



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 03:58 pm GMT

PDB ID : 2W96  
Title : CRYSTAL STRUCTURE OF CDK4 IN COMPLEX WITH A D-TYPE CYCLIN  
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Deposited on : 2009-01-21  
Resolution : 2.30 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

<http://wwpdb.org/validation/2016/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 : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc28949

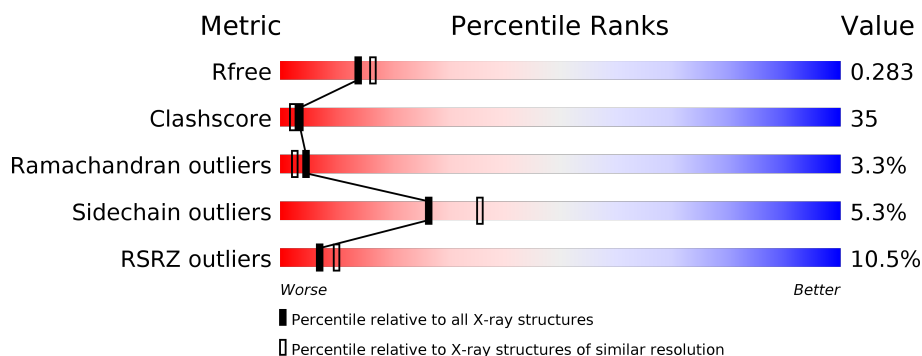
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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))
$R_{free}$	100719	4130 (2.30-2.30)
Clashscore	112137	4751 (2.30-2.30)
Ramachandran outliers	110173	4705 (2.30-2.30)
Sidechain outliers	110143	4704 (2.30-2.30)
RSRZ outliers	101464	4156 (2.30-2.30)

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. 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	271	<div> <div>4%</div> <div>62%</div> <div>27%</div> <div>•</div> <div>8%</div> </div>
2	B	306	<div> <div>14%</div> <div>31%</div> <div>48%</div> <div>7%</div> <div>•</div> <div>13%</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
3	GOL	A	1266	-	-	-	X

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4306 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 G1/S-SPECIFIC CYCLIN-D1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	249	Total	C	N	O	S	0	1	0
			1983	1260	336	365	22			

- Molecule 2 is a protein called CELL DIVISION PROTEIN KINASE 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	267	Total	C	N	O	S	0	1	0
			2127	1365	366	385	11			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	43	GLU	GLY	ENGINEERED MUTATION	UNP P11802
B	44	GLU	GLY	ENGINEERED MUTATION	UNP P11802
B	172	ASP	THR	ENGINEERED MUTATION	UNP P11802

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		

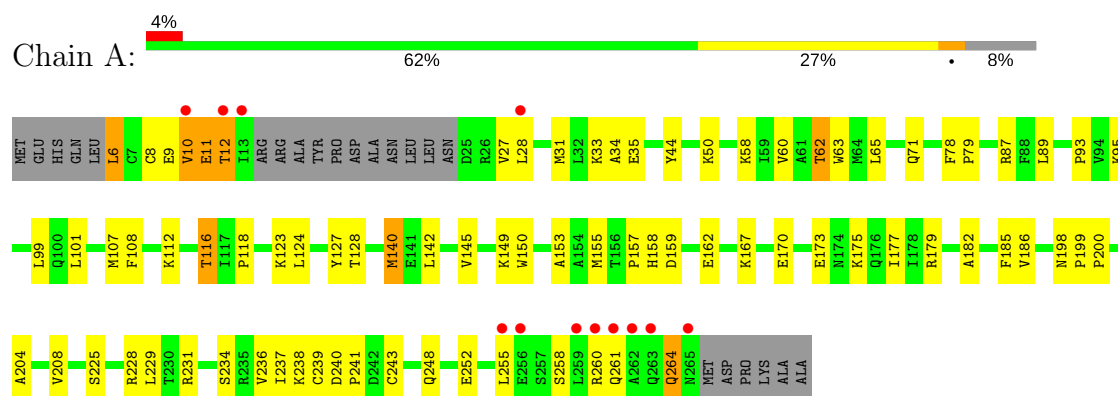
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	122	Total	O	0	0
			122	122		
4	B	68	Total	O	0	0
			68	68		

