU:HD23	1:A:441:LEU:H	1.77	0.50
1:A:144:SER:CB	1:A:204:VAL:CG1	2.72	0.50
1:A:178:VAL:O	1:A:182:PRO:HD2	2.12	0.50
2:B:14:THR:C	2:B:16:THR:H	2.15	0.50
2:B:13:ALA:HB2	2:B:18:LEU:HG	1.94	0.50
1:A:238:LYS:CB	1:A:239:PRO:HD2	2.41	0.49
2:B:27:GLU:HG3	2:B:52:GLY:O	2.12	0.49
1:A:109:ILE:HA	1:A:112:MET:HB2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:317:PHE:CD2	1:A:455:SER:HB2	2.47	0.49
1:A:177:PHE:O	1:A:181:VAL:HG23	2.12	0.49
1:A:458:ALA:HB3	2:B:9:GLU:HA	1.95	0.49
2:B:10:VAL:HG12	2:B:18:LEU:HD21	1.93	0.49
1:A:183:LEU:HD21	1:A:209:VAL:HG23	1.90	0.49
1:A:384:SER:C	1:A:386:ALA:H	2.15	0.49
1:A:158:ALA:HB2	1:A:217:LEU:CD1	2.43	0.49
1:A:391:LYS:HZ3	1:A:451:GLU:HG3	1.76	0.49
1:A:456:HIS:CD2	1:A:459:VAL:HA	2.48	0.49
1:A:40:VAL:HG22	1:A:177:PHE:HB2	1.94	0.49
2:B:4:VAL:HG12	2:B:83:SER:HB3	1.95	0.49
1:A:224:GLU:CG	1:A:225:LYS:N	2.53	0.49
1:A:253:PRO:HB3	1:A:394:LYS:O	2.13	0.49
1:A:31:GLN:NE2	1:A:300:VAL:HA	2.28	0.49
2:B:42:ASN:ND2	2:B:43:SER:H	2.11	0.49
1:A:103:PHE:O	1:A:106:ILE:N	2.42	0.49
2:B:21:SER:HA	2:B:56:THR:HA	1.94	0.49
2:B:29:VAL:H	2:B:76:SER:HA	1.77	0.48
1:A:297:PRO:HB3	1:A:378:PHE:CZ	2.48	0.48
1:A:322:TYR:CE1	1:A:449:SER:HB3	2.48	0.48
1:A:74:MET:O	1:A:76:ALA:N	2.46	0.48
1:A:256:LEU:HB3	1:A:398:PHE:CE1	2.46	0.48
1:A:377:ASP:O	1:A:378:PHE:C	2.51	0.48
1:A:387:LEU:HD21	1:A:444:CYS:O	2.13	0.48
1:A:119:ILE:HG13	1:A:119:ILE:H	1.45	0.48
1:A:187:PHE:HB2	1:A:201:GLY:O	2.13	0.48
2:B:14:THR:O	2:B:16:THR:N	2.38	0.48
1:A:127:THR:HG22	1:A:128:LEU:H	1.78	0.48
1:A:448:TYR:CD1	1:A:451:GLU:HG2	2.48	0.48
1:A:317:PHE:HE2	1:A:455:SER:HB3	1.78	0.48
1:A:221:ILE:HD13	1:A:228:ARG:HG3	1.95	0.48
1:A:334:LEU:N	1:A:334:LEU:HD22	2.27	0.48
1:A:95:GLU:O	1:A:99:GLN:HG3	2.14	0.48
2:B:73:TYR:CE2	2:B:84:PRO:CB	2.95	0.48
1:A:180:ASN:HB2	1:A:209:VAL:HG21	1.94	0.48
1:A:340:LEU:HD12	1:A:341:SER:H	1.79	0.48
1:A:33:ALA:CB	1:A:170:MET:HA	2.43	0.48
1:A:461:SER:OG	1:A:462:GLY:N	2.47	0.48
2:B:74:ALA:O	2:B:81:TRP:HE3	1.97	0.48
1:A:159:TYR:HB3	1:A:169:ILE:HD13	1.96	0.47
1:A:322:TYR:CE1	1:A:449:SER:CB	2.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:394:LYS:C	1:A:397:MET:H	2.17	0.47
1:A:38:GLY:O	1:A:41:ASP:CB	2.62	0.47
1:A:387:LEU:HD21	1:A:445:LEU:CD1	2.42	0.47
1:A:19:LEU:C	1:A:21:THR:N	2.67	0.47
1:A:399:ILE:CG2	1:A:402:ALA:HB3	2.43	0.47
1:A:147:MET:SD	1:A:148:PRO:HD3	2.54	0.47
1:A:204:VAL:O	1:A:208:ALA:HB2	2.14	0.47
2:B:16:THR:HG23	2:B:17:SER:N	2.30	0.47
1:A:101:ILE:CD1	1:A:217:LEU:HD22	2.45	0.47
1:A:369:PHE:C	1:A:371:GLY:H	2.17	0.47
1:A:186:ILE:O	1:A:190:GLY:HA3	2.15	0.47
1:A:408:GLY:CA	1:A:430:LEU:HG	2.39	0.47
1:A:63:PHE:O	1:A:65:THR:N	2.46	0.47
2:B:55:SER:HB2	2:B:72:VAL:HG21	1.96	0.47
1:A:99:GLN:OE1	1:A:241:TRP:HD1	1.98	0.47
1:A:120:THR:C	1:A:122:PHE:N	2.67	0.47
1:A:368:LEU:O	1:A:372:LEU:HG	2.14	0.47
1:A:384:SER:O	1:A:388:ARG:HG3	2.15	0.47
1:A:430:LEU:HA	1:A:433:SER:HB3	1.96	0.47
1:A:437:ALA:C	1:A:439:VAL:H	2.18	0.47
1:A:95:GLU:O	1:A:99:GLN:CG	2.62	0.47
2:B:8:LEU:HA	2:B:22:TRP:CD2	2.49	0.47
1:A:172:VAL:HG21	1:A:216:ALA:HB2	1.96	0.47
1:A:445:LEU:N	1:A:448:TYR:HB2	2.28	0.47
1:A:289:LEU:HD13	1:A:292:ILE:CD1	2.44	0.47
1:A:248:TRP:HZ3	1:A:252:ALA:CB	2.15	0.46
1:A:366:VAL:HA	1:A:369:PHE:CZ	2.50	0.46
1:A:158:ALA:HB2	1:A:217:LEU:CG	2.45	0.46
1:A:9:SER:OG	1:A:443:TRP:HA	2.15	0.46
1:A:74:MET:C	1:A:76:ALA:N	2.68	0.46
1:A:120:THR:N	1:A:121:PRO:CD	2.78	0.46
1:A:201:GLY:HA2	1:A:204:VAL:HG13	1.97	0.46
1:A:274:PRO:C	1:A:276:GLY:N	2.69	0.46
1:A:317:PHE:HB3	1:A:452:LEU:CB	2.26	0.46
1:A:377:ASP:HB2	1:A:434:LEU:HD21	1.96	0.46
2:B:59:ILE:HD12	2:B:61:GLY:CA	2.45	0.46
1:A:458:ALA:HB3	2:B:9:GLU:CA	2.45	0.46
1:A:143:THR:HG23	1:A:144:SER:N	2.31	0.46
1:A:369:PHE:HA	1:A:372:LEU:HG	1.97	0.46
1:A:305:THR:OG1	1:A:389:GLY:HA2	2.15	0.46
2:B:8:LEU:HD13	2:B:87:ILE:CD1	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:181:VAL:CB	1:A:182:PRO:CD	2.89	0.46
1:A:68:ILE:HA	1:A:71:MET:HB3	1.97	0.46
1:A:82:ALA:O	1:A:310:PHE:HA	2.15	0.46
