



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 25, 2020 – 02:45 PM BST

PDB ID : 2ZFK  
Title : Crystal Structure of the Kif1A Motor Domain during Mg release: Mg-releasing Transition-2  
Authors : Nitta, R.; Okada, Y.; Hirokawa, N.  
Deposited on : 2008-01-08  
Resolution : 3.61 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 : 2.13  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.13

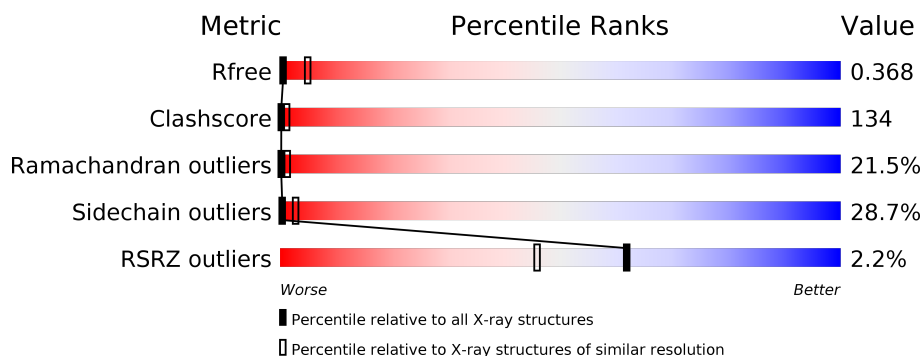
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.61 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	1290 (3.74-3.50)
Clashscore	141614	1387 (3.74-3.50)
Ramachandran outliers	138981	1339 (3.74-3.50)
Sidechain outliers	138945	1339 (3.74-3.50)
RSRZ outliers	127900	1191 (3.74-3.50)

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	366	<div> <div>2%</div> <div>8%</div> <div>49%</div> <div>27%</div> <div>•</div> <div>12%</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	TRS	A	2003	-	-	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 2504 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 Kinesin-like protein KIF1A, Kinesin heavy chain isoform 5C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	321	2433	1518	417	486	12	0	0	0

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	362	HIS	-	EXPRESSION TAG	UNP P28738
A	363	HIS	-	EXPRESSION TAG	UNP P28738
A	364	HIS	-	EXPRESSION TAG	UNP P28738
A	365	HIS	-	EXPRESSION TAG	UNP P28738
A	366	HIS	-	EXPRESSION TAG	UNP P28738

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

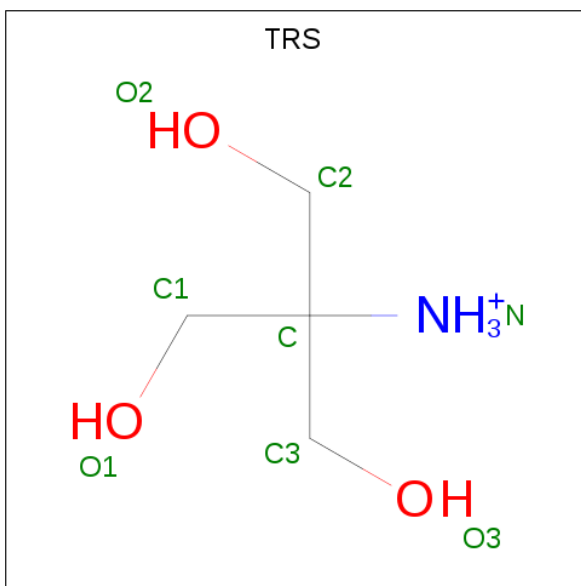
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: C<sub>10</sub>H<sub>15</sub>N<sub>5</sub>O<sub>10</sub>P<sub>2</sub>).



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

- Molecule 4 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula:  $\text{C}_4\text{H}_{12}\text{NO}_3$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total 8	C 4	N 1	O 3	0	0
4	A	1	Total 8	C 4	N 1	O 3	0	0

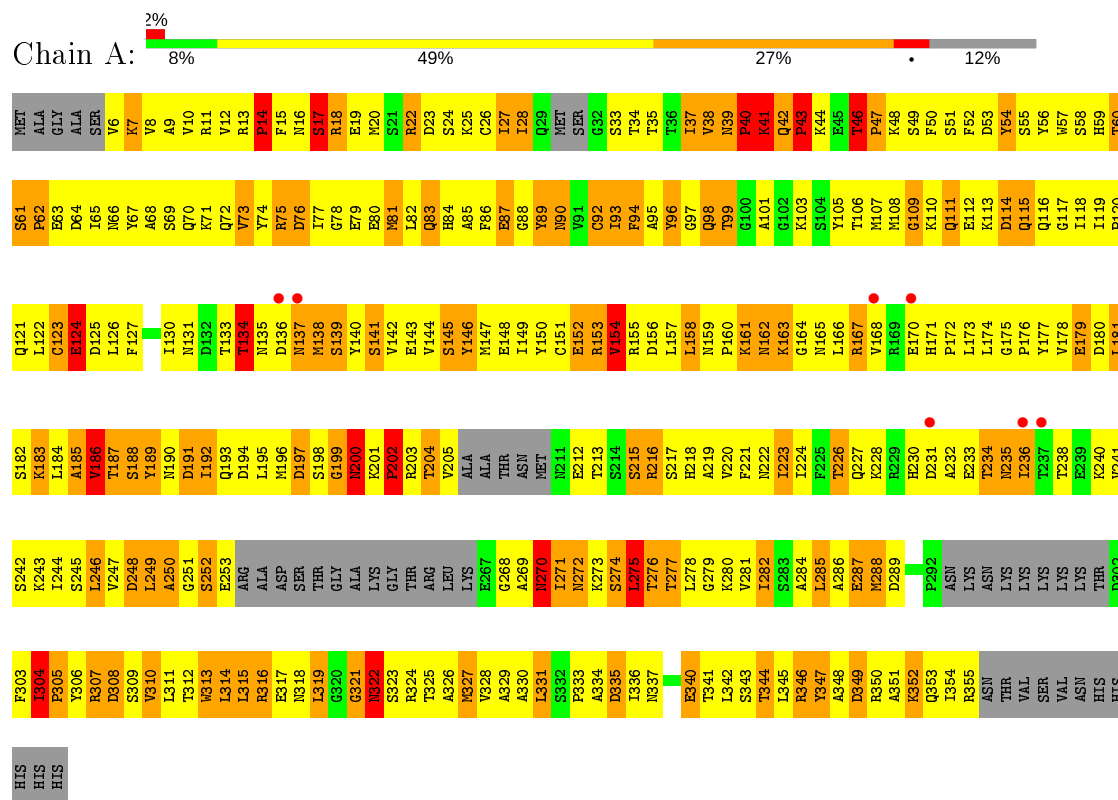
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	27	Total	O	0	0
			27	27		

### 3 Residue-property plots

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

- Molecule 1: Kinesin-like protein KIF1A, Kinesin heavy chain isoform 5C



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	39.48 Å 50.16 Å 157.06 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	14.99 – 3.61 47.78 – 3.61	Depositor EDS
% Data completeness (in resolution range)	69.5 (14.99-3.61) 70.0 (47.78-3.61)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.35 (at 3.57 Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.292 , 0.349 0.285 , 0.368	Depositor DCC
$R_{free}$ test set	315 reflections (9.82%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	73.7	Xtriage
Anisotropy	1.010	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.22 , 104.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.84	EDS
Total number of atoms	2504	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.30% 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: TRS, MG, ADP

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.52	0/2470	0.77	2/3346 (0.1%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	43	PRO	N-CA-CB	6.58	111.20	103.30
1	A	202	PRO	N-CA-CB	5.48	109.88	103.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2433	0	2304	646	0
2	A	1	0	0	0	0
3	A	27	0	12	0	0
4	A	16	0	24	0	0
5	A	27	0	0	8	0
All	All	2504	0	2340	646	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 134.



