



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 09:49 AM GMT

PDB ID : 3JUH
Title : Crystal structure of a mutant of human protein kinase CK2alpha with altered cosubstrate specificity
Authors : Niefind, K.; Issinger, O.-G.
Deposited on : 2009-09-15
Resolution : 1.66 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
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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) : trunk26865

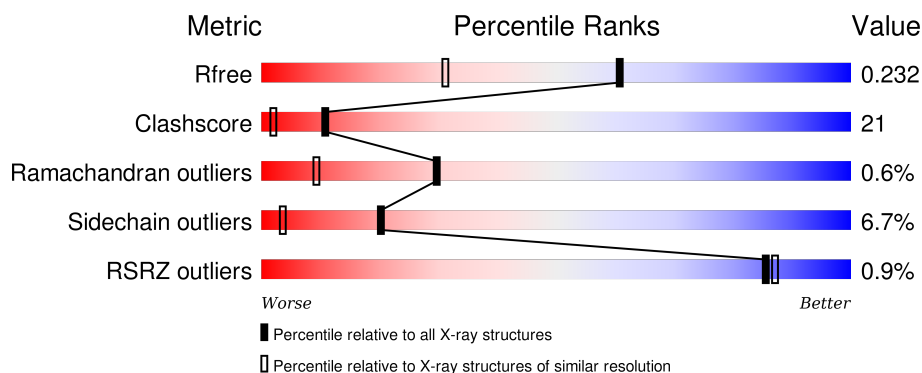
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.66 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}	91344	1226 (1.66-1.66)
Clashscore	102246	1323 (1.66-1.66)
Ramachandran outliers	100387	1295 (1.66-1.66)
Sidechain outliers	100360	1295 (1.66-1.66)
RSRZ outliers	91569	1227 (1.66-1.66)

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 ≥ 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	335	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red, orange, yellow, green);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> % 64% 31% • • </div> </div>
1	B	335	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red, orange, yellow, green);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> % 63% 32% • • </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	ANP	B	339	-	-	-	X

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 6308 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 Casein kinase II subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	334	Total	C	N	O	S	0	5	0
			2857	1826	505	514	12			
1	B	334	Total	C	N	O	S	0	5	0
			2853	1825	503	512	13			

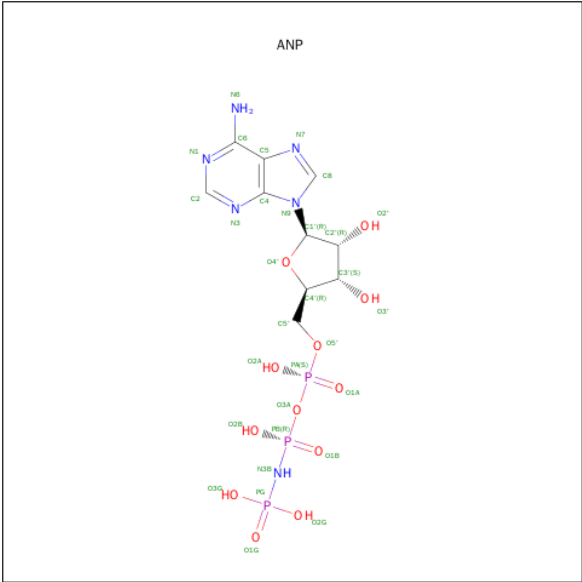
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	66	ALA	VAL	ENGINEERED MUTATION	UNP P68400
A	163	LEU	MET	ENGINEERED MUTATION	UNP P68400
B	66	ALA	VAL	ENGINEERED MUTATION	UNP P68400
B	163	LEU	MET	ENGINEERED MUTATION	UNP P68400

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	3	Total	Cl	0	0
			3	3		
2	A	3	Total	Cl	0	0
			3	3		

- Molecule 3 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (three-letter code: ANP) (formula: C₁₀H₁₇N₆O₁₂P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 31	C 10	N 6	O 12	P 3	0	0
3	B	1	Total 31	C 10	N 6	O 12	P 3	0	0