2:B:8:LEU:CD1	2:B:87:ILE:HD11	2.45	0.46
1:A:188:VAL:HA	1:A:198:GLY:CA	2.34	0.46
2:B:37:GLY:H	2:B:70:ILE:CD1	2.27	0.46
1:A:207:MET:SD	1:A:207:MET:C	2.94	0.46
1:A:258:TYR:C	1:A:260:LEU:H	2.19	0.46
1:A:298:GLN:NE2	1:A:299:SER:HB2	2.31	0.46
1:A:76:ALA:O	1:A:250:ILE:HD13	2.16	0.46
2:B:50:VAL:HA	2:B:51:PRO:HD3	1.67	0.46
1:A:143:THR:CG2	1:A:144:SER:N	2.79	0.45
1:A:396:PRO:HA	1:A:398:PHE:HB3	1.98	0.45
1:A:109:ILE:O	1:A:113:ILE:HB	2.15	0.45
1:A:122:PHE:O	1:A:122:PHE:CD2	2.69	0.45
1:A:148:PRO:HA	1:A:211:TRP:HE1	1.82	0.45
1:A:408:GLY:CA	1:A:411:PRO:HG2	2.39	0.45
2:B:29:VAL:HG23	2:B:77:TYR:N	2.30	0.45
2:B:71:THR:HG23	2:B:85:ILE:C	2.37	0.45
1:A:159:TYR:CB	1:A:169:ILE:HD13	2.46	0.45
1:A:164:ASN:C	1:A:166:PRO:CD	2.81	0.45
1:A:268:ILE:HG21	1:A:287:ILE:HD13	1.98	0.45
1:A:301:GLY:C	1:A:303:ALA:H	2.18	0.45
1:A:56:VAL:O	1:A:138:GLN:OE1	2.34	0.45
1:A:265:PHE:CZ	3:A:501:P4P:C4A	2.99	0.45
1:A:100:GLY:HA2	1:A:103:PHE:HB2	1.99	0.45
1:A:325:GLY:O	1:A:328:LEU:N	2.50	0.45
1:A:400:HIS:CD2	1:A:404:PHE:CE1	3.02	0.45
1:A:410:LEU:C	1:A:412:GLY:H	2.20	0.45
1:A:176:ALA:HA	1:A:212:PHE:CE2	2.52	0.45
1:A:325:GLY:O	1:A:328:LEU:HB3	2.17	0.45
1:A:416:ALA:O	1:A:417:TYR:CB	2.65	0.45
1:A:116:TRP:N	1:A:116:TRP:HE3	2.15	0.44
1:A:40:VAL:HA	1:A:177:PHE:HD1	1.81	0.44
1:A:26:PRO:HA	1:A:29:LEU:HG	1.99	0.44
1:A:68:ILE:HA	1:A:71:MET:HB2	1.99	0.44
2:B:19:LEU:CA	2:B:58:THR:HG22	2.43	0.44
1:A:111:GLY:O	1:A:113:ILE:N	2.51	0.44
1:A:166:PRO:HB3	1:A:168:LEU:HD12	1.99	0.44
1:A:168:LEU:HD23	1:A:171:LEU:HD22	1.99	0.44
1:A:173:SER:HA	1:A:176:ALA:HB3	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:372:LEU:HD11	1:A:424:TYR:HB2	1.98	0.44
1:A:414:LEU:O	1:A:418:ARG:NH1	2.47	0.44
1:A:69:THR:HG23	1:A:70:PHE:HD1	1.82	0.44
2:B:39:THR:OG1	2:B:69:THR:OG1	2.18	0.44
2:B:7:LYS:HG2	2:B:8:LEU:N	2.32	0.44
2:B:71:THR:OG1	2:B:86:SER:HB2	2.17	0.44
1:A:301:GLY:C	1:A:303:ALA:N	2.71	0.44
1:A:346:ARG:O	1:A:348:PRO:HD3	2.17	0.44
1:A:381:CYS:C	1:A:384:SER:H	2.18	0.44
2:B:38:GLU:CD	2:B:38:GLU:N	2.70	0.44
1:A:232:LEU:O	1:A:234:ALA:N	2.47	0.44
1:A:447:LYS:CD	1:A:448:TYR:CD1	2.89	0.44
2:B:87:ILE:CG2	2:B:88:ASN:N	2.80	0.44
1:A:397:MET:SD	1:A:400:HIS:HB3	2.58	0.44
1:A:158:ALA:CB	1:A:217:LEU:HG	2.47	0.44
1:A:59:GLY:O	1:A:63:PHE:N	2.51	0.44
1:A:74:MET:HE3	1:A:107:LEU:HD22	2.00	0.44
1:A:142:PHE:O	1:A:146:ALA:CB	2.58	0.43
1:A:172:VAL:HG21	1:A:216:ALA:HB1	1.97	0.43
1:A:251:GLY:O	1:A:252:ALA:C	2.57	0.43
2:B:29:VAL:O	2:B:30:VAL:CG1	2.64	0.43
1:A:103:PHE:HA	1:A:106:ILE:HG22	2.01	0.43
1:A:145:LEU:HD11	1:A:206:THR:HB	1.98	0.43
1:A:388:ARG:CB	1:A:394:LYS:HB3	2.40	0.43
1:A:417:TYR:O	1:A:417:TYR:CG	2.70	0.43
1:A:297:PRO:HB3	1:A:378:PHE:HE2	1.72	0.43
1:A:437:ALA:C	1:A:439:VAL:N	2.72	0.43
1:A:180:ASN:HA	1:A:183:LEU:HD23	2.00	0.43
1:A:33:ALA:HB2	1:A:170:MET:CA	2.45	0.43
1:A:369:PHE:HD2	1:A:424:TYR:CB	2.31	0.43
1:A:441:LEU:HB2	1:A:442:VAL:H	1.56	0.43
1:A:458:ALA:CB	2:B:8:LEU:CB	2.95	0.43
2:B:3:SER:O	2:B:83:SER:HB2	2.18	0.43
1:A:98:ARG:HA	1:A:101:ILE:HG22	1.99	0.43
1:A:180:ASN:ND2	1:A:180:ASN:C	2.72	0.43
1:A:180:ASN:HD22	1:A:181:VAL:N	2.16	0.43
1:A:297:PRO:O	1:A:298:GLN:C	2.56	0.43
1:A:38:GLY:O	1:A:41:ASP:HB2	2.17	0.43
2:B:30:VAL:O	2:B:31:TYR:CB	2.64	0.43
1:A:282:ALA:HB2	1:A:362:ILE:HD12	2.01	0.43
2:B:16:THR:HG23	2:B:17:SER:H	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:247:ILE:HG23	1:A:250:ILE:HD11	2.00	0.43
1:A:103:PHE:HD2	1:A:103:PHE:HA	1.79	0.43
1:A:283:GLN:CG	1:A:283:GLN:O	2.61	0.43
1:A:294:TYR:O	1:A:297:PRO:HB2	2.18	0.43
1:A:342:LEU:HB3	1:A:370:ALA:HB1	2.00	0.43
1:A:447:LYS:C	1:A:448:TYR:CD1	2.87	0.43
1:A:140:MET:HE3	1:A:197:LEU:HD11	2.01	0.43
1:A:181:VAL:HB	1:A:182:PRO:HD3	1.99	0.43
1:A:346:ARG:CZ	1:A:364:SER:HB2	2.49	0.43
1:A:96:THR:HB	1:A:97:GLY:H	1.74	0.43
1:A:60:SER:CB	1:A:141:LEU:HD11	2.48	0.42
1:A:242:ALA:O	1:A:243:VAL:HG22	2.19	0.42
1:A:352:MET:O	1:A:353:TYR:HB3	2.19	0.42
1:A:396:PRO:HB3	1:A:399:ILE:HD12	2.00	0.42
2:B:22:TRP:O	2:B:56:THR:HG23	2.19	0.42