All (646) 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:93:ILE:HB	1:A:246:LEU:HD12	1.25	1.18
1:A:90:ASN:N	1:A:90:ASN:HD22	1.38	1.11
1:A:38:VAL:HG13	1:A:40:PRO:HD2	1.31	1.11
1:A:37:ILE:HG21	1:A:345:LEU:HD21	1.30	1.09
1:A:275:LEU:HD22	1:A:275:LEU:H	1.11	1.07
1:A:37:ILE:HG21	1:A:345:LEU:CD2	1.85	1.05
1:A:28:ILE:HD12	1:A:28:ILE:H	1.20	1.04
1:A:145:SER:HA	1:A:158:LEU:HD21	1.38	1.04
1:A:192:ILE:HA	1:A:195:LEU:HD13	1.36	1.03
1:A:47:PRO:HG3	1:A:342:LEU:HD21	1.37	1.03
1:A:203:ARG:NH2	1:A:219:ALA:HB2	1.74	1.01
1:A:203:ARG:HH22	1:A:219:ALA:HB2	1.19	1.01
1:A:7:LYS:HA	1:A:326:ALA:HA	1.41	1.00
1:A:101:ALA:HB1	1:A:330:ALA:O	1.61	1.00
1:A:223:ILE:HD13	1:A:224:ILE:N	1.77	0.99
1:A:205:VAL:HG21	1:A:213:THR:HG22	1.01	0.98
1:A:28:ILE:HD11	1:A:333:PRO:HA	1.46	0.97
1:A:334:ALA:HB1	1:A:336:ILE:HG12	1.45	0.97
1:A:37:ILE:H	1:A:37:ILE:HD12	1.24	0.97
1:A:133:THR:CG2	1:A:134:THR:H	1.78	0.96
1:A:200:ASN:H	1:A:200:ASN:ND2	1.63	0.96
1:A:92:CYS:HB2	1:A:325:THR:HG23	1.47	0.95
1:A:162:ASN:O	1:A:163:LYS:HB2	1.64	0.95
1:A:205:VAL:CG2	1:A:213:THR:HG22	1.94	0.95
1:A:304:ILE:HB	1:A:306:TYR:CE1	2.02	0.94
1:A:28:ILE:CD1	1:A:333:PRO:HA	1.95	0.94
1:A:226:THR:HG22	1:A:241:VAL:HG22	1.49	0.94
1:A:127:PHE:CZ	1:A:188:SER:HA	2.04	0.93
1:A:287:GLU:H	1:A:288:MET:HE3	1.33	0.93
1:A:200:ASN:H	1:A:200:ASN:HD22	1.17	0.92
1:A:60:THR:HG22	1:A:61:SER:H	1.34	0.92
1:A:144:VAL:HG11	1:A:192:ILE:HD11	1.49	0.92
1:A:60:THR:HG22	1:A:61:SER:N	1.85	0.92
1:A:354:ILE:HG12	1:A:355:ARG:H	1.34	0.92
1:A:96:TYR:CD1	1:A:97:GLY:N	2.37	0.92
1:A:54:TYR:HD2	1:A:56:TYR:HH	1.01	0.91
1:A:94:PHE:HB2	1:A:327:MET:SD	2.10	0.91
1:A:90:ASN:H	1:A:90:ASN:ND2	1.55	0.91
1:A:6:VAL:O	1:A:7:LYS:HB2	1.71	0.90
1:A:137:ASN:HB2	1:A:230:HIS:HB2	1.51	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:37:ILE:HD11	1:A:48:LYS:O	1.72	0.89
1:A:6:VAL:HG12	1:A:7:LYS:H	1.35	0.89
1:A:93:ILE:HB	1:A:246:LEU:CD1	2.02	0.89
1:A:278:LEU:O	1:A:281:VAL:HG12	1.73	0.89
1:A:253:GLU:HA	5:A:2028:HOH:O	1.72	0.88
1:A:282:ILE:HA	1:A:285:LEU:HD22	1.54	0.88
1:A:37:ILE:HG12	1:A:47:PRO:HG2	1.53	0.88
1:A:223:ILE:HG22	1:A:244:ILE:HB	1.54	0.88
1:A:342:LEU:HA	1:A:345:LEU:HD13	1.56	0.87
1:A:133:THR:HG22	1:A:134:THR:N	1.90	0.87
1:A:90:ASN:H	1:A:90:ASN:HD22	0.92	0.87
1:A:321:GLY:HA2	1:A:355:ARG:HG2	1.55	0.87
1:A:275:LEU:CD2	1:A:275:LEU:H	1.88	0.86
1:A:96:TYR:HD1	1:A:97:GLY:N	1.73	0.86
1:A:148:GLU:HG3	1:A:203:ARG:HH21	1.37	0.86
1:A:133:THR:HG22	1:A:134:THR:H	1.40	0.85
1:A:143:GLU:HB2	1:A:224:ILE:HB	1.57	0.85
1:A:205:VAL:HG21	1:A:213:THR:CG2	1.98	0.85
1:A:61:SER:HB3	1:A:63:GLU:OE1	1.77	0.85
1:A:269:ALA:O	1:A:270:ASN:HB2	1.77	0.84
1:A:153:ARG:NH1	1:A:153:ARG:HA	1.93	0.84
1:A:352:LYS:HD3	1:A:352:LYS:O	1.78	0.84
1:A:184:LEU:HD13	1:A:185:ALA:O	1.78	0.83
1:A:275:LEU:N	1:A:275:LEU:HD22	1.92	0.83
1:A:70:GLN:NE2	1:A:114:ASP:HA	1.93	0.82
1:A:158:LEU:HD12	1:A:158:LEU:H	1.43	0.82
1:A:77:ILE:N	1:A:77:ILE:HD12	1.94	0.82
1:A:92:CYS:CB	1:A:325:THR:HG23	2.10	0.82
1:A:37:ILE:HD12	1:A:37:ILE:N	1.95	0.81
1:A:70:GLN:HG3	1:A:71:LYS:H	1.42	0.81
1:A:26:CYS:SG	1:A:28:ILE:HD12	2.20	0.81
1:A:53:ASP:C	1:A:54:TYR:HD1	1.84	0.81
1:A:171:HIS:CE1	1:A:174:LEU:HD23	2.15	0.81
1:A:146:TYR:H	1:A:158:LEU:HD11	1.44	0.80
1:A:223:ILE:HD13	1:A:224:ILE:H	1.42	0.80
1:A:12:VAL:HG22	1:A:331:LEU:HD12	1.62	0.80
1:A:27:ILE:N	1:A:27:ILE:HD13	1.95	0.80
1:A:133:THR:CG2	1:A:134:THR:N	2.43	0.80
1:A:282:ILE:HA	1:A:285:LEU:CD2	2.12	0.80
1:A:345:LEU:O	1:A:348:ALA:HB3	1.82	0.79
1:A:282:ILE:HD13	1:A:282:ILE:H	1.44	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:142:VAL:HG13	1:A:223:ILE:HD11	1.65	0.79
1:A:344:THR:O	1:A:348:ALA:HB2	1.83	0.79
1:A:303:PHE:O	1:A:304:ILE:HG12	1.82	0.79
1:A:9:ALA:CB	1:A:54:TYR:HB2	2.12	0.79
1:A:200:ASN:N	1:A:200:ASN:HD22	1.78	0.78
1:A:279:GLY:HA2	1:A:282:ILE:HD11	1.63	0.78
1:A:278:LEU:HD22	1:A:281:VAL:HG11	1.65	0.78
1:A:47:PRO:HG3	1:A:342:LEU:CD2	2.12	0.78
1:A:354:ILE:HG12	1:A:355:ARG:N	1.98	0.77
1:A:62:PRO:HG3	1:A:67:TYR:CZ	2.19	0.77
1:A:133:THR:O	1:A:134:THR:HG23	1.82	0.77
1:A:304:ILE:HB	1:A:306:TYR:HE1	1.49	0.77
1:A:101:ALA:O	1:A:330:ALA:HB1	1.84	0.77
1:A:26:CYS:CB	1:A:59:HIS:HE2	1.97	0.77
1:A:7:LYS:HG3	1:A:325:THR:O	1.85	0.77
1:A:137:ASN:CB	1:A:230:HIS:HB2	2.15	0.76
1:A:235:ASN:H	1:A:235:ASN:HD22	1.29	0.76
1:A:127:PHE:CE1	1:A:188:SER:HA	2.20	0.76
1:A:9:ALA:HB2	1:A:54:TYR:HB2	1.66	0.76
1:A:108:MET:HE1	1:A:196:MET:HB3	1.67	0.75
1:A:195:LEU:H	1:A:195:LEU:HD12	1.50	0.75
1:A:106:THR:HG21	1:A:328:VAL:HG11	1.68	0.75
1:A:105:TYR:HA	1:A:109:GLY:HA2	1.69	0.75
1:A:150:TYR:HE1	1:A:216:ARG:HB2	1.52	0.75
1:A:11:ARG:O	1:A:330:ALA:HA	1.87	0.74
1:A:161:LYS:N	1:A:161:LYS:HD2	2.01	0.74
1:A:37:ILE:CG2	1:A:345:LEU:HD21	2.13	0.74
1:A:39:ASN:H	1:A:40:PRO:HD2	1.49	0.74
1:A:282:ILE:O	1:A:285:LEU:HD23	1.88	0.74
1:A:163:LYS:HD2	1:A:164:GLY:H	1.53	0.74
1:A:90:ASN:OD1	1:A:243:LYS:HG2	1.88	0.74
1:A:69:SER:O	1:A:72:GLN:HB3	1.88	0.73
1:A:278:LEU:O	1:A:282:ILE:HD13	1.87	0.73
1:A:12:VAL:CG1	1:A:333:PRO:HG3	2.17	0.73
1:A:8:VAL:O	1:A:53:ASP:HB2	1.88	0.73
1:A:178:VAL:HB	1:A:181:LEU:CD2	2.19	0.73
1:A:285:LEU:HB2	1:A:354:ILE:HB	1.72	0.72
1:A:12:VAL:HG12	1:A:333:PRO:HG3	1.70	0.72
1:A:46:THR:OG1	1:A:47:PRO:HA	1.90	0.71
1:A:277:THR:HG23	1:A:309:SER:HB2	1.73	0.71
1:A:306:TYR:HA	1:A:309:SER:OG	1.90	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:135:ASN:ND2	1:A:137:ASN:OD1	2.23	0.71
1:A:37:ILE:HD13	1:A:37:ILE:O	1.89	0.71
1:A:94:PHE:HB3	1:A:249:LEU:CD2	2.20	0.71
1:A:70:GLN:HE21	1:A:114:ASP:HA	1.55	0.71
1:A:12:VAL:CG2	1:A:331:LEU:HD12	2.21	0.70
1:A:168:VAL:O	1:A:168:VAL:HG13	1.91	0.70
1:A:342:LEU:CA	1:A:345:LEU:HD13	2.21	0.70
1:A:188:SER:O	1:A:191:ASP:N	2.24	0.70
1:A:315:LEU:HD13	1:A:315:LEU:N	2.06	0.70
1:A:7:LYS:CA	1:A:326:ALA:HA	2.20	0.70
1:A:17:SER:HA	1:A:20:MET:HE3	1.72	0.70
1:A:315:LEU:HB2	1:A:318:ASN:OD1	1.91	0.70
1:A:122:LEU:CD1	1:A:246:LEU:HD21	2.21	0.70
1:A:110:LYS:O	1:A:116:GLN:NE2	2.25	0.70
1:A:194:ASP:HA	1:A:197:ASP:OD1	1.90	0.70
1:A:192:ILE:CA	1:A:195:LEU:HD13	2.17	0.70
1:A:318:ASN:HA	1:A:323:SER:CB	2.21	0.70
1:A:28:ILE:HD12	1:A:28:ILE:N	2.03	0.69
1:A:53:ASP:C	1:A:54:TYR:CD1	2.66	0.69
1:A:90:ASN:N	1:A:90:ASN:ND2	2.14	0.69
1:A:13:ARG:HH12	1:A:19:GLU:CD	1.95	0.69
1:A:151:CYS:C	1:A:152:GLU:HG2	2.13	0.69
1:A:185:ALA:O	1:A:186:VAL:HG13	1.93	0.69
1:A:268:GLY:HA3	5:A:2020:HOH:O	1.92	0.69
1:A:183:LYS:NZ	1:A:184:LEU:C	2.47	0.68
1:A:236:ILE:HG23	1:A:236:ILE:O	1.92	0.68
1:A:145:SER:CA	1:A:158:LEU:HD21	2.20	0.68
1:A:317:GLU:O	1:A:321:GLY:O	2.12	0.68
1:A:181:LEU:N	1:A:181:LEU:HD22	2.09	0.68
1:A:178:VAL:HB	1:A:181:LEU:HD21	1.75	0.68
1:A:140:TYR:CD1	1:A:227:GLN:HA	2.29	0.67
1:A:178:VAL:CG1	1:A:181:LEU:HD21	2.23	0.67
1:A:117:GLY:O	1:A:121:GLN:HG3	1.94	0.67
1:A:121:GLN:HA	1:A:124:GLU:OE1	1.95	0.67
1:A:160:PRO:HB2	1:A:161:LYS:HE3	1.76	0.67
1:A:192:ILE:HD13	1:A:195:LEU:HD22	1.74	0.67
1:A:287:GLU:H	1:A:288:MET:CE	2.08	0.67