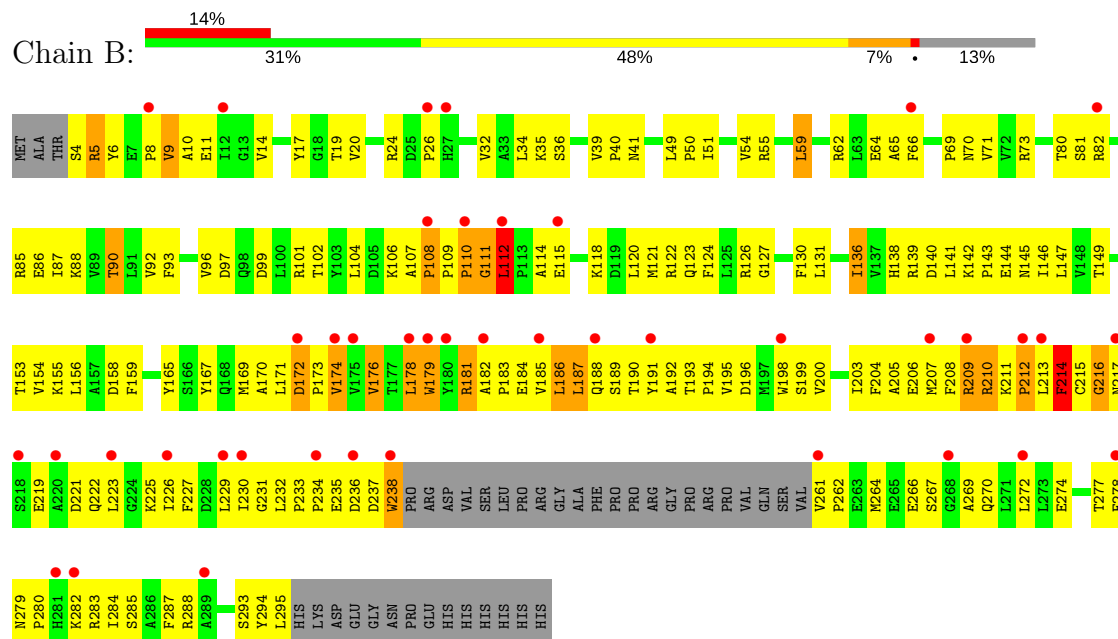
### 3 Residue-property plots

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: G1/S-SPECIFIC CYCLIN-D1



#### • Molecule 2: CELL DIVISION PROTEIN KINASE 4



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	55.91Å 64.69Å 168.69Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	84.22 – 2.30 84.34 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.1 (84.22-2.30) 99.2 (84.34-2.30)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.06 (at 2.29Å)	Xtriage
Refinement program	BUSTER-TNT 2.1.1	Depositor
R, $R_{free}$	0.203 , 0.259 0.218 , 0.283	Depositor DCC
$R_{free}$ test set	1356 reflections (5.13%)	DCC
Wilson B-factor (Å <sup>2</sup> )	45.1	Xtriage
Anisotropy	0.327	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 85.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.42$ , $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	4306	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.69% 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: GOL

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	0.33	0/2018	0.48	0/2723
2	B	0.25	0/2181	0.48	1/2963 (0.0%)
All	All	0.29	0/4199	0.48	1/5686 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	112	LEU	C-N-CD	-6.67	105.92	120.60

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1983	0	2036	78	0
2	B	2127	0	2133	224	0
3	A	6	0	8	3	0
4	A	122	0	0	8	0
4	B	68	0	0	8	0
All	All	4306	0	4177	291	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including



hydrogen atoms). The all-atom clashscore for this structure is 35.