1:A:116:TRP:CE3	1:A:116:TRP:N	2.88	0.42
1:A:64:ALA:HA	1:A:67:TYR:HB3	2.00	0.42
1:A:71:MET:O	1:A:72:GLY:C	2.57	0.42
2:B:76:SER:OG	2:B:77:TYR:N	2.52	0.42
1:A:140:MET:HB3	1:A:200:ALA:HB1	2.00	0.42
1:A:260:LEU:O	1:A:262:ALA:N	2.51	0.42
1:A:400:HIS:CG	1:A:401:ALA:N	2.88	0.42
1:A:172:VAL:C	1:A:174:PHE:N	2.71	0.42
1:A:246:GLN:C	1:A:248:TRP:N	2.72	0.42
1:A:261:GLU:O	1:A:265:PHE:HB2	2.20	0.42
1:A:131:TYR:O	1:A:133:GLU:HG2	2.19	0.42
1:A:231:GLY:O	1:A:233:THR:N	2.52	0.42
1:A:74:MET:SD	1:A:157:HIS:HD2	2.42	0.42
1:A:127:THR:HG22	1:A:128:LEU:N	2.33	0.42
1:A:289:LEU:HA	1:A:292:ILE:CG1	2.44	0.42
1:A:403:ALA:O	1:A:407:CYS:HB2	2.19	0.42
1:A:77:LEU:C	1:A:79:PRO:HD2	2.40	0.42
2:B:63:SER:CB	2:B:64:PRO:HD2	2.49	0.42
1:A:269:VAL:HG12	1:A:269:VAL:O	2.20	0.42
1:A:297:PRO:O	1:A:299:SER:N	2.53	0.42
2:B:13:ALA:HA	2:B:18:LEU:HA	2.01	0.42
1:A:154:ARG:O	1:A:217:LEU:HD11	2.19	0.42
1:A:260:LEU:C	1:A:262:ALA:N	2.73	0.42
1:A:335:ALA:HA	1:A:378:PHE:CZ	2.54	0.42
1:A:392:VAL:O	1:A:394:LYS:N	2.35	0.42
1:A:44:MET:HE1	1:A:180:ASN:CG	2.29	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:12:ALA:O	2:B:18:LEU:CD2	2.66	0.42
1:A:250:ILE:O	1:A:394:LYS:NZ	2.47	0.42
1:A:254:ILE:O	1:A:258:TYR:N	2.53	0.42
1:A:263:SER:C	1:A:265:PHE:N	2.73	0.42
1:A:40:VAL:HA	1:A:177:PHE:CD1	2.55	0.42
2:B:87:ILE:HG22	2:B:88:ASN:N	2.34	0.42
1:A:217:LEU:O	1:A:218:TRP:C	2.57	0.41
1:A:260:LEU:HB3	1:A:261:GLU:H	1.74	0.41
1:A:380:GLN:HB3	1:A:437:ALA:CB	2.49	0.41
2:B:7:LYS:HB3	2:B:23:ASP:HB2	2.00	0.41
2:B:8:LEU:HD13	2:B:87:ILE:HG12	2.02	0.41
2:B:90:ARG:HB2	2:B:91:THR:H	1.49	0.41
1:A:183:LEU:CD2	1:A:209:VAL:CG2	2.87	0.41
1:A:236:PHE:C	1:A:241:TRP:HB2	2.40	0.41
1:A:72:GLY:HA2	1:A:258:TYR:CE1	2.55	0.41
1:A:150:ALA:C	1:A:152:VAL:H	2.24	0.41
1:A:397:MET:C	1:A:400:HIS:H	2.22	0.41
1:A:98:ARG:O	1:A:101:ILE:HG22	2.20	0.41
1:A:15:LYS:HA	1:A:322:TYR:CD2	2.55	0.41
1:A:81:ILE:HG12	1:A:163:LEU:HD12	1.99	0.41
2:B:2:SER:HB3	2:B:3:SER:H	1.58	0.41
2:B:35:THR:HG1	2:B:71:THR:H	1.66	0.41
1:A:317:PHE:CE2	1:A:455:SER:HB3	2.54	0.41
1:A:152:VAL:HG12	1:A:210:PHE:CG	2.56	0.41
1:A:32:VAL:HA	1:A:296:ILE:HD11	2.02	0.41
1:A:32:VAL:HG12	1:A:32:VAL:O	2.21	0.41
3:A:501:P4P:H6D	3:A:501:P4P:C6B	2.50	0.41
2:B:71:THR:HG23	2:B:85:ILE:O	2.20	0.41
1:A:128:LEU:HD13	1:A:132:VAL:CG1	2.50	0.41
1:A:282:ALA:C	1:A:284:GLN:H	2.24	0.41
1:A:36:GLY:HA2	1:A:39:PHE:CE2	2.56	0.41
1:A:460:SER:O	2:B:8:LEU:CG	2.69	0.41
1:A:120:THR:HG22	1:A:120:THR:O	2.21	0.41
1:A:148:PRO:CB	1:A:207:MET:HB2	2.51	0.41
1:A:252:ALA:O	1:A:254:ILE:N	2.54	0.41
1:A:290:SER:O	1:A:294:TYR:CB	2.64	0.41
1:A:315:ARG:O	1:A:317:PHE:CD1	2.73	0.41
1:A:369:PHE:HD2	1:A:424:TYR:HB3	1.86	0.41
1:A:424:TYR:CA	1:A:427:TRP:CD1	2.99	0.41
1:A:435:THR:HG22	1:A:438:ALA:HB2	2.03	0.41
2:B:34:ILE:HA	2:B:71:THR:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:384:SER:C	1:A:386:ALA:N	2.74	0.41
1:A:40:VAL:HB	1:A:41:ASP:H	1.72	0.41
1:A:72:GLY:O	1:A:73:ILE:C	2.60	0.41
2:B:76:SER:O	2:B:77:TYR:C	2.60	0.41
2:B:77:TYR:HB3	2:B:78:TYR:H	1.71	0.41
1:A:252:ALA:HB3	1:A:253:PRO:CD	2.46	0.40
1:A:447:LYS:O	1:A:451:GLU:HG2	2.21	0.40
2:B:52:GLY:C	2:B:54:SER:H	2.24	0.40
1:A:289:LEU:HD13	1:A:292:ILE:HG12	2.03	0.40
1:A:418:ARG:HD2	1:A:418:ARG:HA	1.95	0.40
1:A:368:LEU:HD12	1:A:423:ILE:CG2	2.51	0.40
1:A:29:LEU:N	1:A:29:LEU:HD23	2.36	0.40
1:A:440:ALA:C	1:A:443:TRP:HB3	2.41	0.40
1:A:91:GLY:HA2	1:A:229:PRO:HG3	2.04	0.40
2:B:21:SER:C	2:B:22:TRP:HD1	2.25	0.40
1:A:174:PHE:C	1:A:176:ALA:N	2.69	0.40
1:A:254:ILE:CB	1:A:394:LYS:HZ1	2.31	0.40
1:A:400:HIS:CE1	1:A:401:ALA:HB2	2.56	0.40
1:A:19:LEU:HD22	1:A:323:ILE:HG22	2.04	0.40
1:A:397:MET:O	1:A:398:PHE:C	2.59	0.40
2:B:29:VAL:O	2:B:30:VAL:CB	2.70	0.40
2:B:30:VAL:CG1	2:B:30:VAL:O	2.69	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	457/459 (100%)	252 (55%)	116 (25%)	89 (20%)	<b>0</b> <b>2</b>
2	B	89/99 (90%)	52 (58%)	19 (21%)	18 (20%)	<b>0</b> <b>1</b>
All	All	546/558 (98%)	304 (56%)	135 (25%)	107 (20%)	<b>0</b> <b>2</b>