1:A:313:TRP:O	1:A:315:LEU:N	2.27	0.67
1:A:139:SER:HB3	1:A:228:LYS:HD2	1.77	0.66
1:A:251:GLY:O	1:A:252:SER:O	2.13	0.66
1:A:123:CYS:O	1:A:126:LEU:N	2.29	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:116:GLN:HA	1:A:116:GLN:NE2	2.11	0.66
1:A:57:TRP:HE3	1:A:57:TRP:O	1.79	0.66
1:A:70:GLN:HG3	1:A:71:LYS:N	2.10	0.66
1:A:312:THR:O	1:A:315:LEU:HD22	1.96	0.66
1:A:28:ILE:HD13	1:A:333:PRO:HA	1.76	0.66
1:A:92:CYS:SG	1:A:94:PHE:HE1	2.18	0.66
1:A:114:ASP:O	1:A:115:GLN:HB2	1.94	0.66
1:A:178:VAL:CB	1:A:181:LEU:HD21	2.26	0.65
1:A:88:GLY:O	1:A:89:TYR:O	2.14	0.65
1:A:6:VAL:HG12	1:A:7:LYS:N	2.11	0.65
1:A:13:ARG:O	1:A:333:PRO:HG2	1.96	0.65
1:A:312:THR:HA	1:A:315:LEU:CD2	2.27	0.65
1:A:39:ASN:H	1:A:40:PRO:CD	2.09	0.65
1:A:178:VAL:HG12	1:A:181:LEU:HD21	1.77	0.65
1:A:92:CYS:O	1:A:93:ILE:HG12	1.97	0.65
1:A:235:ASN:N	1:A:235:ASN:HD22	1.93	0.64
1:A:234:THR:HG23	1:A:234:THR:O	1.96	0.64
1:A:93:ILE:CB	1:A:246:LEU:HD12	2.16	0.64
1:A:277:THR:HG23	1:A:309:SER:CB	2.28	0.64
1:A:307:ARG:C	1:A:309:SER:H	2.00	0.64
1:A:354:ILE:HG12	1:A:355:ARG:CD	2.27	0.64
1:A:150:TYR:O	1:A:153:ARG:HB3	1.98	0.64
1:A:321:GLY:HA2	1:A:355:ARG:CG	2.28	0.64
1:A:38:VAL:HG13	1:A:39:ASN:N	2.12	0.64
1:A:17:SER:HA	1:A:20:MET:CE	2.28	0.64
1:A:247:VAL:HG12	1:A:248:ASP:N	2.12	0.64
1:A:346:ARG:C	1:A:348:ALA:H	2.02	0.64
1:A:7:LYS:O	1:A:327:MET:N	2.29	0.63
1:A:143:GLU:HA	1:A:183:LYS:HZ2	1.63	0.63
1:A:57:TRP:HH2	1:A:60:THR:CB	2.11	0.63
1:A:61:SER:C	1:A:63:GLU:H	2.00	0.63
1:A:183:LYS:HE2	1:A:184:LEU:N	2.12	0.63
1:A:306:TYR:HB2	1:A:312:THR:OG1	1.98	0.63
1:A:61:SER:O	1:A:63:GLU:N	2.29	0.63
1:A:145:SER:OG	1:A:182:SER:O	2.16	0.63
1:A:315:LEU:HD23	1:A:319:LEU:HG	1.81	0.63
1:A:46:THR:HA	1:A:47:PRO:O	1.97	0.63
1:A:183:LYS:HZ3	1:A:184:LEU:C	2.02	0.63
1:A:277:THR:HG22	1:A:278:LEU:N	2.12	0.63
1:A:340:GLU:O	1:A:343:SER:HB3	1.99	0.63
1:A:68:ALA:HA	1:A:72:GLN:OE1	1.99	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:342:LEU:HD13	1:A:342:LEU:O	1.99	0.62
1:A:41:LYS:HE3	5:A:2006:HOH:O	1.98	0.62
1:A:35:THR:O	1:A:49:SER:HA	1.99	0.62
1:A:7:LYS:HA	1:A:326:ALA:CA	2.25	0.62
1:A:192:ILE:HA	1:A:195:LEU:CD1	2.22	0.62
1:A:19:GLU:HG2	1:A:334:ALA:HB2	1.81	0.62
1:A:156:ASP:OD2	1:A:158:LEU:HD13	1.99	0.62
1:A:77:ILE:CD1	1:A:77:ILE:N	2.60	0.62
1:A:98:GLN:O	1:A:99:THR:C	2.36	0.62
1:A:112:GLU:HG2	1:A:113:LYS:N	2.14	0.62
1:A:200:ASN:O	1:A:203:ARG:HG3	2.00	0.62
1:A:218:HIS:CB	1:A:249:LEU:HA	2.30	0.62
1:A:144:VAL:HG22	1:A:145:SER:N	2.14	0.61
1:A:148:GLU:HG3	1:A:203:ARG:NH2	2.13	0.61
1:A:26:CYS:SG	1:A:28:ILE:CD1	2.88	0.61
1:A:39:ASN:N	1:A:40:PRO:HD2	2.15	0.61
1:A:213:THR:C	1:A:215:SER:H	2.02	0.61
1:A:10:VAL:HG21	1:A:35:THR:HG21	1.83	0.61
1:A:354:ILE:HG12	1:A:355:ARG:HD3	1.82	0.61
1:A:112:GLU:O	1:A:116:GLN:OE1	2.18	0.61
1:A:312:THR:HA	1:A:315:LEU:HD21	1.82	0.61
1:A:52:PHE:HE1	1:A:349:ASP:CB	2.13	0.61
1:A:57:TRP:HH2	1:A:60:THR:OG1	1.83	0.61
1:A:127:PHE:CD2	1:A:189:TYR:HB2	2.36	0.61
1:A:38:VAL:CG1	1:A:39:ASN:N	2.63	0.61
1:A:149:ILE:HG23	1:A:149:ILE:O	2.00	0.60
1:A:135:ASN:OD1	1:A:137:ASN:ND2	2.34	0.60
1:A:27:ILE:HD12	1:A:335:ASP:HA	1.83	0.60
1:A:188:SER:O	1:A:189:TYR:C	2.40	0.60
1:A:189:TYR:O	1:A:192:ILE:HG22	2.01	0.60
1:A:277:THR:OG1	1:A:309:SER:HA	2.01	0.60
1:A:37:ILE:N	1:A:37:ILE:CD1	2.63	0.60
1:A:316:ARG:NH1	1:A:317:GLU:HG3	2.17	0.60
1:A:192:ILE:CD1	1:A:195:LEU:HD22	2.32	0.60
1:A:52:PHE:HE1	1:A:349:ASP:CA	2.15	0.60
1:A:52:PHE:HE1	1:A:349:ASP:HB2	1.64	0.60
1:A:205:VAL:HG11	1:A:213:THR:HG23	1.84	0.59
1:A:37:ILE:CD1	1:A:48:LYS:O	2.47	0.59
1:A:287:GLU:C	1:A:288:MET:HE2	2.23	0.59
1:A:26:CYS:HB2	1:A:59:HIS:HE2	1.64	0.59
1:A:143:GLU:O	1:A:224:ILE:N	2.31	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:273:LYS:O	1:A:274:SER:C	2.41	0.59
1:A:341:THR:O	1:A:344:THR:N	2.36	0.59
1:A:37:ILE:CG1	1:A:47:PRO:HG2	2.29	0.59
1:A:215:SER:C	1:A:217:SER:H	2.06	0.59
1:A:57:TRP:HH2	1:A:60:THR:HG1	1.49	0.59
1:A:143:GLU:HA	1:A:183:LYS:NZ	2.18	0.59
1:A:110:LYS:N	1:A:115:GLN:O	2.28	0.59
1:A:279:GLY:CA	1:A:282:ILE:HD11	2.31	0.59
1:A:201:LYS:HE3	1:A:201:LYS:HA	1.84	0.58
1:A:285:LEU:HD12	1:A:354:ILE:HG21	1.86	0.58
1:A:122:LEU:HD13	1:A:246:LEU:HD21	1.84	0.58
1:A:133:THR:HG23	1:A:134:THR:H	1.62	0.58
1:A:146:TYR:N	1:A:158:LEU:HD11	2.15	0.58
1:A:276:THR:O	1:A:277:THR:C	2.42	0.58
1:A:285:LEU:HB2	1:A:354:ILE:CB	2.34	0.58
1:A:60:THR:CG2	1:A:61:SER:N	2.56	0.58
1:A:106:THR:HG22	1:A:106:THR:O	2.02	0.58
1:A:119:ILE:HB	1:A:120:PRO:CD	2.34	0.58
1:A:250:ALA:HB3	1:A:275:LEU:HD11	1.85	0.58
1:A:57:TRP:CH2	1:A:60:THR:OG1	2.56	0.58
1:A:138:MET:O	1:A:228:LYS:O	2.22	0.58
1:A:153:ARG:CZ	1:A:153:ARG:HA	2.34	0.58
1:A:274:SER:HB2	1:A:275:LEU:HD22	1.85	0.58
1:A:27:ILE:HD12	1:A:335:ASP:CA	2.34	0.58
1:A:94:PHE:CB	1:A:327:MET:SD	2.89	0.58
1:A:186:VAL:O	1:A:187:THR:O	2.22	0.57
1:A:278:LEU:O	1:A:282:ILE:CD1	2.51	0.57
1:A:342:LEU:HD22	1:A:345:LEU:HD22	1.85	0.57
1:A:234:THR:CG2	1:A:234:THR:O	2.51	0.57
1:A:304:ILE:HG13	1:A:306:TYR:CZ	2.40	0.57
1:A:241:VAL:HG12	1:A:242:SER:N	2.20	0.57
1:A:10:VAL:HG22	1:A:55:SER:HA	1.86	0.57
1:A:197:ASP:O	1:A:198:SER:C	2.43	0.57
1:A:6:VAL:O	1:A:7:LYS:CB	2.50	0.57
1:A:123:CYS:O	1:A:126:LEU:HB3	2.05	0.57
1:A:22:ARG:HH11	1:A:22:ARG:HB2	1.69	0.57
1:A:146:TYR:HE2	1:A:200:ASN:ND2	2.03	0.57
1:A:346:ARG:O	1:A:349:ASP:N	2.37	0.57
1:A:172:PRO:HB2	1:A:173:LEU:HD22	1.87	0.56
1:A:192:ILE:CG2	1:A:193:GLN:N	2.68	0.56
1:A:59:HIS:CE1	1:A:333:PRO:HB3	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:315:LEU:CB	1:A:318:ASN:HD21	2.19	0.56
1:A:26:CYS:HA	1:A:333:PRO:O	2.05	0.56
1:A:205:VAL:HG11	1:A:213:THR:CG2	2.35	0.56
1:A:34:THR:OG1	1:A:49:SER:HB3	2.05	0.56
1:A:233:GLU:O	1:A:234:THR:HG22	2.06	0.56
1:A:179:GLU:O	1:A:181:LEU:HD22	2.06	0.56
1:A:27:ILE:H	1:A:27:ILE:HD13	1.69	0.56
1:A:278:LEU:O	1:A:281:VAL:CG1	2.51	0.56
1:A:158:LEU:HD12	1:A:158:LEU:N	2.15	0.56
1:A:94:PHE:HB3	1:A:249:LEU:HD23	1.88	0.56
1:A:187:THR:HG23	1:A:187:THR:O	2.05	0.56
1:A:191:ASP:O	1:A:195:LEU:HD12	2.06	0.56
1:A:220:VAL:HG22	1:A:247:VAL:HG22	1.87	0.56
1:A:42:GLN:O	1:A:43:PRO:CB	2.54	0.56
1:A:277:THR:HG21	1:A:311:LEU:H	1.70	0.55
1:A:52:PHE:CE1	1:A:349:ASP:HB2	2.39	0.55
1:A:83:GLN:HA	1:A:83:GLN:HE21	1.71	0.55
1:A:316:ARG:HH11	1:A:317:GLU:HG3	1.71	0.55
1:A:307:ARG:C	1:A:309:SER:N	2.58	0.55
1:A:171:HIS:CE1	1:A:174:LEU:H	2.24	0.55
1:A:201:LYS:O	1:A:203:ARG:N	2.40	0.55
1:A:354:ILE:HG13	1:A:355:ARG:HH11	1.71	0.55
1:A:140:TYR:CE1	1:A:227:GLN:HG2	2.41	0.55
1:A:352:LYS:CD	1:A:352:LYS:O	2.54	0.55
1:A:96:TYR:CD1	1:A:96:TYR:C	2.80	0.55
1:A:153:ARG:HH11	1:A:154:VAL:H	1.54	0.55
1:A:171:HIS:CE1	1:A:173:LEU:H	2.24	0.55
1:A:355:ARG:HD2	1:A:355:ARG:H	1.72	0.55
1:A:54:TYR:CD1	1:A:54:TYR:N	2.74	0.55
1:A:145:SER:HA	1:A:158:LEU:CD2	2.27	0.55
1:A:181:LEU:N	1:A:181:LEU:CD2	2.70	0.55
1:A:278:LEU:HD22	1:A:281:VAL:CG1	2.35	0.55
1:A:306:TYR:CA	1:A:309:SER:OG	2.55	0.55
1:A:156:ASP:OD2	1:A:158:LEU:HB2	2.07	0.55
1:A:316:ARG:HD2	1:A:317:GLU:N	2.22	0.55