All (291) 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)
2:B:32:VAL:HG11	2:B:92:VAL:HG13	1.38	1.06
2:B:173:PRO:HA	2:B:174:VAL:HB	1.38	1.03
2:B:190:THR:HA	2:B:191:TYR:HB2	1.46	0.98
1:A:142:LEU:HD13	2:B:82:ARG:HD3	1.48	0.95
2:B:279:ASN:HD22	2:B:282:LYS:HG2	1.29	0.95
2:B:178:LEU:HD13	2:B:181:ARG:HB2	1.51	0.92
2:B:193:THR:HG22	2:B:194:PRO:HD3	1.53	0.91
2:B:179:TRP:CH2	2:B:216:GLY:HA2	2.06	0.90
2:B:179:TRP:CZ3	2:B:216:GLY:HA2	2.07	0.88
2:B:64:GLU:HG3	2:B:73:ARG:HD2	1.55	0.88
2:B:186:LEU:HD13	2:B:223:LEU:HD12	1.54	0.87
1:A:58:LYS:O	1:A:62:THR:HG22	1.77	0.83
2:B:232:LEU:HD12	2:B:233:PRO:HD2	1.59	0.83
1:A:142:LEU:HD13	2:B:82:ARG:CD	2.08	0.83
1:A:60:VAL:HG21	1:A:99:LEU:HG	1.60	0.81
2:B:196:ASP:O	2:B:200:VAL:HG23	1.80	0.80
2:B:32:VAL:HG11	2:B:92:VAL:CG1	2.11	0.80
2:B:213:LEU:H	2:B:213:LEU:HD23	1.45	0.80
2:B:59:LEU:HD21	4:B:2009:HOH:O	1.81	0.80
2:B:102:THR:HG22	2:B:106:LYS:HE3	1.64	0.80
2:B:188:GLN:HB3	2:B:189:SER:OG	1.82	0.80
2:B:226:ILE:O	2:B:230:ILE:HG22	1.84	0.78
2:B:136[A]:ILE:HD11	2:B:159:PHE:HB2	1.66	0.77
2:B:122:ARG:O	2:B:126:ARG:HG3	1.86	0.76
2:B:118:LYS:HE2	2:B:294:TYR:CE1	2.18	0.76
2:B:187:LEU:HG	2:B:188:GLN:HA	1.68	0.76
1:A:116:THR:HG22	4:A:2038:HOH:O	1.84	0.76
2:B:198:TRP:HB2	2:B:283:ARG:NH2	2.01	0.75
1:A:237:ILE:CG2	1:A:239:CYS:HB3	2.17	0.75
2:B:187:LEU:CG	2:B:188:GLN:HA	2.17	0.75
2:B:140:ASP:OD1	2:B:142:LYS:HE3	1.86	0.74
2:B:187:LEU:CD2	2:B:188:GLN:HA	2.18	0.74
2:B:170:ALA:C	2:B:171:LEU:HD12	2.09	0.73
1:A:237:ILE:HG21	1:A:239:CYS:HB3	1.69	0.73
2:B:172:ASP:H	2:B:173:PRO:CD	2.03	0.72
2:B:190:THR:HA	2:B:191:TYR:CB	2.18	0.72
2:B:51:ILE:O	2:B:54:VAL:HG22	1.90	0.71
2:B:187:LEU:HD23	2:B:188:GLN:HA	1.73	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:79:PRO:HG2	1:A:158:HIS:CE1	2.26	0.70
2:B:24:ARG:O	2:B:26:PRO:HD3	1.90	0.70
2:B:215:CYS:H	2:B:225:LYS:HD3	1.56	0.70
2:B:261:VAL:HG23	4:B:2064:HOH:O	1.91	0.69
2:B:199:SER:O	2:B:203:ILE:HG12	1.93	0.69
1:A:237:ILE:HG22	1:A:239:CYS:N	2.07	0.69
2:B:170:ALA:O	2:B:171:LEU:HD12	1.92	0.69
2:B:227:PHE:CE2	2:B:233:PRO:HD3	2.28	0.69
2:B:101:ARG:NE	2:B:144:GLU:HG3	2.08	0.68
2:B:279:ASN:ND2	2:B:282:LYS:HG2	2.07	0.68
2:B:101:ARG:CZ	2:B:144:GLU:HG3	2.24	0.68
2:B:184:GLU:HB3	2:B:190:THR:O	1.93	0.68
2:B:55:ARG:O	2:B:59:LEU:HD13	1.94	0.68
1:A:10:VAL:HG12	1:A:11:GLU:N	2.08	0.68
1:A:185:PHE:HE1	1:A:255:LEU:HD22	1.59	0.67
2:B:229:LEU:HD23	2:B:229:LEU:O	1.93	0.67
2:B:171:LEU:N	2:B:172:ASP:HA	2.10	0.67
2:B:101:ARG:HD3	2:B:144:GLU:OE2	1.95	0.67
2:B:193:THR:CG2	2:B:194:PRO:HD3	2.24	0.67