All (107) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	10	PHE
1	A	41	ASP
1	A	80	MET
1	A	105	LEU
1	A	112	MET
1	A	119	ILE
1	A	133	GLU
1	A	139	TYR
1	A	164	ASN
1	A	165	ARG
1	A	194	MET
1	A	200	ALA
1	A	229	PRO
1	A	233	THR
1	A	238	LYS
1	A	277	GLU
1	A	278	ASP
1	A	297	PRO
1	A	298	GLN
1	A	353	TYR
1	A	361	SER
1	A	395	VAL
1	A	417	TYR
1	A	440	ALA
1	A	441	LEU
1	A	442	VAL
2	B	11	VAL
2	B	15	PRO
2	B	30	VAL
2	B	31	TYR
2	B	51	PRO
2	B	52	GLY
2	B	61	GLY
2	B	77	TYR
2	B	79	TRP
2	B	90	ARG
1	A	15	LYS
1	A	75	ALA
1	A	79	PRO
1	A	131	TYR
1	A	149	ALA
1	A	173	SER

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Mol	Chain	Res	Type
1	A	224	GLU
1	A	236	PHE
1	A	237	GLY
1	A	275	PHE
1	A	284	GLN
1	A	306	VAL
1	A	307	ARG
1	A	315	ARG
1	A	324	SER
1	A	348	PRO
1	A	354	ASN
1	A	376	ALA
1	A	378	PHE
1	A	386	ALA
1	A	405	TRP
1	A	445	LEU
2	B	38	GLU
2	B	64	PRO
1	A	17	ILE
1	A	40	VAL
1	A	58	LEU
1	A	64	ALA
1	A	67	TYR
1	A	121	PRO
1	A	130	ASP
1	A	182	PRO
1	A	232	LEU
1	A	242	ALA
1	A	244	PHE
1	A	261	GLU
1	A	404	PHE
2	B	5	PRO
2	B	9	GLU
2	B	44	PRO
1	A	127	THR
1	A	155	ALA
1	A	314	ARG
1	A	371	GLY
1	A	438	ALA
2	B	62	LEU
2	B	84	PRO
1	A	20	LEU