1:A:146:TYR:H	1:A:158:LEU:CD1	2.17	0.54
1:A:54:TYR:N	1:A:54:TYR:HD1	2.05	0.54
1:A:173:LEU:N	1:A:173:LEU:HD22	2.22	0.54
1:A:38:VAL:HG13	1:A:39:ASN:H	1.70	0.54
1:A:94:PHE:N	1:A:94:PHE:HD1	2.05	0.54
1:A:98:GLN:HA	1:A:252:SER:N	2.23	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:13:ARG:O	1:A:14:PRO:C	2.45	0.54
1:A:171:HIS:ND1	1:A:173:LEU:N	2.49	0.54
1:A:201:LYS:C	1:A:203:ARG:H	2.09	0.54
1:A:236:ILE:O	1:A:236:ILE:CG2	2.56	0.54
1:A:308:ASP:OD2	1:A:308:ASP:N	2.28	0.54
1:A:98:GLN:OE1	1:A:337:ASN:OD1	2.24	0.54
1:A:75:ARG:HA	1:A:79:GLU:HB2	1.90	0.54
1:A:199:GLY:O	1:A:202:PRO:N	2.40	0.54
1:A:271:ILE:O	1:A:272:ASN:ND2	2.40	0.54
1:A:342:LEU:HD13	1:A:342:LEU:C	2.27	0.54
1:A:191:ASP:O	1:A:195:LEU:CD1	2.55	0.53
1:A:22:ARG:O	1:A:24:SER:N	2.41	0.53
1:A:227:GLN:HB2	1:A:240:LYS:O	2.08	0.53
1:A:276:THR:O	1:A:279:GLY:N	2.42	0.53
1:A:315:LEU:CA	1:A:318:ASN:HD21	2.20	0.53
1:A:303:PHE:C	1:A:304:ILE:HG12	2.28	0.53
1:A:183:LYS:CE	1:A:184:LEU:N	2.72	0.53
1:A:185:ALA:C	1:A:186:VAL:HG22	2.28	0.53
1:A:271:ILE:O	1:A:272:ASN:HB2	2.08	0.53
1:A:277:THR:HG23	1:A:309:SER:CA	2.39	0.53
1:A:167:ARG:HG3	1:A:168:VAL:N	2.22	0.53
1:A:27:ILE:HD11	1:A:334:ALA:C	2.29	0.53
1:A:192:ILE:HD13	1:A:195:LEU:HD13	1.91	0.53
1:A:213:THR:C	1:A:215:SER:N	2.62	0.53
1:A:151:CYS:O	1:A:152:GLU:HG2	2.08	0.53
1:A:183:LYS:HZ3	1:A:185:ALA:N	2.07	0.52
1:A:15:PHE:CZ	1:A:333:PRO:HB2	2.44	0.52
1:A:227:GLN:HB2	1:A:240:LYS:HB3	1.92	0.52
1:A:284:ALA:C	1:A:286:ALA:N	2.62	0.52
1:A:345:LEU:HD12	1:A:345:LEU:H	1.74	0.52
1:A:247:VAL:CG1	1:A:248:ASP:N	2.72	0.52
1:A:17:SER:O	1:A:18:ARG:C	2.48	0.52
1:A:271:ILE:O	1:A:272:ASN:CB	2.57	0.52
1:A:158:LEU:CD1	1:A:158:LEU:H	2.18	0.52
1:A:163:LYS:HD2	1:A:164:GLY:N	2.22	0.52
1:A:103:LYS:O	1:A:107:MET:HG2	2.10	0.52
1:A:26:CYS:SG	1:A:28:ILE:O	2.68	0.52
1:A:346:ARG:O	1:A:348:ALA:N	2.42	0.52
1:A:57:TRP:HH2	1:A:60:THR:HB	1.75	0.52
1:A:63:GLU:CD	1:A:63:GLU:N	2.63	0.52
1:A:60:THR:HG21	1:A:64:ASP:HB2	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:119:ILE:N	1:A:120:PRO:HD2	2.24	0.52
1:A:226:THR:HG22	1:A:241:VAL:CG2	2.32	0.52
1:A:307:ARG:CG	1:A:307:ARG:HH11	2.21	0.52
1:A:110:LYS:HD2	1:A:115:GLN:OE1	2.10	0.52
1:A:126:LEU:C	1:A:126:LEU:HD13	2.30	0.52
1:A:15:PHE:CE1	1:A:333:PRO:HB2	2.45	0.52
1:A:52:PHE:CD1	1:A:52:PHE:N	2.77	0.52
1:A:219:ALA:HB3	1:A:248:ASP:OD2	2.10	0.51
1:A:171:HIS:NE2	1:A:174:LEU:HD23	2.24	0.51
1:A:116:GLN:CA	1:A:116:GLN:NE2	2.73	0.51
1:A:199:GLY:O	1:A:201:LYS:N	2.42	0.51
1:A:147:MET:CE	1:A:222:ASN:HD21	2.23	0.51
1:A:146:TYR:CE1	1:A:221:PHE:HB2	2.46	0.51
1:A:200:ASN:ND2	1:A:200:ASN:N	2.35	0.51
1:A:26:CYS:HG	1:A:59:HIS:HE2	1.57	0.51
1:A:140:TYR:HD1	1:A:227:GLN:HA	1.72	0.51
1:A:235:ASN:H	1:A:235:ASN:ND2	2.04	0.51
1:A:27:ILE:CD1	1:A:335:ASP:HA	2.41	0.51
1:A:354:ILE:HG12	1:A:355:ARG:HD2	1.92	0.51
1:A:94:PHE:CD1	1:A:94:PHE:N	2.77	0.51
1:A:28:ILE:N	1:A:28:ILE:CD1	2.71	0.51
1:A:281:VAL:O	1:A:284:ALA:HB3	2.11	0.51
1:A:231:ASP:O	1:A:232:ALA:HB3	2.11	0.51
1:A:285:LEU:CB	1:A:354:ILE:HB	2.41	0.50
1:A:334:ALA:CB	1:A:336:ILE:HG12	2.29	0.50
1:A:159:ASN:OD1	1:A:162:ASN:N	2.45	0.50
1:A:165:ASN:HA	1:A:179:GLU:HB3	1.93	0.50
1:A:34:THR:HG21	5:A:2007:HOH:O	2.10	0.50
1:A:108:MET:O	1:A:109:GLY:C	2.50	0.50
1:A:156:ASP:OD1	1:A:182:SER:CB	2.60	0.50
1:A:17:SER:O	1:A:19:GLU:N	2.44	0.50
1:A:201:LYS:C	1:A:203:ARG:N	2.65	0.50
1:A:123:CYS:O	1:A:124:GLU:C	2.49	0.50
1:A:183:LYS:C	1:A:183:LYS:HD3	2.32	0.50
1:A:46:THR:HG23	1:A:47:PRO:N	2.26	0.50
1:A:144:VAL:HG23	1:A:222:ASN:O	2.12	0.50
1:A:171:HIS:CG	1:A:174:LEU:HB2	2.46	0.50
1:A:242:SER:C	1:A:243:LYS:HD3	2.32	0.50
1:A:305:PRO:HB3	5:A:2029:HOH:O	2.12	0.50
1:A:6:VAL:CG1	1:A:7:LYS:H	2.16	0.50
1:A:13:ARG:O	1:A:333:PRO:CG	2.59	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:140:TYR:HA	1:A:226:THR:O	2.12	0.50
1:A:16:ASN:O	1:A:19:GLU:HB2	2.12	0.50
1:A:234:THR:O	1:A:235:ASN:C	2.50	0.50
1:A:277:THR:O	1:A:309:SER:HB3	2.12	0.50
1:A:188:SER:HB2	1:A:191:ASP:OD1	2.11	0.49
1:A:313:TRP:O	1:A:314:LEU:C	2.50	0.49
1:A:11:ARG:HG3	1:A:56:TYR:HB3	1.94	0.49
1:A:183:LYS:HZ1	1:A:184:LEU:C	2.15	0.49
1:A:46:THR:CB	1:A:47:PRO:HA	2.42	0.49
1:A:57:TRP:CE3	1:A:57:TRP:C	2.85	0.49
1:A:95:ALA:HB2	1:A:107:MET:CG	2.43	0.49
1:A:243:LYS:N	1:A:243:LYS:HD3	2.28	0.49
1:A:64:ASP:OD2	1:A:66:ASN:O	2.30	0.49
1:A:114:ASP:O	1:A:115:GLN:CB	2.61	0.49
1:A:12:VAL:HG12	1:A:333:PRO:CG	2.40	0.49
1:A:135:ASN:OD1	1:A:137:ASN:CG	2.51	0.49
1:A:148:GLU:O	1:A:154:VAL:HA	2.13	0.49
1:A:22:ARG:HG2	1:A:336:ILE:HG21	1.93	0.49
1:A:153:ARG:HH11	1:A:154:VAL:N	2.11	0.49
1:A:146:TYR:HE2	1:A:200:ASN:HD21	1.61	0.49
1:A:220:VAL:HG22	1:A:247:VAL:CG2	2.43	0.49
1:A:281:VAL:HB	1:A:312:THR:HG21	1.94	0.49
1:A:39:ASN:O	1:A:40:PRO:C	2.51	0.49
1:A:86:PHE:C	1:A:88:GLY:H	2.16	0.49
1:A:322:ASN:N	1:A:322:ASN:OD1	2.45	0.48
1:A:98:GLN:HA	1:A:252:SER:HB2	1.95	0.48
1:A:223:ILE:CG2	1:A:244:ILE:HB	2.34	0.48
1:A:282:ILE:O	1:A:285:LEU:CD2	2.60	0.48
1:A:153:ARG:HH11	1:A:153:ARG:HA	1.73	0.48
1:A:98:GLN:OE1	1:A:340:GLU:HB2	2.12	0.48
1:A:52:PHE:O	1:A:53:ASP:C	2.51	0.48
1:A:167:ARG:O	1:A:178:VAL:HG13	2.14	0.48
1:A:62:PRO:HG3	1:A:67:TYR:OH	2.12	0.48
1:A:124:GLU:HG2	1:A:125:ASP:N	2.28	0.48
1:A:345:LEU:CD1	1:A:345:LEU:H	2.26	0.48
1:A:354:ILE:CG1	1:A:355:ARG:HH11	2.26	0.48
1:A:85:ALA:HA	1:A:88:GLY:O	2.14	0.48
1:A:122:LEU:C	1:A:122:LEU:HD23	2.34	0.48
1:A:248:ASP:OD1	1:A:248:ASP:N	2.47	0.48
1:A:312:THR:O	1:A:313:TRP:C	2.52	0.48
1:A:9:ALA:HB1	1:A:54:TYR:HB2	1.93	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:304:ILE:HG13	1:A:306:TYR:OH	2.14	0.48
1:A:354:ILE:CG1	1:A:355:ARG:HD3	2.43	0.48
1:A:94:PHE:HB3	1:A:249:LEU:HD21	1.95	0.48
1:A:16:ASN:O	1:A:20:MET:HG3	2.14	0.47
1:A:270:ASN:ND2	5:A:2024:HOH:O	2.39	0.47
1:A:57:TRP:CE3	1:A:57:TRP:O	2.63	0.47
1:A:12:VAL:HG22	1:A:331:LEU:CD1	2.41	0.47
1:A:11:ARG:N	1:A:329:ALA:O	2.39	0.47
1:A:116:GLN:HA	1:A:116:GLN:HE21	1.78	0.47
1:A:144:VAL:HB	1:A:223:ILE:HG12	1.95	0.47
1:A:276:THR:O	1:A:280:LYS:HG3	2.15	0.47
1:A:28:ILE:H	1:A:28:ILE:CD1	1.94	0.47
1:A:56:TYR:CE2	1:A:73:VAL:HG23	2.49	0.47
1:A:105:TYR:OH	1:A:115:GLN:HG2	2.14	0.47
1:A:272:ASN:O	1:A:273:LYS:C	2.52	0.47
1:A:162:ASN:CG	1:A:163:LYS:H	2.18	0.47
1:A:304:ILE:CB	1:A:306:TYR:CE1	2.88	0.47
1:A:13:ARG:O	1:A:333:PRO:CD	2.63	0.47
1:A:278:LEU:HD13	1:A:278:LEU:O	2.14	0.47
1:A:94:PHE:N	1:A:327:MET:SD	2.84	0.47
1:A:99:THR:HG23	1:A:99:THR:O	2.15	0.47
1:A:84:HIS:CD2	1:A:84:HIS:H	2.33	0.46
1:A:281:VAL:HG13	1:A:282:ILE:N	2.30	0.46
1:A:287:GLU:HG3	1:A:287:GLU:O	2.15	0.46
1:A:46:THR:HG23	1:A:47:PRO:CA	2.45	0.46
1:A:144:VAL:CG2	1:A:145:SER:N	2.79	0.46
1:A:172:PRO:C	1:A:173:LEU:HD22	2.35	0.46
1:A:125:ASP:O	1:A:126:LEU:C	2.52	0.46
1:A:195:LEU:H	1:A:195:LEU:CD1	2.24	0.46
1:A:154:VAL:HG23	1:A:155:ARG:N	2.29	0.46
1:A:162:ASN:OD1	1:A:163:LYS:N	2.48	0.46
1:A:52:PHE:HD1	1:A:52:PHE:N	2.13	0.46
1:A:96:TYR:C	1:A:96:TYR:HD1	2.17	0.46
1:A:135:ASN:ND2	1:A:136:ASP:N	2.63	0.46