2:B:235:GLU:HA	2:B:237:ASP:H	1.59	0.66
2:B:49:LEU:HD23	2:B:87:ILE:HD13	1.77	0.66
2:B:81:SER:O	2:B:82:ARG:HG3	1.96	0.66
2:B:65:ALA:HB2	4:B:2021:HOH:O	1.96	0.66
2:B:178:LEU:CD1	2:B:181:ARG:HB2	2.26	0.66
2:B:187:LEU:HD12	2:B:191:TYR:CE2	2.32	0.65
2:B:144:GLU:OE1	2:B:144:GLU:N	2.28	0.65
2:B:36:SER:OG	2:B:88:LYS:HE2	1.95	0.65
1:A:28:LEU:HD21	1:A:236:VAL:HG12	1.79	0.65
2:B:192:ALA:O	2:B:195:VAL:HG22	1.96	0.65
1:A:123[B]:LYS:NZ	4:A:2064:HOH:O	2.28	0.65
1:A:204:ALA:O	1:A:208:VAL:HG23	1.97	0.64
1:A:248:GLN:NE2	1:A:252:GLU:OE2	2.30	0.64
2:B:140:ASP:O	2:B:145:ASN:ND2	2.30	0.64
2:B:186:LEU:CD1	2:B:223:LEU:HD12	2.27	0.64
2:B:149:THR:CG2	2:B:153:THR:H	2.09	0.64
2:B:232:LEU:CD1	2:B:233:PRO:HD2	2.27	0.64
1:A:71:GLN:NE2	1:A:127:TYR:OH	2.25	0.64
2:B:187:LEU:HA	2:B:188:GLN:C	2.18	0.64
1:A:162:GLU:OE1	1:A:179:ARG:NH1	2.30	0.64
1:A:145:VAL:HG12	1:A:150:TRP:CD1	2.33	0.64
2:B:40:PRO:HA	2:B:85:ARG:O	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:190:THR:CA	2:B:191:TYR:HB2	2.27	0.63
2:B:149:THR:HG21	2:B:153:THR:HB	1.78	0.63
2:B:186:LEU:HD11	2:B:219:GLU:HB3	1.81	0.63
2:B:5:ARG:O	2:B:26:PRO:HG2	1.97	0.63
2:B:115:GLU:OE1	2:B:118:LYS:HD2	1.98	0.63
2:B:184:GLU:OE2	2:B:280:PRO:HB3	1.99	0.63
2:B:149:THR:CG2	2:B:153:THR:HB	2.29	0.62
2:B:80:THR:OG1	2:B:88:LYS:HD2	1.98	0.62
2:B:187:LEU:HD23	2:B:188:GLN:CA	2.30	0.62
2:B:213:LEU:N	2:B:213:LEU:HD23	2.13	0.62
2:B:142:LYS:N	2:B:145:ASN:HD22	1.98	0.61
2:B:102:THR:O	2:B:106:LYS:HG2	2.01	0.61
1:A:101:LEU:HG	1:A:140:MET:HG3	1.83	0.60
1:A:9:GLU:OE2	2:B:288:ARG:NH1	2.34	0.60
2:B:264:MET:HE1	2:B:269:ALA:HA	1.82	0.60
2:B:39:VAL:HG22	2:B:87:ILE:O	2.01	0.60
2:B:96:VAL:HB	2:B:147:LEU:HD13	1.83	0.60
2:B:176:VAL:HB	2:B:178:LEU:HD23	1.83	0.60
2:B:32:VAL:HG13	2:B:93:PHE:O	2.01	0.59
1:A:162:GLU:OE2	1:A:179:ARG:HD3	2.02	0.59
2:B:35:LYS:NZ	2:B:158:ASP:OD1	2.29	0.59
1:A:10:VAL:HG21	2:B:287:PHE:CE2	2.38	0.59
1:A:185:PHE:CE1	1:A:255:LEU:HD22	2.36	0.59
1:A:261:GLN:HA	1:A:264:GLN:HG2	1.85	0.59
2:B:209:ARG:NH2	2:B:213:LEU:HD13	2.18	0.59
2:B:70:ASN:HD21	2:B:123:GLN:HE21	1.51	0.59
2:B:213:LEU:H	2:B:213:LEU:CD2	2.15	0.59
2:B:123:GLN:HE22	2:B:153:THR:HA	1.68	0.58
2:B:167:TYR:O	2:B:171:LEU:HD13	2.02	0.58
1:A:118:PRO:HG2	2:B:51:ILE:CD1	2.33	0.58
2:B:215:CYS:O	2:B:222:GLN:NE2	2.36	0.58
2:B:49:LEU:CD2	2:B:87:ILE:HD13	2.34	0.58
2:B:173:PRO:HA	2:B:174:VAL:CB	2.20	0.58
1:A:34:ALA:HB1	4:A:2078:HOH:O	2.03	0.57
2:B:223:LEU:HD23	2:B:223:LEU:O	2.04	0.57
2:B:71:VAL:HG13	2:B:159:PHE:CE2	2.39	0.57
2:B:217:ASN:HB3	2:B:221:ASP:CB	2.35	0.57
2:B:186:LEU:CD1	2:B:219:GLU:HB3	2.34	0.57