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Mol	Chain	Res	Type
1	A	88	GLY
1	A	104	GLY
1	A	175	ALA
1	A	193	GLY
1	A	260	LEU
1	A	365	THR
1	A	377	ASP
1	A	439	VAL
2	B	43	SER
1	A	47	GLY
1	A	73	ILE
1	A	259	PHE
1	A	274	PRO
1	A	347	SER
1	A	396	PRO
1	A	12	VAL
1	A	134	GLY
1	A	252	ALA
1	A	273	ALA
1	A	97	GLY
1	A	120	THR
1	A	72	GLY
1	A	243	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	353/353 (100%)	234 (66%)	119 (34%)	0	1
2	B	78/85 (92%)	52 (67%)	26 (33%)	0	2
All	All	431/438 (98%)	286 (66%)	145 (34%)	0	1

All (145) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	PHE
1	A	12	VAL
1	A	14	LEU
1	A	15	LYS
1	A	27	MET
1	A	39	PHE
1	A	52	ASP
1	A	56	VAL
1	A	58	LEU
1	A	61	SER
1	A	63	PHE
1	A	71	MET
1	A	80	MET
1	A	81	ILE
1	A	89	LYS
1	A	95	GLU
1	A	101	ILE
1	A	102	TRP
1	A	103	PHE
1	A	106	ILE
1	A	107	LEU
1	A	109	ILE
1	A	112	MET
1	A	113	ILE
1	A	116	TRP
1	A	119	ILE
1	A	123	ARG
1	A	124	ASN
1	A	126	LEU
1	A	127	THR
1	A	130	ASP
1	A	131	TYR
1	A	132	VAL
1	A	135	THR
1	A	136	MET
1	A	140	MET
1	A	141	LEU
1	A	147	MET
1	A	154	ARG
1	A	156	LEU
1	A	159	TYR
1	A	165	ARG
1	A	167	ARG