1:A:142:VAL:O	1:A:185:ALA:HA	2.15	0.46
1:A:148:GLU:HG2	1:A:217:SER:HB2	1.98	0.46
1:A:92:CYS:HA	1:A:245:SER:O	2.16	0.46
1:A:277:THR:CG2	1:A:278:LEU:N	2.78	0.46
1:A:350:ARG:O	1:A:352:LYS:N	2.48	0.46
1:A:26:CYS:SG	1:A:27:ILE:N	2.89	0.46
1:A:347:TYR:HA	1:A:350:ARG:CB	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:307:ARG:CG	1:A:307:ARG:NH1	2.74	0.46
1:A:12:VAL:O	1:A:58:SER:OG	2.30	0.46
1:A:148:GLU:HB2	1:A:157:LEU:HD21	1.97	0.46
1:A:95:ALA:HB2	1:A:107:MET:HG3	1.97	0.46
1:A:14:PRO:O	1:A:15:PHE:CG	2.69	0.45
1:A:183:LYS:HE2	1:A:184:LEU:H	1.79	0.45
1:A:90:ASN:CG	1:A:243:LYS:HG2	2.36	0.45
1:A:46:THR:HG23	1:A:47:PRO:HA	1.99	0.45
1:A:52:PHE:HE1	1:A:349:ASP:HA	1.80	0.45
1:A:146:TYR:O	1:A:158:LEU:HD12	2.17	0.45
1:A:196:MET:O	1:A:197:ASP:C	2.54	0.45
1:A:18:ARG:O	1:A:22:ARG:HB2	2.17	0.45
1:A:81:MET:CE	1:A:325:THR:HA	2.45	0.45
1:A:113:LYS:O	1:A:114:ASP:HB3	2.17	0.45
1:A:149:ILE:O	1:A:149:ILE:CG2	2.63	0.45
1:A:10:VAL:HG11	1:A:52:PHE:CD2	2.51	0.45
1:A:60:THR:CG2	1:A:64:ASP:HB2	2.45	0.45
1:A:106:THR:O	1:A:118:ILE:HG13	2.16	0.45
1:A:180:ASP:O	1:A:181:LEU:HB2	2.16	0.45
1:A:70:GLN:CG	1:A:71:LYS:N	2.79	0.45
1:A:78:GLY:O	1:A:79:GLU:C	2.55	0.45
1:A:127:PHE:CE1	1:A:188:SER:CA	2.95	0.45
1:A:171:HIS:ND1	1:A:171:HIS:C	2.70	0.45
1:A:87:GLU:CD	1:A:87:GLU:N	2.70	0.45
1:A:87:GLU:OE1	1:A:87:GLU:N	2.49	0.45
1:A:183:LYS:NZ	1:A:185:ALA:N	2.65	0.45
1:A:187:THR:O	1:A:188:SER:CB	2.64	0.45
1:A:146:TYR:CD1	1:A:221:PHE:HD1	2.34	0.45
1:A:346:ARG:C	1:A:348:ALA:N	2.68	0.45
1:A:8:VAL:CG1	1:A:9:ALA:N	2.80	0.45
1:A:124:GLU:HB2	1:A:189:TYR:CZ	2.52	0.45
1:A:168:VAL:O	1:A:168:VAL:CG1	2.63	0.45
1:A:186:VAL:HB	1:A:191:ASP:HB3	1.98	0.45
1:A:147:MET:HE2	1:A:222:ASN:HD21	1.82	0.45
1:A:273:LYS:O	1:A:275:LEU:N	2.50	0.45
1:A:355:ARG:H	1:A:355:ARG:CD	2.30	0.44
1:A:60:THR:CG2	1:A:61:SER:H	2.02	0.44
1:A:26:CYS:SG	1:A:59:HIS:NE2	2.80	0.44
1:A:285:LEU:HB2	1:A:354:ILE:HD12	1.99	0.44
1:A:321:GLY:HA2	1:A:355:ARG:CD	2.48	0.44
1:A:37:ILE:O	1:A:37:ILE:CD1	2.63	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:15:PHE:HD1	1:A:19:GLU:OE1	2.00	0.44
1:A:27:ILE:CD1	1:A:335:ASP:CA	2.96	0.44
1:A:340:GLU:OE1	1:A:340:GLU:HA	2.17	0.44
1:A:354:ILE:CD1	1:A:355:ARG:HD3	2.48	0.44
1:A:284:ALA:O	1:A:286:ALA:N	2.51	0.44
1:A:54:TYR:HD2	1:A:56:TYR:OH	1.81	0.44
1:A:70:GLN:HE22	1:A:114:ASP:HA	1.81	0.44
1:A:184:LEU:HD22	1:A:185:ALA:N	2.33	0.44
1:A:275:LEU:O	1:A:276:THR:C	2.56	0.44
1:A:284:ALA:C	1:A:286:ALA:H	2.20	0.44
1:A:61:SER:C	1:A:63:GLU:N	2.68	0.44
1:A:231:ASP:CB	1:A:236:ILE:HG22	2.48	0.44
1:A:12:VAL:HG11	1:A:333:PRO:HG3	1.99	0.44
1:A:50:PHE:HB3	1:A:349:ASP:HB2	2.00	0.43
1:A:171:HIS:HB3	1:A:175:GLY:O	2.17	0.43
1:A:270:ASN:HD22	1:A:270:ASN:HA	1.55	0.43
1:A:285:LEU:HD12	1:A:354:ILE:CG2	2.47	0.43
1:A:11:ARG:HG3	1:A:56:TYR:CB	2.48	0.43
1:A:140:TYR:O	1:A:141:SER:OG	2.28	0.43
1:A:16:ASN:C	1:A:20:MET:HG3	2.39	0.43
1:A:174:LEU:CD2	1:A:174:LEU:N	2.81	0.43
1:A:285:LEU:O	1:A:288:MET:HE1	2.19	0.43
1:A:341:THR:O	1:A:342:LEU:C	2.56	0.43
1:A:139:SER:CB	1:A:228:LYS:HD2	2.46	0.43
1:A:249:LEU:HD12	1:A:250:ALA:O	2.19	0.43
1:A:9:ALA:HA	1:A:54:TYR:O	2.18	0.43
1:A:171:HIS:ND1	1:A:174:LEU:N	2.61	0.43
1:A:183:LYS:CD	1:A:183:LYS:C	2.87	0.43
1:A:22:ARG:C	1:A:24:SER:N	2.71	0.43
1:A:286:ALA:O	1:A:287:GLU:HB2	2.19	0.43
1:A:54:TYR:HE2	1:A:76:ASP:HB3	1.84	0.43
1:A:111:GLN:HG2	1:A:111:GLN:H	1.56	0.43
1:A:315:LEU:HB2	1:A:318:ASN:CG	2.38	0.43
1:A:108:MET:HE2	1:A:196:MET:HE3	2.01	0.43
1:A:192:ILE:O	1:A:193:GLN:C	2.56	0.43
1:A:83:GLN:HG3	1:A:87:GLU:OE2	2.17	0.43
1:A:162:ASN:O	1:A:163:LYS:CB	2.49	0.43
1:A:315:LEU:HB2	1:A:318:ASN:ND2	2.34	0.43
1:A:39:ASN:N	1:A:40:PRO:CD	2.77	0.43
1:A:85:ALA:O	1:A:88:GLY:N	2.51	0.43
1:A:187:THR:O	1:A:188:SER:OG	2.27	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:41:LYS:HD3	1:A:41:LYS:HA	1.26	0.42
1:A:13:ARG:HG2	1:A:13:ARG:O	2.18	0.42
1:A:144:VAL:HG21	1:A:221:PHE:CZ	2.54	0.42
1:A:98:GLN:O	1:A:101:ALA:N	2.53	0.42
1:A:126:LEU:HD11	1:A:130:ILE:HD11	2.00	0.42
1:A:167:ARG:CG	1:A:168:VAL:N	2.78	0.42
1:A:307:ARG:O	1:A:309:SER:N	2.53	0.42
1:A:96:TYR:HD1	1:A:97:GLY:CA	2.32	0.42
1:A:98:GLN:O	1:A:99:THR:O	2.38	0.42
1:A:203:ARG:O	1:A:204:THR:HG23	2.19	0.42
1:A:10:VAL:N	1:A:54:TYR:O	2.45	0.42
1:A:98:GLN:O	1:A:101:ALA:HB2	2.20	0.42
1:A:98:GLN:OE1	1:A:340:GLU:CB	2.67	0.42
1:A:140:TYR:CE1	1:A:227:GLN:HA	2.54	0.42
1:A:227:GLN:O	1:A:240:LYS:N	2.42	0.42
1:A:235:ASN:N	1:A:235:ASN:ND2	2.64	0.42
1:A:227:GLN:N	1:A:240:LYS:O	2.52	0.42
1:A:285:LEU:HD23	1:A:286:ALA:N	2.34	0.42
1:A:306:TYR:CB	1:A:312:THR:OG1	2.65	0.42
1:A:156:ASP:C	1:A:158:LEU:N	2.73	0.42
1:A:14:PRO:O	1:A:15:PHE:CD2	2.72	0.42
1:A:10:VAL:HG21	1:A:35:THR:CG2	2.47	0.42
1:A:278:LEU:C	1:A:278:LEU:HD13	2.40	0.42
1:A:151:CYS:C	1:A:153:ARG:N	2.73	0.42
1:A:215:SER:O	1:A:217:SER:N	2.53	0.42
1:A:7:LYS:C	1:A:326:ALA:HA	2.40	0.42
1:A:117:GLY:H	1:A:120:PRO:HG3	1.85	0.42
1:A:146:TYR:O	1:A:158:LEU:CD1	2.68	0.42
1:A:188:SER:O	1:A:190:ASN:N	2.53	0.42
1:A:84:HIS:CD2	1:A:84:HIS:N	2.88	0.42
1:A:26:CYS:HB2	1:A:59:HIS:NE2	2.30	0.41
1:A:26:CYS:SG	1:A:28:ILE:N	2.92	0.41
1:A:22:ARG:HG3	1:A:22:ARG:O	2.19	0.41
1:A:238:THR:HG23	1:A:238:THR:O	2.20	0.41
1:A:8:VAL:HG21	1:A:351:ALA:HB3	2.02	0.41
1:A:66:ASN:HD22	1:A:66:ASN:HA	1.75	0.41
1:A:215:SER:C	1:A:217:SER:N	2.72	0.41
1:A:247:VAL:CG1	1:A:248:ASP:H	2.33	0.41
1:A:27:ILE:HD12	1:A:335:ASP:CB	2.50	0.41
1:A:57:TRP:O	1:A:68:ALA:CB	2.68	0.41
1:A:156:ASP:OD2	1:A:158:LEU:CD1	2.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:271:ILE:H	1:A:271:ILE:HD13	1.84	0.41
1:A:275:LEU:O	1:A:278:LEU:N	2.51	0.41
1:A:14:PRO:O	1:A:333:PRO:HG2	2.20	0.41
1:A:13:ARG:HH11	1:A:13:ARG:HG2	1.86	0.41
1:A:172:PRO:CB	1:A:173:LEU:HD22	2.49	0.41
1:A:186:VAL:C	1:A:187:THR:HG22	2.40	0.41
1:A:17:SER:OG	1:A:18:ARG:N	2.53	0.41
1:A:196:MET:O	1:A:199:GLY:N	2.54	0.41
1:A:200:ASN:O	1:A:203:ARG:CG	2.67	0.41
1:A:17:SER:O	1:A:20:MET:N	2.54	0.41
1:A:280:LYS:CG	5:A:2022:HOH:O	2.68	0.41
1:A:315:LEU:N	1:A:315:LEU:CD1	2.78	0.41
1:A:150:TYR:CE1	1:A:216:ARG:HB2	2.43	0.41
1:A:7:LYS:CG	1:A:325:THR:O	2.64	0.41
1:A:64:ASP:O	1:A:65:ILE:C	2.58	0.41
1:A:131:ASN:C	1:A:133:THR:N	2.74	0.41
1:A:280:LYS:HG3	5:A:2022:HOH:O	2.21	0.41
1:A:282:ILE:O	1:A:286:ALA:HB3	2.19	0.41
1:A:82:LEU:O	1:A:85:ALA:HB3	2.21	0.41
1:A:17:SER:C	1:A:19:GLU:N	2.74	0.41
1:A:143:GLU:HB3	1:A:183:LYS:HE3	2.01	0.41
1:A:179:GLU:C	1:A:181:LEU:HD22	2.41	0.41
1:A:241:VAL:CG1	1:A:242:SER:N	2.84	0.41
1:A:315:LEU:HB2	1:A:318:ASN:HD21	1.86	0.41
1:A:341:THR:O	1:A:345:LEU:CD1	2.68	0.40
1:A:74:TYR:C	1:A:76:ASP:H	2.23	0.40
1:A:13:ARG:NH1	1:A:19:GLU:OE1	2.41	0.40
1:A:321:GLY:O	1:A:322:ASN:O	2.39	0.40
1:A:133:THR:O	1:A:134:THR:CG2	2.62	0.40
1:A:54:TYR:HD2	1:A:56:TYR:CZ	2.39	0.40
1:A:170:GLU:OE2	1:A:176:PRO:HD3	2.21	0.40
1:A:57:TRP:CH2	1:A:60:THR:CB	2.98	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	311/366 (85%)	178 (57%)	66 (21%)	67 (22%)	0 1