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

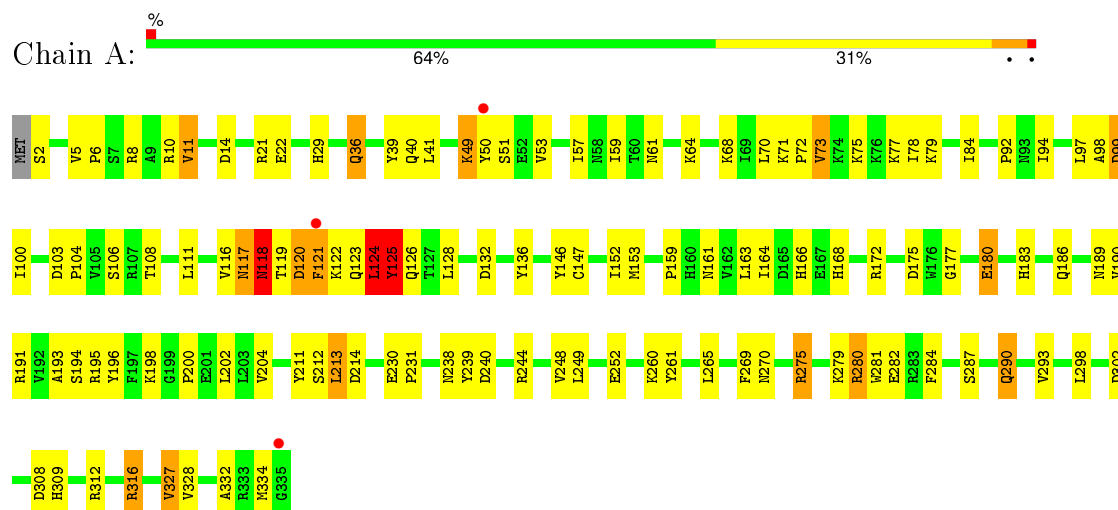
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	274	Total 274	O 274	0	0
5	B	244	Total 244	O 244	0	0

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 errors 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: Casein kinase II subunit alpha



• Molecule 1: Casein kinase II subunit alpha



4 Data and refinement statistics

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, α , β , γ	71.37Å 71.37Å 126.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.45 – 1.66 39.44 – 1.66	Depositor EDS
% Data completeness (in resolution range)	97.3 (39.45-1.66) 97.4 (39.44-1.66)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.75 (at 1.66Å)	Xtriage
Refinement program	REFMAC 5.6.0039	Depositor
R, R_{free}	0.156 , 0.218 0.190 , 0.232	Depositor DCC
R_{free} test set	2161 reflections (3.06%)	DCC
Wilson B-factor (Å ²)	22.0	Xtriage
Anisotropy	0.109	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 19.5	EDS
Estimated twinning fraction	0.500 for H, K, L 0.500 for -H, K, -L 0.487 for h,-k,-l	Xtriage
Reported twinning fraction	0.500 for H, K, L 0.500 for -H, K, -L	Depositor
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 72776 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6308	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.08% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: GOL, ANP, CL

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	1.14	4/2935 (0.1%)	1.11	12/3964 (0.3%)
1	B	1.10	6/2928 (0.2%)	1.13	18/3955 (0.5%)
All	All	1.12	10/5863 (0.2%)	1.12	30/7919 (0.4%)

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	1
1	B	0	2
All	All	0	3

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	213	LEU	CG-CD1	6.63	1.76	1.51
1	B	320	GLU	CD-OE1	6.54	1.32	1.25
1	A	147	CYS	CB-SG	-6.07	1.72	1.82
1	B	11	VAL	CB-CG1	5.86	1.65	1.52
1	A	180	GLU	CB-CG	-5.77	1.41	1.52
1	B	147	CYS	CB-SG	-5.74	1.72	1.81
1	A	332	ALA	CA-CB	5.57	1.64	1.52
1	B	139	GLU	CD-OE1	-5.48	1.19	1.25
1	B	42	VAL	CB-CG1	5.25	1.63	1.52
1	B	180	GLU	CD-OE1	5.09	1.31	1.25

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	11	VAL	CG1-CB-CG2	8.52	124.53	110.90
1	A	172	ARG	NE-CZ-NH1	7.64	124.12	120.30
1	B	89	ARG	NE-CZ-NH2	-7.40	116.60	120.30
1	B	215	MET	CG-SD-CE	7.23	111.77	100.20
1	B	175	ASP	CB-CG-OD2	-7.22	111.80	118.30
1	A	308	ASP	CB-CG-OD1	7.14	124.73	118.30
1	B	312	ARG	NE-CZ-NH1	7.05	123.82	120.30
1	A	316	ARG	NE-CZ-NH1	-7.01	116.80	120.30
1	B	280	ARG	NE-CZ-NH1	6.70	123.65	120.30
1	B	132	ASP	CB-CG-OD2	6.62	124.26	118.30
1	B	89	ARG	NE-CZ-NH1	6.53	123.56	120.30
1	B	191	ARG	NE-CZ-NH1	6.48	123.54	120.30
1	A	124	LEU	CA-CB-CG	6.30	129.78	115.30
1	A	213	LEU	CB-CG-CD1	6.26	121.64	111.00
1	B	134	ARG	NE-CZ-NH2	-6.09	117.26	120.30
1	A	163	LEU	CB-CG-CD2	6.05	121.28	111.00
1	B	312	ARG	NE-CZ-NH2	-6.01	117.29	120.30
1	A	308	ASP	CB-CG-OD2	-5.99	112.91	118.30
1	B	153	MET	CG-SD-CE	5.91	109.65	100.20
1	A	327	VAL	CG1-CB-CG2	5.72	120.06	110.90
1	B	47	ARG	NE-CZ-NH1	5.64	123.12	120.30
1	B	280	ARG	NE-CZ-NH2	-5.56	117.52	120.30
1	B	335	GLY	N-CA-C	5.40	126.61	113.10
1	A	11	VAL	CB-CA-C	-5.34	101.26	111.40
1	A	280	ARG	NE-CZ-NH1	5.33	122.97	120.30
1	A	312	ARG	NE-CZ-NH1	5.33	122.96	120.30
1	A	214	ASP	CB-CG-OD2	5.13	122.92	118.30
1	B	134	ARG	NE-CZ-NH1	5.06	122.83	120.30
1	B	191	ARG	NE-CZ-NH2	-5.05	117.78	120.30
1	B	172	ARG	NE-CZ-NH1	5.02	122.81	120.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	117	ASN	Peptide
1	B	117	ASN	Peptide
1	B	118	ASN	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	2857	0	2799	122	1
1	B	2853	0	2798	118	1
2	A	3	0	0	1	0
2	B	3	0	0	2	0
3	A	31	0	13	5	0
3	B	31	0	13	5	0
4	A	6	0	8	3	0
4	B	6	0	8	0	0
5	A	274	0	0	23	0
5	B	244	0	0	20	0
All	All	6308	0	5639	241	1