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Mol	Chain	Res	Type
1	A	177	PHE
1	A	178	VAL
1	A	179	LEU
1	A	180	ASN
1	A	183	LEU
1	A	184	ASN
1	A	197	LEU
1	A	204	VAL
1	A	207	MET
1	A	210	PHE
1	A	212	PHE
1	A	213	SER
1	A	217	LEU
1	A	218	TRP
1	A	224	GLU
1	A	225	LYS
1	A	228	ARG
1	A	232	LEU
1	A	235	LYS
1	A	236	PHE
1	A	240	ASP
1	A	248	TRP
1	A	257	SER
1	A	259	PHE
1	A	261	GLU
1	A	275	PHE
1	A	284	GLN
1	A	287	ILE
1	A	288	SER
1	A	289	LEU
1	A	294	TYR
1	A	295	MET
1	A	296	ILE
1	A	298	GLN
1	A	300	VAL
1	A	302	SER
1	A	307	ARG
1	A	310	PHE
1	A	311	SER
1	A	312	LEU
1	A	315	ARG
1	A	321	ARG

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Mol	Chain	Res	Type
1	A	326	VAL
1	A	328	LEU
1	A	329	VAL
1	A	332	TRP
1	A	334	LEU
1	A	338	THR
1	A	339	VAL
1	A	340	LEU
1	A	347	SER
1	A	353	TYR
1	A	362	ILE
1	A	368	LEU
1	A	374	GLN
1	A	377	ASP
1	A	379	THR
1	A	382	ILE
1	A	384	SER
1	A	387	LEU
1	A	388	ARG
1	A	394	LYS
1	A	397	MET
1	A	407	CYS
1	A	413	TYR
1	A	428	THR
1	A	435	THR
1	A	436	ILE
1	A	441	LEU
1	A	446	GLU
1	A	447	LYS
1	A	451	GLU
1	A	452	LEU
1	A	457	LYS
1	A	460	SER
1	A	463	LEU
2	B	2	SER
2	B	3	SER
2	B	4	VAL
2	B	6	THR
2	B	10	VAL
2	B	18	LEU
2	B	19	LEU
2	B	20	ILE