1:A:10:VAL:HG21	2:B:287:PHE:CD2	2.39	0.57
1:A:234:SER:OG	1:A:241:PRO:HA	2.04	0.57
2:B:214:PHE:HA	2:B:225:LYS:HD3	1.85	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:142:LEU:HD21	2:B:49:LEU:HD21	1.88	0.56
2:B:124:PHE:CD1	2:B:156:LEU:HD21	2.40	0.56
2:B:206:GLU:OE2	2:B:212:PRO:HD3	2.04	0.56
1:A:95:LYS:NZ	4:A:2051:HOH:O	2.37	0.56
2:B:179:TRP:N	2:B:179:TRP:CE3	2.74	0.56
1:A:33:LYS:HB3	4:B:2024:HOH:O	2.06	0.56
1:A:11:GLU:O	1:A:11:GLU:HG2	2.05	0.56
1:A:87:ARG:HH21	3:A:1266:GOL:H2	1.71	0.56
2:B:32:VAL:CG1	2:B:92:VAL:HG13	2.26	0.56
2:B:142:LYS:HB3	2:B:144:GLU:OE1	2.06	0.55
2:B:264:MET:CE	2:B:269:ALA:HA	2.36	0.55
1:A:182:ALA:O	1:A:186:VAL:HG23	2.07	0.55
2:B:183:PRO:HG2	4:B:2059:HOH:O	2.06	0.55
2:B:49:LEU:HD23	2:B:87:ILE:CD1	2.37	0.55
2:B:209:ARG:O	2:B:210:ARG:HG3	2.07	0.54
1:A:240:ASP:HB3	1:A:243:CYS:SG	2.47	0.54
1:A:27:VAL:HG13	1:A:28:LEU:H	1.73	0.54
2:B:172:ASP:N	2:B:173:PRO:CD	2.71	0.54
2:B:294:TYR:O	2:B:295:LEU:HB2	2.07	0.54
2:B:142:LYS:O	2:B:146:ILE:HG13	2.08	0.53
1:A:228:ARG:HH12	1:A:231:ARG:NH1	2.06	0.53
2:B:14:VAL:HG12	2:B:14:VAL:O	2.08	0.53
2:B:204:PHE:HA	2:B:207:MET:CE	2.39	0.53
2:B:41:ASN:HB2	2:B:87:ILE:HG13	1.89	0.53
1:A:142:LEU:HD13	2:B:82:ARG:HH11	1.75	0.52
1:A:170:GLU:O	1:A:175:LYS:HE3	2.09	0.52
1:A:31:MET:HE3	1:A:155:MET:HE1	1.91	0.52
2:B:217:ASN:HB3	2:B:221:ASP:HB2	1.92	0.52
2:B:227:PHE:O	2:B:231:GLY:N	2.39	0.51
2:B:205:ALA:HB2	2:B:272:LEU:HD21	1.92	0.51
1:A:157:PRO:HG2	1:A:186:VAL:HG13	1.93	0.51
1:A:79:PRO:HG2	1:A:158:HIS:HE1	1.72	0.51
2:B:205:ALA:HB1	2:B:209:ARG:HE	1.75	0.51
2:B:64:GLU:HB2	4:B:2023:HOH:O	2.10	0.51
2:B:215:CYS:O	2:B:216:GLY:O	2.28	0.51
2:B:4:SER:HB3	2:B:6:TYR:CZ	2.46	0.51
1:A:108:PHE:CE2	1:A:112:LYS:HE3	2.46	0.50
2:B:172:ASP:O	2:B:172:ASP:OD1	2.29	0.50
2:B:190:THR:HB	2:B:191:TYR:C	2.31	0.50
1:A:225:SER:O	1:A:229:LEU:HD13	2.12	0.50
2:B:178:LEU:HD12	2:B:222:GLN:HG2	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:190:THR:CA	2:B:191:TYR:CB	2.89	0.50
2:B:172:ASP:H	2:B:173:PRO:HD2	1.76	0.50
2:B:17:TYR:CD2	2:B:165:TYR:CG	2.99	0.50
2:B:227:PHE:CD2	2:B:233:PRO:HD3	2.46	0.49
1:A:79:PRO:CG	1:A:158:HIS:HE1	2.25	0.49
2:B:235:GLU:HB3	2:B:236:ASP:HA	1.94	0.49
2:B:111:GLY:HA3	2:B:112:LEU:HB3	1.93	0.49
2:B:274:GLU:OE1	2:B:284:ILE:HD12	2.13	0.49
1:A:237:ILE:O	1:A:238:LYS:HB2	2.12	0.49
2:B:71:VAL:HG21	2:B:131:LEU:HD13	1.93	0.49
2:B:261:VAL:N	2:B:262:PRO:HD3	2.27	0.49
2:B:114:ALA:O	2:B:118:LYS:HG3	2.12	0.49
2:B:17:TYR:HD2	2:B:165:TYR:CD2	2.31	0.49
2:B:261:VAL:O	2:B:261:VAL:HG12	2.13	0.49
2:B:277:THR:O	2:B:279:ASN:N	2.45	0.49