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 21.

All (241) 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:213:LEU:CD1	1:A:213:LEU:CG	1.76	1.59
1:B:73:VAL:CG1	1:B:78:ILE:HD11	1.34	1.57
1:B:73:VAL:HG11	1:B:78:ILE:CD1	1.57	1.32
1:A:49:LYS:NZ	1:A:50:TYR:OH	1.91	1.03
1:B:73:VAL:CG1	1:B:78:ILE:CD1	2.21	1.03
1:B:73:VAL:CB	1:B:78:ILE:HD11	1.89	1.02
1:A:57:ILE:O	1:A:57:ILE:HD12	1.60	0.99
1:A:36:GLN:HE22	1:A:104:PRO:HG3	1.30	0.96
1:B:73:VAL:HG11	1:B:78:ILE:HD11	0.97	0.95
1:B:275:ARG:NH1	5:B:550:HOH:O	2.03	0.91
1:B:137[A]:MET:HE1	1:B:218:LEU:HD11	1.51	0.91
1:B:73:VAL:CG2	1:B:78:ILE:HD11	2.00	0.90
1:B:117:ASN:HD22	1:B:117:ASN:C	1.75	0.89
1:A:119:THR:HG23	1:A:164:ILE:O	1.73	0.89
1:B:70:LEU:N	1:B:70:LEU:HD23	1.90	0.86
1:B:137[A]:MET:CE	1:B:218:LEU:HD11	2.04	0.86
1:A:249:LEU:HD21	1:A:281:TRP:CH2	2.11	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:73:VAL:HG21	1:B:78:ILE:CD1	2.05	0.86
1:B:320:GLU:HG2	5:B:389:HOH:O	1.76	0.85
1:A:213:LEU:HG	1:A:213:LEU:CD1	2.05	0.84
1:B:137[A]:MET:HE1	1:B:218:LEU:CD1	2.08	0.84
1:B:73:VAL:CG2	1:B:78:ILE:CD1	2.56	0.83
1:A:57:ILE:C	1:A:57:ILE:HD12	1.99	0.81
1:B:121:PHE:CD1	1:B:164:ILE:HD12	2.16	0.80
1:B:137[B]:MET:HE2	1:B:140:ILE:HD12	1.64	0.78
1:B:73:VAL:HG13	1:B:78:ILE:HD11	1.59	0.78
1:B:137[B]:MET:CE	1:B:140:ILE:HD12	2.15	0.77
1:B:73:VAL:HG21	1:B:78:ILE:HD13	1.66	0.76
1:A:279:LYS:O	5:A:484:HOH:O	2.05	0.75
1:A:70:LEU:HD12	1:A:78:ILE:HD12	1.68	0.75
1:A:265:LEU:HD12	5:A:490:HOH:O	1.87	0.75
1:B:121:PHE:CE1	1:B:164:ILE:HD12	2.22	0.74
1:A:72:PRO:C	1:A:73:VAL:HG12	2.07	0.74
1:A:70:LEU:CD1	1:A:78:ILE:CD1	2.65	0.74
1:A:70:LEU:HD21	1:A:111:LEU:HD12	1.71	0.73
1:A:196:TYR:CD2	5:A:430:HOH:O	2.40	0.73
1:A:36:GLN:NE2	1:A:104:PRO:HG3	2.02	0.73
1:A:106:SER:OG	1:A:108:THR:HG23	1.88	0.73
1:B:73:VAL:HG11	1:B:78:ILE:HD12	1.67	0.73
1:B:148:HIS:HE1	1:B:214:ASP:OD2	1.71	0.71
1:A:21[B]:ARG:HH11	1:A:21[B]:ARG:HG2	1.56	0.71
1:A:70:LEU:HD12	1:A:78:ILE:CD1	2.21	0.70
1:A:116:VAL:HG12	1:A:117:ASN:H	1.55	0.70
1:B:324:PHE:O	1:B:328[A]:VAL:HG23	1.92	0.70
1:B:169:ARG:HD2	5:B:458:HOH:O	1.92	0.69
1:B:121:PHE:CE1	1:B:164:ILE:CD1	2.76	0.69
1:B:118:ASN:ND2	3:B:339:ANP:H1'	2.07	0.69
1:B:249:LEU:HD22	1:B:278:ARG:HH12	1.58	0.69
1:B:117:ASN:HD22	1:B:118:ASN:N	1.91	0.68
1:B:37:ASP:O	1:B:59:ILE:HD11	1.92	0.68
3:A:339:ANP:N7	5:A:503:HOH:O	2.26	0.68
1:B:125:TYR:HA	1:B:128:LEU:HG	1.76	0.67
1:B:121:PHE:CD1	1:B:164:ILE:CD1	2.76	0.67
1:A:121:PHE:HE1	1:A:128:LEU:HD11	1.59	0.67
1:A:128:LEU:HA	5:A:603:HOH:O	1.94	0.67
1:B:118:ASN:HD21	3:B:339:ANP:H1'	1.61	0.66
1:A:136:TYR:OH	1:A:166:HIS:HD2	1.77	0.66