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Mol	Chain	Res	Type
2	B	25	ARG
2	B	28	TYR
2	B	31	TYR
2	B	34	ILE
2	B	36	TYR
2	B	38	GLU
2	B	39	THR
2	B	45	VAL
2	B	46	GLN
2	B	48	PHE
2	B	50	VAL
2	B	53	SER
2	B	56	THR
2	B	70	ILE
2	B	71	THR
2	B	75	ARG
2	B	83	SER
2	B	90	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	31	GLN
1	A	138	GLN
1	A	153	HIS
1	A	180	ASN
2	B	42	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

1 ligand 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	$\# Z  > 2$
3	P4P	A	501	-	28,28,28	0.86	1 (3%)	38,38,38	1.55	5 (13%)

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	P4P	A	501	-	-	0/24/24/24	0/4/4/4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	501	P4P	P-C1C	-2.30	1.75	1.79

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	501	P4P	C1B-P-C1A	5.62	120.68	109.43
3	A	501	P4P	C1C-P-C1A	-4.11	101.21	109.43
3	A	501	P4P	C1D-P-C1C	3.37	116.17	109.43
3	A	501	P4P	C1D-P-C1A	-3.08	103.25	109.43
3	A	501	P4P	C1B-P-C1C	-2.17	105.09	109.43

There are no chirality outliers.

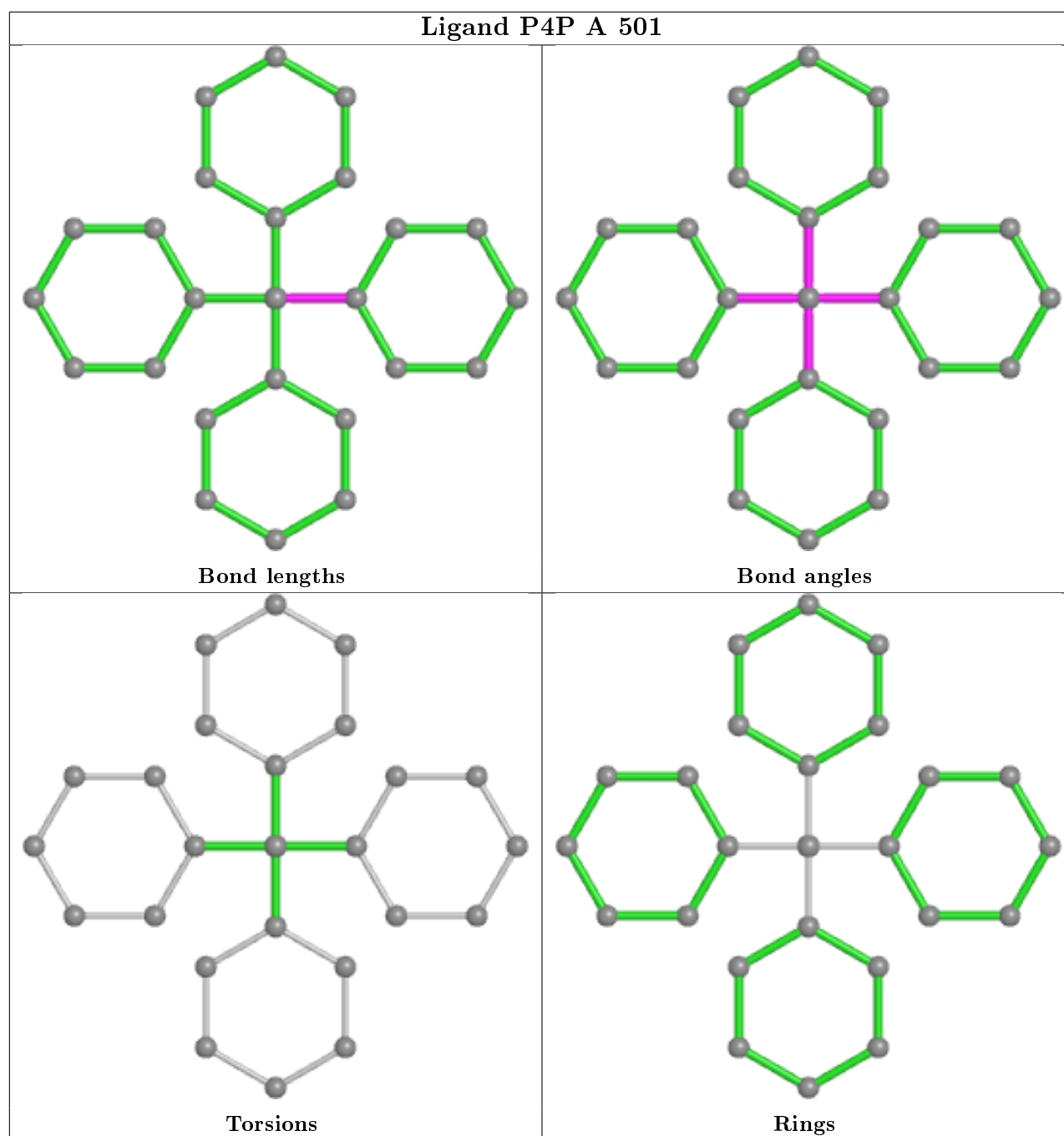
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	501	P4P	9	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	459/459 (100%)	-0.31	14 (3%)	49	33	74, 190, 316, 361	0
2	B	91/99 (91%)	-0.03	6 (6%)	18	10	87, 166, 235, 256	0
All	All	550/558 (98%)	-0.27	20 (3%)	42	28	74, 186, 308, 361	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	2	SER	19.5
2	B	1	VAL	13.6
1	A	9	SER	6.7
1	A	457	LYS	3.8
1	A	421	MET	3.4
2	B	89	TYR	3.4
2	B	11	VAL	3.2
1	A	129	SER	2.8
1	A	378	PHE	2.7
1	A	6	ASP	2.6
1	A	278	ASP	2.6
1	A	456	HIS	2.6
1	A	349	LEU	2.5
2	B	9	GLU	2.4
1	A	273	ALA	2.3
1	A	279	TYR	2.2
1	A	272	ILE	2.2
1	A	127	THR	2.2
1	A	130	ASP	2.1
2	B	77	TYR	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.