All (67) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	7	LYS
1	A	23	ASP
1	A	39	ASN
1	A	40	PRO
1	A	41	LYS
1	A	42	GLN
1	A	43	PRO
1	A	44	LYS
1	A	89	TYR
1	A	115	GLN
1	A	134	THR
1	A	138	MET
1	A	163	LYS
1	A	186	VAL
1	A	187	THR
1	A	188	SER
1	A	236	ILE
1	A	252	SER
1	A	272	ASN
1	A	274	SER
1	A	287	GLU
1	A	289	ASP
1	A	304	ILE
1	A	314	LEU
1	A	316	ARG
1	A	346	ARG
1	A	62	PRO
1	A	93	ILE
1	A	109	GLY
1	A	166	LEU
1	A	185	ALA
1	A	197	ASP
1	A	200	ASN
1	A	216	ARG

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Mol	Chain	Res	Type
1	A	275	LEU
1	A	353	GLN
1	A	14	PRO
1	A	17	SER
1	A	18	ARG
1	A	99	THR
1	A	114	ASP
1	A	250	ALA
1	A	270	ASN
1	A	305	PRO
1	A	322	ASN
1	A	347	TYR
1	A	51	SER
1	A	60	THR
1	A	124	GLU
1	A	141	SER
1	A	179	GLU
1	A	234	THR
1	A	313	TRP
1	A	46	THR
1	A	123	CYS
1	A	139	SER
1	A	154	VAL
1	A	162	ASN
1	A	181	LEU
1	A	189	TYR
1	A	202	PRO
1	A	324	ARG
1	A	75	ARG
1	A	321	GLY
1	A	310	VAL
1	A	199	GLY
1	A	47	PRO