1:A:71:LYS:O	1:A:73:VAL:HG12	1.95	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:119:THR:HG21	5:A:524:HOH:O	1.95	0.65
1:A:123:GLN:O	5:A:541:HOH:O	2.15	0.64
1:A:121:PHE:HE1	1:A:128:LEU:CD1	2.10	0.64
1:A:94:ILE:O	5:A:346:HOH:O	2.15	0.63
1:B:313:LEU:HD23	5:B:559:HOH:O	1.98	0.63
1:A:41:LEU:HG	4:A:340:GOL:H2	1.81	0.63
1:A:118:ASN:HA	3:A:339:ANP:O2'	2.00	0.62
1:A:21[B]:ARG:NH1	1:A:21[B]:ARG:HG2	2.12	0.62
1:A:61:ASN:O	1:B:32:GLU:HG2	2.00	0.61
1:B:117:ASN:HB3	1:B:165:ASP:HB2	1.81	0.61
1:A:116:VAL:HG12	1:A:117:ASN:N	2.15	0.61
1:A:119:THR:CG2	1:A:164:ILE:O	2.48	0.61
1:A:70:LEU:CD1	1:A:78:ILE:HD12	2.30	0.61
1:B:136:TYR:OH	1:B:166:HIS:HD2	1.84	0.61
1:A:70:LEU:HD13	1:A:78:ILE:CD1	2.30	0.60
1:A:57:ILE:CD1	1:A:57:ILE:C	2.69	0.60
1:A:238:ASN:ND2	5:A:448:HOH:O	2.08	0.60
1:B:277:SER:O	1:B:279:LYS:NZ	2.32	0.59
1:B:118:ASN:ND2	3:B:339:ANP:O2'	2.35	0.59
1:B:116:VAL:HG12	1:B:117:ASN:O	2.04	0.58
1:A:70:LEU:CD1	1:A:78:ILE:HD11	2.34	0.58
1:A:198:LYS:HD3	5:A:526:HOH:O	2.03	0.58
1:B:159:PRO:HD3	1:B:221[B]:MET:HE2	1.85	0.58
1:B:73:VAL:CG1	1:B:78:ILE:CG1	2.82	0.57
1:B:191:ARG:HG2	5:B:511:HOH:O	2.03	0.57
1:B:56:ALA:HB3	1:B:65:VAL:HG23	1.86	0.57
1:B:137[A]:MET:SD	1:B:225:MET:HE1	2.44	0.57
1:B:70:LEU:CD2	1:B:70:LEU:N	2.63	0.57
1:B:8:ARG:NH1	5:B:531:HOH:O	2.33	0.56
1:A:117:ASN:HB3	1:A:119:THR:HG22	1.87	0.56
1:A:128:LEU:HD22	1:A:132:ASP:HB3	1.88	0.56
1:A:119:THR:HA	1:A:123:GLN:OE1	2.06	0.56
1:B:189:ASN:HD21	1:B:191:ARG:HD3	1.70	0.56
1:B:73:VAL:HG13	1:B:78:ILE:CG1	2.37	0.55
1:A:159:PRO:HD2	2:A:338:CL:CL	2.43	0.55
1:A:121:PHE:CE1	1:A:128:LEU:HD11	2.41	0.55
1:A:77:LYS:HE2	1:A:177:GLY:O	2.07	0.55
1:A:117:ASN:CB	1:A:119:THR:HG22	2.37	0.55
1:A:70:LEU:HD13	1:A:78:ILE:HD11	1.89	0.55
1:A:193:ALA:CB	5:A:547:HOH:O	2.54	0.54
1:A:36:GLN:NE2	1:A:104:PRO:HD3	2.23	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:249:LEU:HD21	1:A:281:TRP:CZ2	2.41	0.54
1:B:89:ARG:HD2	1:B:97:LEU:O	2.06	0.54
1:A:120:ASP:OD1	1:A:123:GLN:HG3	2.07	0.54
1:B:61:ASN:OD1	1:B:63:GLU:HB2	2.06	0.54
1:A:193:ALA:HB2	5:A:547:HOH:O	2.06	0.54
1:A:293:VAL:HG13	1:A:298:LEU:HD21	1.89	0.54
1:A:68:LYS:HE2	1:A:70:LEU:CD2	2.37	0.54
1:B:158:LYS:C	1:B:221[B]:MET:HE1	2.28	0.54
1:A:125:TYR:CD2	1:A:125:TYR:C	2.81	0.54
1:B:10:ARG:HG2	5:B:547:HOH:O	2.08	0.53
1:A:84:ILE:HG23	1:A:152:ILE:HD13	1.90	0.53
1:B:117:ASN:ND2	1:B:117:ASN:C	2.48	0.53
1:A:213:LEU:HD11	5:A:547:HOH:O	2.09	0.53
1:A:29:HIS:HD2	5:A:413:HOH:O	1.91	0.53
1:B:178:LEU:HD22	1:B:192:VAL:HG12	1.90	0.53
1:A:213:LEU:CD2	1:A:213:LEU:CD1	2.80	0.53
1:B:148:HIS:HD2	2:B:336:CL:CL	2.30	0.52
1:B:34:GLY:N	5:B:539:HOH:O	2.41	0.52
1:A:240:ASP:O	1:A:244:ARG:HG2	2.09	0.52
1:A:29:HIS:HE1	5:A:384:HOH:O	1.93	0.52