2:B:35:LYS:HZ2	2:B:158:ASP:CG	2.15	0.49
2:B:20:VAL:HB	2:B:35:LYS:HG2	1.94	0.49
2:B:8:PRO:O	2:B:9:VAL:HG23	2.12	0.49
2:B:96:VAL:HB	2:B:147:LEU:CD1	2.43	0.49
2:B:34:LEU:CD2	2:B:92:VAL:HG22	2.43	0.48
2:B:209:ARG:HH21	2:B:213:LEU:HD13	1.77	0.48
1:A:87:ARG:HH21	3:A:1266:GOL:C2	2.26	0.48
2:B:149:THR:HG22	2:B:153:THR:O	2.14	0.48
1:A:112:LYS:O	2:B:55:ARG:NH1	2.43	0.48
2:B:206:GLU:HA	2:B:209:ARG:HB2	1.95	0.48
2:B:142:LYS:H	2:B:145:ASN:HD22	1.61	0.48
2:B:223:LEU:HD22	2:B:227:PHE:CE1	2.49	0.48
1:A:63:TRP:CZ3	1:A:107:MET:HE2	2.48	0.48
2:B:71:VAL:CG1	2:B:159:PHE:CZ	2.97	0.47
2:B:138:HIS:CD2	2:B:141:LEU:HD13	2.49	0.47
2:B:121:MET:SD	2:B:207:MET:HE3	2.54	0.47
2:B:235:GLU:CB	2:B:236:ASP:HA	2.43	0.47
2:B:88:LYS:NZ	2:B:90:THR:HG22	2.30	0.47
1:A:155:MET:HE3	1:A:159:ASP:CB	2.45	0.47
2:B:9:VAL:O	2:B:10:ALA:HB2	2.15	0.47
2:B:149:THR:HG22	2:B:153:THR:N	2.29	0.47
2:B:285:SER:HB2	2:B:288:ARG:HG3	1.96	0.47
2:B:143:PRO:HD3	2:B:203:ILE:HD11	1.96	0.46
2:B:97:ASP:OD1	2:B:97:ASP:O	2.32	0.46
1:A:145:VAL:HG12	1:A:150:TRP:CG	2.51	0.46
2:B:69:PRO:O	2:B:155:LYS:HD3	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:88:LYS:NZ	2:B:90:THR:CG2	2.79	0.46
1:A:93:PRO:HG3	4:A:2018:HOH:O	2.14	0.46
2:B:193:THR:N	2:B:194:PRO:CD	2.79	0.45
1:A:63:TRP:CZ3	1:A:107:MET:CE	3.00	0.45
2:B:149:THR:CG2	2:B:153:THR:N	2.79	0.45
2:B:188:GLN:HB3	2:B:189:SER:HG	1.80	0.45
1:A:237:ILE:HG22	1:A:239:CYS:HB3	1.98	0.45
1:A:173:GLU:O	1:A:177:ILE:HG13	2.15	0.45
1:A:9:GLU:HG3	1:A:9:GLU:O	2.17	0.45
2:B:214:PHE:CD1	2:B:214:PHE:N	2.84	0.45
2:B:223:LEU:CD2	2:B:227:PHE:CE1	2.99	0.45
2:B:227:PHE:CE2	2:B:233:PRO:CD	2.99	0.45
1:A:28:LEU:CD2	1:A:236:VAL:CG1	2.95	0.45
1:A:237:ILE:HG22	1:A:239:CYS:H	1.80	0.45
2:B:101:ARG:O	2:B:104:LEU:N	2.50	0.45
1:A:142:LEU:HD13	2:B:82:ARG:HD2	1.94	0.45
2:B:66:PHE:CD2	2:B:130:PHE:HE1	2.34	0.45
2:B:293:SER:O	2:B:295:LEU:HD12	2.16	0.45
2:B:235:GLU:HA	2:B:237:ASP:N	2.29	0.45
1:A:6:LEU:HD12	1:A:6:LEU:N	2.32	0.44
2:B:82:ARG:NH1	4:B:2030:HOH:O	2.30	0.44
1:A:28:LEU:HD21	1:A:236:VAL:CG1	2.44	0.44
2:B:51:ILE:O	2:B:55:ARG:HG3	2.17	0.44
2:B:62:ARG:HG2	2:B:62:ARG:O	2.18	0.44
1:A:167:LYS:HG2	4:A:2086:HOH:O	2.16	0.44
1:A:255:LEU:O	1:A:258:SER:HB2	2.18	0.44
2:B:111:GLY:CA	2:B:112:LEU:CB	2.95	0.44
2:B:96:VAL:CG1	2:B:147:LEU:HB3	2.48	0.44
1:A:123[B]:LYS:NZ	4:A:2065:HOH:O	2.49	0.43
2:B:209:ARG:HH22	2:B:229:LEU:HD11	1.83	0.43
2:B:127:GLY:O	2:B:130:PHE:HB3	2.18	0.43
2:B:187:LEU:HD23	2:B:188:GLN:N	2.33	0.43
1:A:149:LYS:HB2	3:A:1266:GOL:H32	1.99	0.43
2:B:111:GLY:HA3	2:B:112:LEU:CB	2.48	0.43