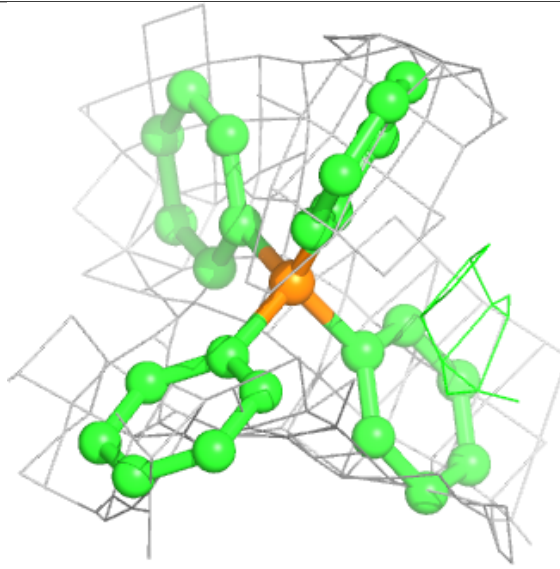
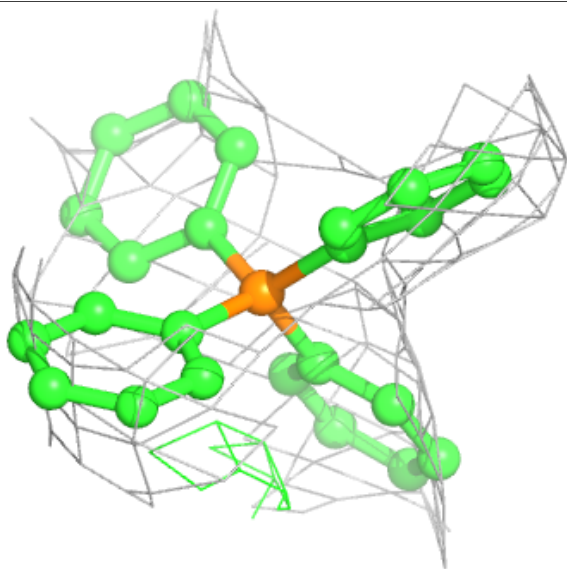
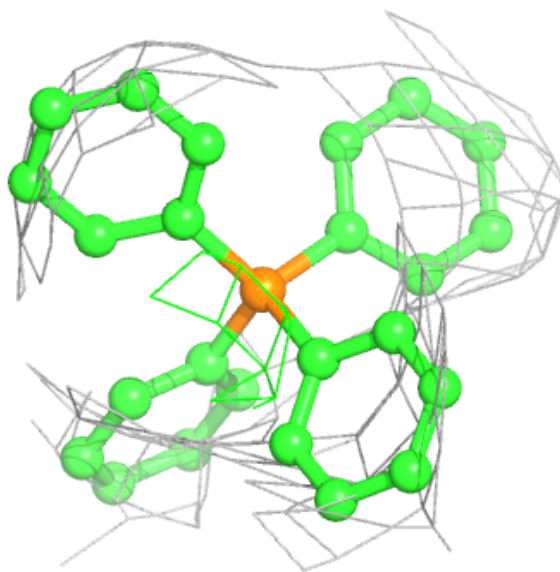
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	P4P	A	501	25/25	0.83	0.34	233,268,303,323	0

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 P4P A 501:**

$2mF_o-DF_c$  (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.