1:B:239:TYR:OH	5:B:428:HOH:O	2.18	0.52
1:A:57:ILE:CD1	1:A:59:ILE:HG22	2.40	0.51
1:B:137[A]:MET:HE3	1:B:218:LEU:HD11	1.90	0.51
1:B:155:ARG:CZ	1:B:192:VAL:HG11	2.40	0.51
1:B:320:GLU:OE1	5:B:389:HOH:O	2.19	0.51
1:A:104:PRO:HD2	4:A:340:GOL:H32	1.93	0.51
1:B:251:THR:HB	1:B:255:TYR:CE2	2.45	0.51
1:B:116:VAL:O	1:B:117:ASN:C	2.47	0.51
1:A:120:ASP:H	1:A:123:GLN:CD	2.14	0.51
1:B:192:VAL:O	1:B:198:LYS:NZ	2.38	0.51
2:B:338:CL:CL	5:B:553:HOH:O	2.55	0.51
1:A:92:PRO:HD2	1:A:146:TYR:CG	2.46	0.51
1:A:72:PRO:C	1:A:73:VAL:CG1	2.76	0.50
1:B:159:PRO:CD	1:B:221[B]:MET:HE2	2.40	0.50
1:A:190:VAL:HB	1:A:202:LEU:HB3	1.92	0.50
1:B:73:VAL:CG2	1:B:78:ILE:HD13	2.32	0.50
1:B:257:TYR:HA	5:B:412:HOH:O	2.09	0.50
1:A:189:ASN:OD1	1:A:191:ARG:N	2.22	0.50
1:A:51:SER:OG	3:A:339:ANP:N3B	2.44	0.50
1:A:72:PRO:O	1:A:73:VAL:HB	2.12	0.50
1:A:248:VAL:HG13	1:A:284:PHE:CZ	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:320:GLU:CG	5:B:389:HOH:O	2.44	0.50
1:A:36:GLN:NE2	1:A:104:PRO:CG	2.74	0.49
1:B:137[B]:MET:HE3	1:B:140:ILE:HD12	1.94	0.49
1:A:29:HIS:CE1	5:A:384:HOH:O	2.65	0.49
1:B:117:ASN:HB3	1:B:165:ASP:CB	2.42	0.49
1:B:44:LYS:HD3	1:B:54:PHE:CE2	2.48	0.49
1:A:118:ASN:ND2	5:A:513:HOH:O	2.30	0.48
1:B:257:TYR:CE1	1:B:308:ASP:HA	2.48	0.48
1:B:135:PHE:HA	1:B:327:VAL:HG21	1.95	0.48
1:A:72:PRO:O	1:A:73:VAL:CB	2.60	0.48
1:B:121:PHE:CE1	1:B:164:ILE:HD11	2.47	0.48
1:A:98:ALA:HB2	5:A:502:HOH:O	2.13	0.48
1:B:217:SER:O	1:B:221[A]:MET:HG3	2.13	0.48
1:B:189:ASN:OD1	1:B:191:ARG:HG3	2.12	0.48
1:B:69:ILE:C	1:B:70:LEU:HD23	2.33	0.48
1:B:117:ASN:ND2	1:B:118:ASN:N	2.62	0.47
1:B:95:ILE:HB	1:B:174:ILE:HG22	1.96	0.47
1:A:97:LEU:HD21	1:A:100:ILE:HD11	1.96	0.47
1:A:103:ASP:OD2	4:A:340:GOL:H32	2.14	0.47
1:A:36:GLN:HE22	1:A:104:PRO:CG	2.16	0.47
1:A:200:PRO:O	1:A:204:VAL:HG22	2.15	0.47
3:B:339:ANP:H3'	3:B:339:ANP:O1A	2.14	0.47
1:A:153:MET:HG2	1:A:211:TYR:HA	1.96	0.47
1:A:168:HIS:HA	1:A:334:MET:SD	2.55	0.47
1:B:313:LEU:CD2	5:B:559:HOH:O	2.60	0.46
1:B:321:HIS:CG	1:B:322:PRO:HD2	2.50	0.46
1:A:77:LYS:CE	1:A:177:GLY:O	2.63	0.46
1:B:200:PRO:HD3	1:B:216:TRP:CE2	2.49	0.46
1:A:117:ASN:C	1:A:119:THR:H	2.19	0.46
1:B:121:PHE:HD1	1:B:164:ILE:HD12	1.72	0.46
1:A:68:LYS:NZ	3:A:339:ANP:O1G	2.44	0.46
1:A:53:VAL:HG21	3:A:339:ANP:O4'	2.16	0.46
1:A:239:TYR:HB3	1:A:269:PHE:CE2	2.51	0.46
1:B:249:LEU:HD22	1:B:278:ARG:NH1	2.27	0.46
1:B:117:ASN:ND2	1:B:119:THR:HB	2.31	0.45
1:A:121:PHE:HA	1:A:164:ILE:HD12	1.98	0.45
1:B:20:PRO:HB2	1:B:22:GLU:HG2	1.98	0.45
1:B:38:ASP:O	1:B:59:ILE:HG12	2.15	0.45
1:A:8:ARG:NH2	1:A:14:ASP:OD1	2.49	0.45
1:B:122:LYS:HB2	1:B:159:PRO:HB2	1.98	0.45
1:A:249:LEU:CD2	1:A:281:TRP:CZ2	2.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:116:VAL:CG1	1:A:117:ASN:N	2.80	0.45