2:B:266:GLU:O	2:B:270:GLN:HG2	2.18	0.43
2:B:66:PHE:HB2	2:B:130:PHE:HZ	1.83	0.43
2:B:99:ASP:HA	2:B:147:LEU:HA	2.00	0.43
1:A:107:MET:HE3	1:A:124:LEU:HD22	2.00	0.43
1:A:198:ASN:HA	1:A:199:PRO:HD3	1.79	0.43
2:B:174:VAL:HG12	2:B:174:VAL:O	2.17	0.43
2:B:212:PRO:HB2	2:B:215:CYS:SG	2.59	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:109:PRO:HA	2:B:110:PRO:HA	1.64	0.43
2:B:179:TRP:HB3	2:B:214:PHE:O	2.19	0.43
2:B:214:PHE:HA	2:B:225:LYS:CD	2.49	0.42
2:B:204:PHE:HA	2:B:207:MET:HE2	2.00	0.42
2:B:211:LYS:HA	2:B:212:PRO:HD2	1.84	0.42
2:B:267:SER:HA	2:B:270:GLN:HG2	2.01	0.42
2:B:34:LEU:HD22	2:B:92:VAL:HG22	2.01	0.42
1:A:153:ALA:HB3	4:B:2019:HOH:O	2.19	0.42
1:A:31:MET:HE3	1:A:159:ASP:HB3	2.01	0.42
1:A:78:PHE:HB3	1:A:79:PRO:HD3	2.01	0.42
2:B:182:ALA:HB3	2:B:185:VAL:HG23	2.01	0.42
2:B:215:CYS:HB3	2:B:216:GLY:H	1.51	0.42
1:A:35:GLU:OE2	1:A:200:PRO:HD2	2.19	0.42
1:A:10:VAL:HG12	1:A:12:THR:H	1.84	0.42
2:B:233:PRO:HA	2:B:234:PRO:HD2	1.91	0.42
2:B:40:PRO:O	2:B:50:PRO:HG3	2.19	0.42
2:B:71:VAL:HG21	2:B:131:LEU:CD1	2.50	0.42
2:B:81:SER:OG	2:B:82:ARG:N	2.53	0.42
1:A:260:ARG:O	1:A:264:GLN:N	2.52	0.42
2:B:107:ALA:HA	2:B:108:PRO:HD2	1.82	0.42
2:B:190:THR:HA	2:B:191:TYR:CD2	2.54	0.42
2:B:39:VAL:O	2:B:86:GLU:HA	2.18	0.42
2:B:110:PRO:HD2	2:B:112:LEU:HD23	2.02	0.42
2:B:217:ASN:CB	2:B:221:ASP:CB	2.97	0.41
2:B:11:GLU:HG3	2:B:19:THR:CG2	2.50	0.41
1:A:123[A]:LYS:HB2	1:A:123[A]:LYS:HE3	1.95	0.41
2:B:233:PRO:HG2	2:B:238:TRP:CZ3	2.55	0.41
2:B:261:VAL:N	2:B:262:PRO:CD	2.83	0.41
2:B:82:ARG:HG2	2:B:87:ILE:HG12	2.02	0.41
2:B:111:GLY:CA	2:B:112:LEU:HB3	2.50	0.41
2:B:203:ILE:O	2:B:207:MET:HE2	2.21	0.41
2:B:169:MET:O	2:B:173:PRO:O	2.38	0.41
2:B:71:VAL:HG13	2:B:159:PHE:CZ	2.55	0.41
1:A:142:LEU:CD1	2:B:82:ARG:HD3	2.33	0.41
1:A:62:THR:HG23	4:A:2026:HOH:O	2.21	0.41
1:A:124:LEU:O	1:A:128:THR:HG23	2.21	0.41
2:B:219:GLU:O	2:B:223:LEU:HB2	2.21	0.41
2:B:208:PHE:CE1	2:B:264:MET:HB3	2.55	0.41
2:B:124:PHE:CZ	2:B:141:LEU:HD21	2.56	0.41
2:B:5:ARG:NE	2:B:5:ARG:HA	2.35	0.40
2:B:215:CYS:N	2:B:225:LYS:HD3	2.31	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:232:LEU:HD12	2:B:233:PRO:CD	2.41	0.40
2:B:51:ILE:CG2	2:B:55:ARG:CZ	2.99	0.40
1:A:27:VAL:HG13	1:A:28:LEU:N	2.35	0.40
2:B:193:THR:CG2	2:B:194:PRO:CD	2.98	0.40
2:B:112:LEU:O	2:B:112:LEU:HD12	2.22	0.40
2:B:208:PHE:HZ	2:B:294:TYR:HH	1.69	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	246/271 (91%)	239 (97%)	4 (2%)	3 (1%)	15	16
2	B	264/306 (86%)	222 (84%)	28 (11%)	14 (5%)	2	1
All	All	510/577 (88%)	461 (90%)	32 (6%)	17 (3%)	4	2