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	258/322 (80%)	184 (71%)	74 (29%)	<b>0</b> <b>3</b>

All (74) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	PRO
1	A	17	SER
1	A	22	ARG
1	A	25	LYS
1	A	27	ILE
1	A	28	ILE
1	A	33	SER
1	A	37	ILE
1	A	38	VAL
1	A	40	PRO
1	A	41	LYS
1	A	46	THR
1	A	54	TYR
1	A	61	SER
1	A	73	VAL
1	A	76	ASP
1	A	80	GLU
1	A	81	MET
1	A	83	GLN
1	A	87	GLU
1	A	90	ASN
1	A	92	CYS
1	A	94	PHE
1	A	96	TYR
1	A	98	GLN
1	A	111	GLN
1	A	124	GLU
1	A	134	THR
1	A	137	ASN
1	A	145	SER
1	A	146	TYR
1	A	152	GLU
1	A	153	ARG
1	A	154	VAL
1	A	158	LEU
1	A	161	LYS
1	A	167	ARG
1	A	177	TYR

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Mol	Chain	Res	Type
1	A	183	LYS
1	A	186	VAL
1	A	191	ASP
1	A	192	ILE
1	A	200	ASN
1	A	204	THR
1	A	212	GLU
1	A	215	SER
1	A	223	ILE
1	A	226	THR
1	A	235	ASN
1	A	246	LEU
1	A	248	ASP
1	A	249	LEU
1	A	270	ASN
1	A	271	ILE
1	A	275	LEU
1	A	276	THR
1	A	277	THR
1	A	282	ILE
1	A	285	LEU
1	A	288	MET
1	A	304	ILE
1	A	307	ARG
1	A	308	ASP
1	A	310	VAL
1	A	315	LEU
1	A	319	LEU
1	A	322	ASN
1	A	327	MET
1	A	331	LEU
1	A	335	ASP
1	A	340	GLU
1	A	344	THR
1	A	349	ASP
1	A	352	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	66	ASN
1	A	83	GLN