1:A:78:ILE:HD12	1:A:78:ILE:HG23	1.74	0.45
1:B:137[B]:MET:HE2	1:B:140:ILE:CD1	2.42	0.44
1:B:169:ARG:HG3	1:B:334:MET:CE	2.47	0.44
1:A:189:ASN:OD1	1:A:190:VAL:N	2.50	0.44
1:A:316:ARG:HD2	1:B:328[A]:VAL:HG12	1.98	0.44
1:A:287:SER:HA	1:A:290:GLN:HG2	1.99	0.44
1:B:280:ARG:HG2	5:B:563:HOH:O	2.17	0.44
1:A:161:ASN:OD1	1:A:175:ASP:OD1	2.35	0.44
5:A:532:HOH:O	1:B:92:PRO:HA	2.18	0.44
1:B:320:GLU:CD	5:B:389:HOH:O	2.56	0.44
1:B:25:ASP:OD2	1:B:28:SER:HB3	2.18	0.44
1:A:212:SER:OG	1:A:309:HIS:HB2	2.18	0.44
1:B:40:GLN:HG3	1:B:59:ILE:HD13	2.00	0.43
1:A:198:LYS:HG2	1:A:202:LEU:HD12	1.99	0.43
1:A:183:HIS:CD2	1:A:186:GLN:HE22	2.36	0.43
1:A:275:ARG:HD3	5:A:497:HOH:O	2.18	0.43
1:B:281:TRP:CG	1:B:298:LEU:HD22	2.53	0.43
1:A:122:LYS:HB2	1:A:159:PRO:HB2	1.99	0.43
1:A:302:ASP:HB2	5:A:440:HOH:O	2.18	0.43
1:B:321:HIS:CE1	1:B:322:PRO:HD2	2.53	0.43
1:A:194:SER:O	1:A:195:ARG:C	2.55	0.43
1:B:49:LYS:HB3	1:B:50:TYR:CE2	2.53	0.43
1:A:36:GLN:HE21	1:A:36:GLN:HB2	1.61	0.43
1:A:5:VAL:HB	1:A:261:TYR:HA	2.00	0.43
1:A:248:VAL:HG13	1:A:284:PHE:HZ	1.83	0.43
1:B:223:ALA:HB2	1:B:301:LEU:HD11	2.00	0.43
1:A:230:GLU:HA	1:A:231:PRO:HA	1.93	0.43
1:A:119:THR:CA	1:A:123:GLN:OE1	2.67	0.42
1:B:74:LYS:O	1:B:75:LYS:C	2.57	0.42
1:B:103:ASP:OD2	1:B:106:SER:N	2.52	0.42
1:B:190:VAL:HG21	1:B:205:ASP:OD2	2.18	0.42
1:B:103:ASP:OD2	1:B:105:VAL:N	2.50	0.42
1:B:233:PHE:CE1	1:B:245:ILE:HA	2.55	0.42
1:B:89:ARG:CD	1:B:97:LEU:O	2.68	0.42
1:A:78:ILE:HA	1:A:78:ILE:HD13	1.69	0.41
1:B:118:ASN:O	3:B:339:ANP:O2'	2.24	0.41
1:A:49:LYS:C	1:A:50:TYR:CD2	2.94	0.41
1:B:137[A]:MET:SD	1:B:225:MET:CE	3.08	0.41
1:B:128:LEU:CD2	1:B:166:HIS:CE1	3.03	0.41
1:B:257:TYR:HB2	5:B:416:HOH:O	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:32:GLU:O	5:B:539:HOH:O	2.22	0.41
1:B:120:ASP:OD2	1:B:160:HIS:ND1	2.51	0.41
1:A:39:TYR:OH	1:A:99:ASP:OD1	2.31	0.41
1:B:310:GLN:HE21	1:B:310:GLN:HB3	1.60	0.41
1:A:213:LEU:O	1:A:213:LEU:HD12	2.21	0.41
1:B:39:TYR:HA	1:B:57:ILE:O	2.21	0.41
1:B:137[B]:MET:CE	1:B:140:ILE:CD1	2.94	0.41
1:B:169:ARG:CD	5:B:458:HOH:O	2.63	0.41
1:A:275:ARG:CD	5:A:497:HOH:O	2.69	0.41
1:A:75:LYS:O	1:A:79:LYS:HG3	2.20	0.41
1:B:199:GLY:HA2	1:B:216:TRP:CD1	2.56	0.40
1:A:260:LYS:HD2	1:A:261:TYR:CE2	2.55	0.40
1:A:282:GLU:CD	1:A:282:GLU:H	2.23	0.40
1:A:124:LEU:HD11	1:A:164:ILE:CD1	2.51	0.40
1:A:68:LYS:HG2	1:A:70:LEU:HD23	2.04	0.40
1:B:328[A]:VAL:HG21	5:B:418:HOH:O	2.20	0.40
1:A:280:ARG:CB	5:A:500:HOH:O	2.68	0.40
1:A:21[B]:ARG:CG	1:A:21[B]:ARG:HH11	2.26	0.40
1:A:92:PRO:HD2	1:A:146:TYR:CD1	2.56	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:40:GLN:NE2	1:B:335:GLY:O[4_365]	2.11	0.09