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	8	CYS
1	A	11	GLU
2	B	9	VAL
2	B	209	ARG
2	B	216	GLY
2	B	278	PHE
2	B	110	PRO
2	B	111	GLY
2	B	172	ASP
2	B	176	VAL
2	B	187	LEU
2	B	210	ARG

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Mol	Chain	Res	Type
1	A	10	VAL
2	B	174	VAL
2	B	212	PRO
2	B	108	PRO
2	B	214	PHE

### 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	225/243 (93%)	215 (96%)	10 (4%)	33	45
2	B	232/265 (88%)	217 (94%)	15 (6%)	20	26
All	All	457/508 (90%)	432 (94%)	25 (6%)	26	34

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	LEU
1	A	12	THR
1	A	44	TYR
1	A	50	LYS
1	A	62	THR
1	A	65	LEU
1	A	89	LEU
1	A	116	THR
1	A	140	MET
1	A	264	GLN
2	B	5	ARG
2	B	59	LEU
2	B	90	THR
2	B	112	LEU
2	B	120	LEU
2	B	136[A]	ILE
2	B	136[B]	ILE
2	B	139	ARG

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Mol	Chain	Res	Type
2	B	154	VAL
2	B	178	LEU
2	B	179	TRP
2	B	181	ARG
2	B	186	LEU
2	B	214	PHE
2	B	238	TRP

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	71	GLN
1	A	139	GLN
1	A	158	HIS
1	A	183	GLN
1	A	261	GLN
2	B	27	HIS
2	B	30	HIS
2	B	98	GLN
2	B	123	GLN
2	B	145	ASN
2	B	279	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

### 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

### 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 5.6 Ligand geometry [i](#)

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	GOL	A	1266	-	5,5,5	0.25	0	5,5,5	0.24	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	A	1266	-	-	0/4/4/4	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1266	GOL	3	0

## 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	249/271 (91%)	0.44	12 (4%) 31 38	25, 44, 97, 163	0
2	B	267/306 (87%)	0.98	42 (15%) 2 3	35, 77, 125, 140	0
All	All	516/577 (89%)	0.72	54 (10%) 7 10	25, 58, 121, 163	0

All (54) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	262	ALA	8.7
2	B	172	ASP	6.7
2	B	220	ALA	6.1
2	B	261	VAL	5.9
1	A	260	ARG	5.7
2	B	212	PRO	5.4
2	B	188	GLN	5.1
1	A	263	GLN	4.8
2	B	223	LEU	4.7
2	B	236	ASP	4.6
2	B	229	LEU	4.4
2	B	8	PRO	4.4
2	B	174	VAL	4.3
2	B	209	ARG	4.3
2	B	282	LYS	4.3
1	A	265	ASN	4.1
2	B	238	TRP	3.9
2	B	234	PRO	3.8
1	A	261	GLN	3.7
2	B	281	HIS	3.6
2	B	278	PHE	3.6
2	B	175	VAL	3.5
2	B	268	GLY	3.4
2	B	82	ARG	3.4

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Mol	Chain	Res	Type	RSRZ
2	B	185	VAL	3.2
1	A	259	LEU	3.2
2	B	191	TYR	3.1
2	B	27	HIS	3.0
2	B	12	ILE	3.0
1	A	256	GLU	2.9
2	B	213	LEU	2.9
2	B	207	MET	2.9
2	B	226	ILE	2.8
2	B	112	LEU	2.8
2	B	178	LEU	2.8
1	A	12	THR	2.8
1	A	255	LEU	2.7
2	B	230	ILE	2.7
1	A	13	ILE	2.6
2	B	182	ALA	2.6
2	B	66	PHE	2.6
2	B	217	ASN	2.6
1	A	28	LEU	2.6
2	B	179	TRP	2.5
1	A	10	VAL	2.4
2	B	115	GLU	2.2
2	B	198	TRP	2.2
2	B	218	SER	2.2
2	B	180	TYR	2.1
2	B	289	ALA	2.1
2	B	26	PRO	2.1
2	B	108	PRO	2.1
2	B	110	PRO	2.1
2	B	272	LEU	2.0

## 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 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	GOL	A	1266	6/6	0.86	0.23	5.42	59,62,63,65	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.