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Mol	Chain	Res	Type
1	A	84	HIS
1	A	90	ASN
1	A	111	GLN
1	A	116	GLN
1	A	193	GLN
1	A	200	ASN
1	A	222	ASN
1	A	235	ASN
1	A	270	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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
4	TRS	A	2003	-	7,7,7	1.19	1 (14%)	9,9,9	0.83	0
4	TRS	A	2002	-	7,7,7	0.51	0	9,9,9	0.53	0
3	ADP	A	2000	-	24,29,29	1.09	3 (12%)	29,45,45	1.40	6 (20%)

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	TRS	A	2003	-	-	0/9/9/9	-
4	TRS	A	2002	-	-	0/9/9/9	-
3	ADP	A	2000	-	-	7/12/32/32	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	2000	ADP	C2-N1	2.56	1.38	1.33
3	A	2000	ADP	C4-N3	2.54	1.39	1.35
3	A	2000	ADP	O4'-C1'	-2.28	1.37	1.41
4	A	2003	TRS	C2-C	2.27	1.60	1.53

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	2000	ADP	C3'-C2'-C1'	3.31	105.97	100.98
3	A	2000	ADP	O2B-PB-O3A	2.48	112.95	104.64
3	A	2000	ADP	O4'-C4'-C3'	2.44	109.94	105.11
3	A	2000	ADP	O5'-C5'-C4'	2.43	117.34	108.99
3	A	2000	ADP	C5-C6-N6	2.25	123.77	120.35
3	A	2000	ADP	O3'-C3'-C2'	2.19	118.89	111.82

There are no chirality outliers.

All (7) torsion outliers are listed below:

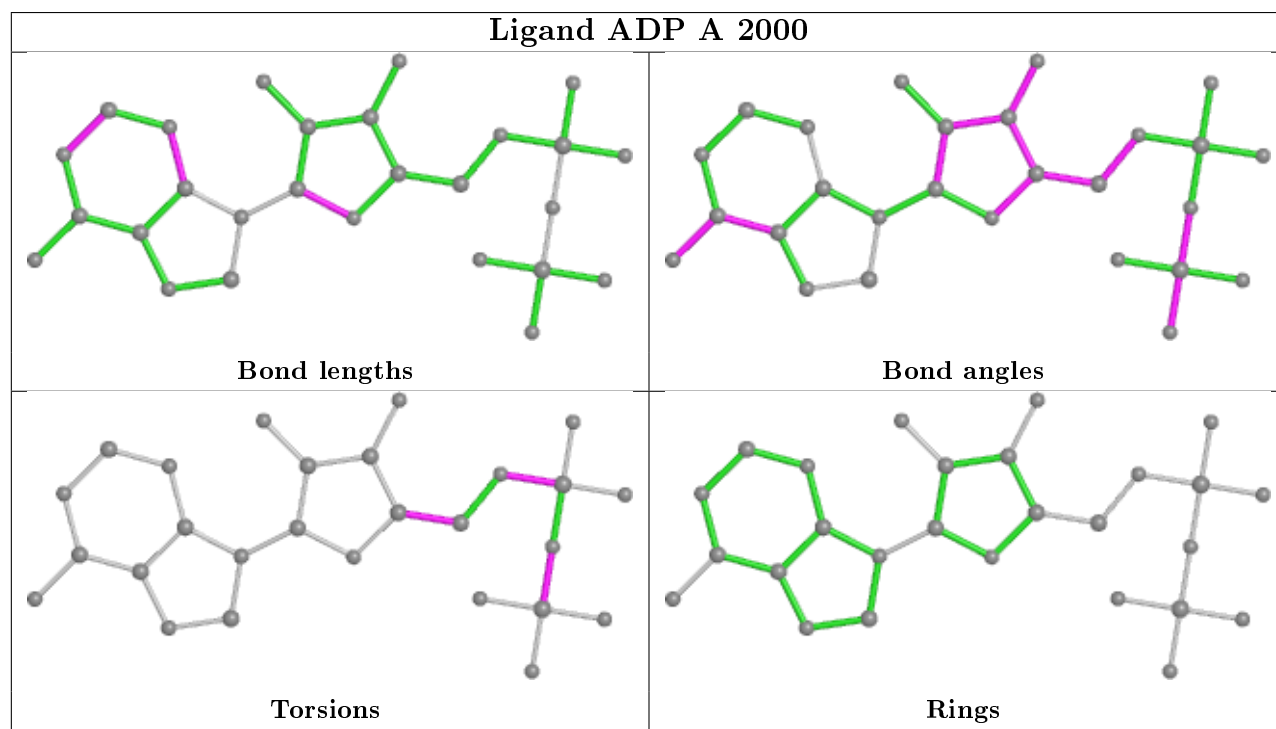
Mol	Chain	Res	Type	Atoms
3	A	2000	ADP	PA-O3A-PB-O3B
3	A	2000	ADP	C5'-O5'-PA-O1A
3	A	2000	ADP	C5'-O5'-PA-O3A
3	A	2000	ADP	O4'-C4'-C5'-O5'
3	A	2000	ADP	PA-O3A-PB-O1B
3	A	2000	ADP	PA-O3A-PB-O2B
3	A	2000	ADP	C3'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

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	321/366 (87%)	-0.28	7 (2%) 62 46	19, 75, 112, 117	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	237	THR	3.1
1	A	170	GLU	2.9
1	A	137	ASN	2.8
1	A	136	ASP	2.7
1	A	236	ILE	2.5
1	A	231	ASP	2.5
1	A	168	VAL	2.1

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

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

### 6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

### 6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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	TRS	A	2003	8/8	0.68	0.44	56,57,57,57	0

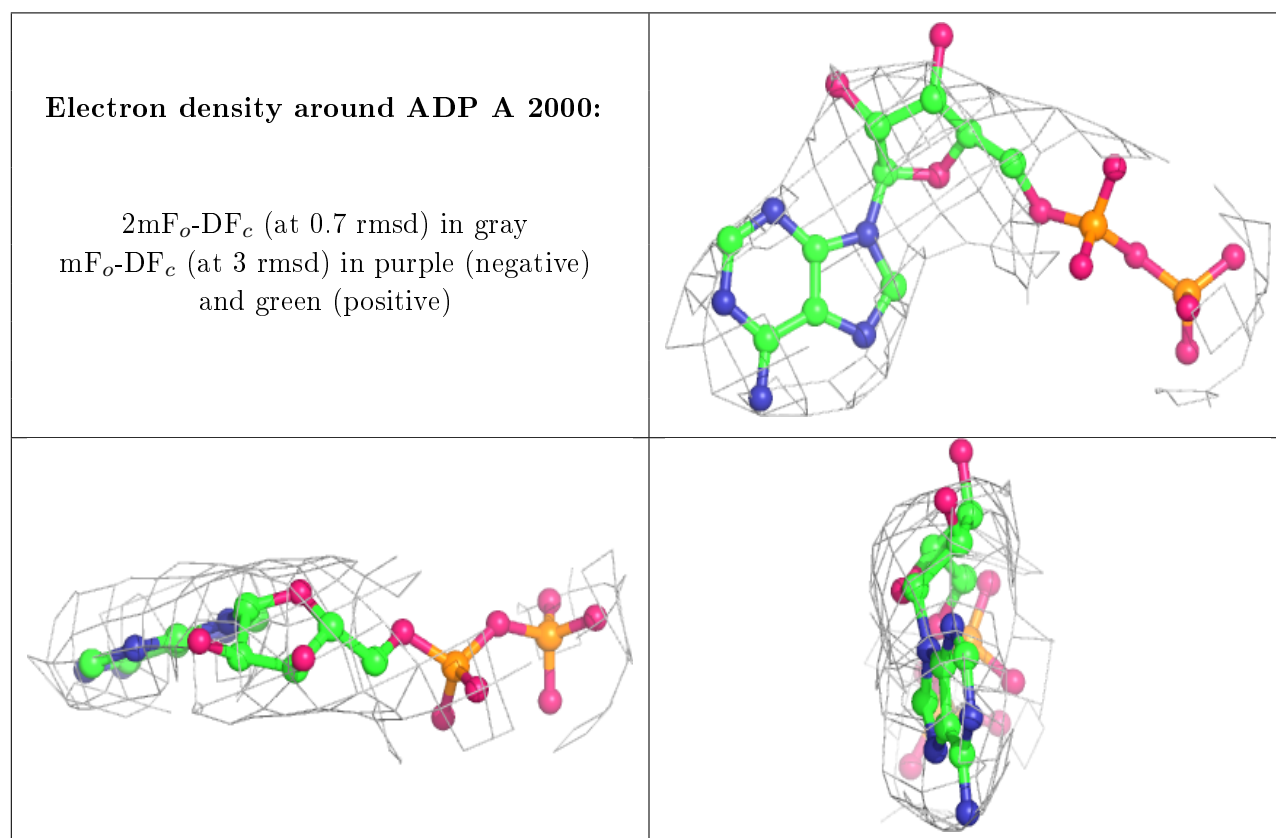
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	TRS	A	2002	8/8	0.80	0.33	106,113,116,116	0
2	MG	A	2001	1/1	0.87	0.95	87,87,87,87	1
3	ADP	A	2000	27/27	0.89	0.21	38,74,91,96	0

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.



## 6.5 Other polymers [i](#)

There are no such residues in this entry.