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	337/335 (101%)	324 (96%)	10 (3%)	3 (1%)	21 4

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	B	337/335 (101%)	321 (95%)	15 (4%)	1 (0%)	46 24
All	All	674/670 (101%)	645 (96%)	25 (4%)	4 (1%)	30 9

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	73	VAL
1	A	118	ASN
1	B	193	ALA
1	A	125	TYR

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	310/306 (101%)	288 (93%)	22 (7%)	18 3
1	B	310/306 (101%)	291 (94%)	19 (6%)	23 4
All	All	620/612 (101%)	579 (93%)	41 (7%)	20 4

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	SER
1	A	6	PRO
1	A	10	ARG
1	A	11	VAL
1	A	22	GLU
1	A	36	GLN
1	A	49	LYS
1	A	64	LYS
1	A	99	ASP
1	A	118	ASN
1	A	120	ASP
1	A	121	PHE

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Mol	Chain	Res	Type
1	A	124	LEU
1	A	125	TYR
1	A	126	GLN
1	A	180	GLU
1	A	252	GLU
1	A	270	ASN
1	A	275	ARG
1	A	290	GLN
1	A	327	VAL
1	A	328	VAL
1	B	21	ARG
1	B	44	LYS
1	B	50	TYR
1	B	52	GLU
1	B	59	ILE
1	B	70	LEU
1	B	103	ASP
1	B	117	ASN
1	B	125	TYR
1	B	126	GLN
1	B	180	GLU
1	B	228	ARG
1	B	244	ARG
1	B	256	ASP
1	B	262	ASN
1	B	269	PHE
1	B	275	ARG
1	B	280	ARG
1	B	290	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	29	HIS
1	A	35	ASN
1	A	36	GLN
1	A	166	HIS
1	A	186	GLN
1	A	207	GLN
1	A	262	ASN
1	A	290	GLN
1	B	29	HIS

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Mol	Chain	Res	Type
1	B	36	GLN
1	B	117	ASN
1	B	118	ASN
1	B	148	HIS
1	B	166	HIS
1	B	234	HIS
1	B	262	ASN
1	B	270	ASN
1	B	286	HIS
1	B	310	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 10 ligands modelled in this entry, 6 are monoatomic - leaving 4 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
3	ANP	A	339	-	27,33,33	2.41	6 (22%)	30,52,52	3.20	13 (43%)
4	GOL	A	340	-	5,5,5	1.35	0	5,5,5	1.78	2 (40%)
3	ANP	B	339	-	27,33,33	2.85	7 (25%)	30,52,52	2.20	9 (30%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	GOL	B	340	-	5,5,5	0.64	0	5,5,5	1.39	1 (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
3	ANP	A	339	-	-	0/12/38/38	0/3/3/3
4	GOL	A	340	-	-	0/4/4/4	0/0/0/0
3	ANP	B	339	-	-	0/12/38/38	0/3/3/3
4	GOL	B	340	-	-	0/4/4/4	0/0/0/0

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	339	ANP	C2-N3	2.15	1.36	1.32
3	B	339	ANP	C2-N3	2.50	1.36	1.32
3	A	339	ANP	C5-C4	2.63	1.46	1.40
3	B	339	ANP	C5-C4	3.40	1.48	1.40
3	B	339	ANP	PG-N3B	4.70	1.75	1.63
3	A	339	ANP	PG-N3B	5.14	1.76	1.63
3	A	339	ANP	PG-O1G	5.26	1.52	1.46
3	B	339	ANP	PB-N3B	5.48	1.77	1.63
3	B	339	ANP	PB-O3A	5.99	1.66	1.59
3	A	339	ANP	PB-N3B	6.18	1.79	1.63
3	A	339	ANP	PB-O1B	6.28	1.53	1.46
3	B	339	ANP	PB-O1B	6.62	1.53	1.46
3	B	339	ANP	PG-O1G	7.06	1.54	1.46

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	339	ANP	N3-C2-N1	-8.38	122.48	128.89
3	B	339	ANP	N3-C2-N1	-8.13	122.67	128.89
3	A	339	ANP	O1G-PG-N3B	-8.12	99.44	111.90
3	A	339	ANP	C1'-N9-C4	-7.77	115.23	126.94
3	A	339	ANP	C4'-O4'-C1'	-4.54	104.73	109.72
3	A	339	ANP	C2'-C1'-N9	-3.68	108.67	114.29
3	B	339	ANP	O1B-PB-N3B	-2.60	107.91	111.90
3	A	339	ANP	PA-O3A-PB	-2.48	124.34	132.67
3	A	339	ANP	O4'-C4'-C5'	-2.48	100.47	109.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	339	ANP	C4-C5-N7	-2.40	107.27	109.48
4	A	340	GOL	O1-C1-C2	-2.31	98.99	110.18
3	A	339	ANP	O1B-PB-N3B	-2.20	108.52	111.90
3	B	339	ANP	C1'-N9-C4	-2.20	123.63	126.94
4	B	340	GOL	O3-C3-C2	2.01	119.91	110.18
3	B	339	ANP	O4'-C1'-N9	2.07	112.43	108.10
3	A	339	ANP	O3G-PG-O2G	2.09	113.77	107.58
3	B	339	ANP	C4'-O4'-C1'	2.19	112.12	109.72
3	B	339	ANP	O3A-PB-N3B	2.24	112.59	106.44
3	B	339	ANP	O3A-PA-O5'	2.25	108.92	102.94
3	A	339	ANP	N6-C6-N1	2.33	124.21	119.20
4	A	340	GOL	C3-C2-C1	2.35	120.35	111.12
3	A	339	ANP	O4'-C4'-C3'	2.37	109.92	105.15
3	B	339	ANP	O2B-PB-O1B	2.84	115.93	110.00
3	B	339	ANP	O3G-PG-O2G	3.73	118.63	107.58
3	A	339	ANP	O4'-C1'-N9	4.18	116.85	108.10

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	339	ANP	5	0
4	A	340	GOL	3	0
3	B	339	ANP	5	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th 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 ²)	Q<0.9
1	A	334/335 (99%)	-0.02	3 (0%) 85 87	14, 25, 39, 51	0
1	B	334/335 (99%)	0.01	3 (0%) 85 87	15, 25, 43, 52	0
All	All	668/670 (99%)	-0.01	6 (0%) 85 87	14, 25, 41, 52	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	50	TYR	4.6
1	B	50	TYR	3.9
1	B	335	GLY	3.8
1	A	335	GLY	2.6
1	B	192	VAL	2.3
1	A	121	PHE	2.1

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. 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, 95th 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(\AA^2)	Q<0.9
3	ANP	B	339	31/31	0.76	0.20	2.14	44,48,55,57	0
3	ANP	A	339	31/31	0.86	0.18	1.63	39,46,51,52	0
4	GOL	B	340	6/6	0.86	0.11	0.04	18,22,27,28	0
4	GOL	A	340	6/6	0.91	0.10	-0.21	18,20,21,24	0
2	CL	A	336	1/1	0.99	0.04	-3.61	16,16,16,16	0
2	CL	B	336	1/1	1.00	0.03	-4.23	17,17,17,17	0
2	CL	B	338	1/1	0.99	0.02	-4.32	26,26,26,26	0
2	CL	A	338	1/1	0.99	0.02	-	27,27,27,27	0
2	CL	A	337	1/1	0.99	0.10	-	30,30,30,30	0
2	CL	B	337	1/1	0.99	0.06	-	26,26,26,26	0

6.5 Other polymers [i](#)

There are no such residues in this entry.