Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 04:26 PM GMT

PDB ID	:	4F1T
Title	:	Crystal Structure of the Roco4 Kinase Domain from D. discoideum bound to the ROCK Inhibitor H1152
Authors	:	Gilsbach, B.K.; Vetter, I.R.; Wittinghofer, A.; Kortholt, A.
Deposited on	:	2012-05-07
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
A user guide is available at
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

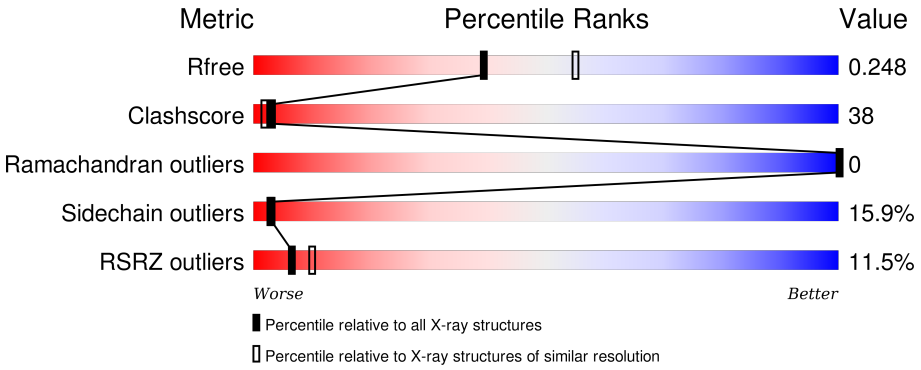
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

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}	91344	3852 (2.30-2.30)
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (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 >=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 <=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	287	11% 63% 22% 8% 6%

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
2	H52	A	1301	-	-	X	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	H52	A	1302	-	-	X	X

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2263 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.

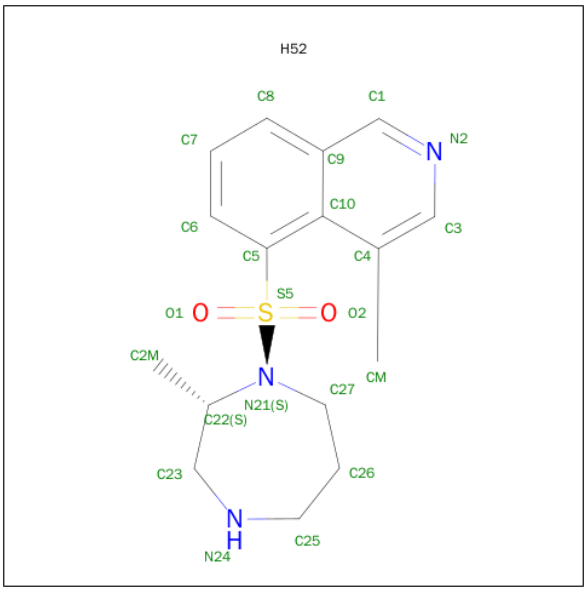
- Molecule 1 is a protein called Serine/threonine-protein kinase roco4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	269	Total	C	N	O	S	0	1	0
			2165	1392	363	395	15			

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1006	GLY	-	EXPRESSION TAG	UNP Q6XHB2
A	1007	ALA	-	EXPRESSION TAG	UNP Q6XHB2
A	1008	MET	-	EXPRESSION TAG	UNP Q6XHB2
A	1009	GLY	-	EXPRESSION TAG	UNP Q6XHB2
A	1010	GLY	-	EXPRESSION TAG	UNP Q6XHB2
A	1011	SER	-	EXPRESSION TAG	UNP Q6XHB2
A	1012	GLU	-	EXPRESSION TAG	UNP Q6XHB2
A	1013	PHE	-	EXPRESSION TAG	UNP Q6XHB2
A	1014	PRO	-	EXPRESSION TAG	UNP Q6XHB2
A	1015	LYS	-	EXPRESSION TAG	UNP Q6XHB2
A	1016	SER	-	EXPRESSION TAG	UNP Q6XHB2
A	1017	ARG	-	EXPRESSION TAG	UNP Q6XHB2
A	1018	LEU	-	EXPRESSION TAG	UNP Q6XHB2

- Molecule 2 is (S)-2-METHYL-1-[(4-METHYL-5-ISOQUINOLINE)SULFONYL]-HOMOPIPERAZINE (three-letter code: H52) (formula: $C_{16}H_{21}N_3O_2S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			22	16	3	2	1		
2	A	1	Total	C	N	O	S	0	0
			22	16	3	2	1		

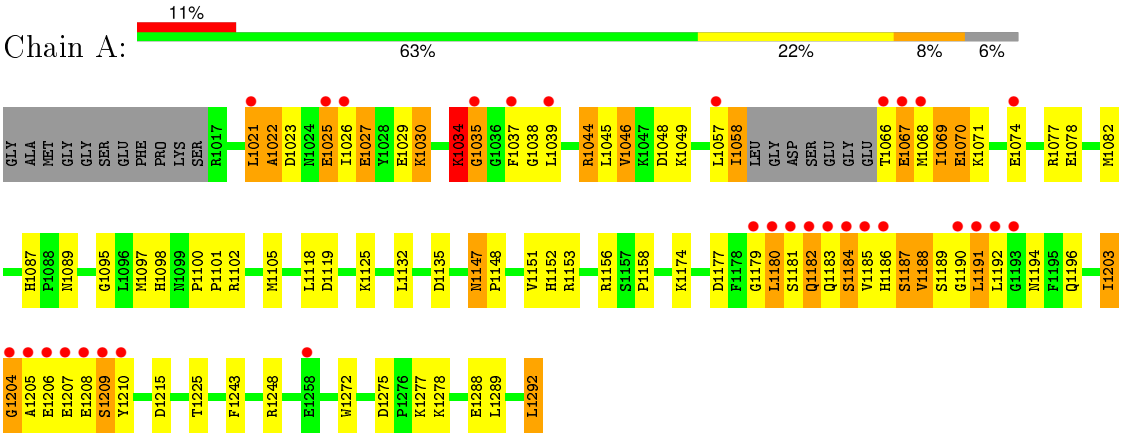
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	54	Total	O	0	0
			54	54		

3 Residue-property plots (i)

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: Serine/threonine-protein kinase roco4



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	43.28Å 43.28Å 352.52Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.00 – 2.30 42.03 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.9 (42.00-2.30) 99.9 (42.03-2.30)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.81 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.6.0093	Depositor
R, R_{free}	0.197 , 0.234 0.217 , 0.248	Depositor DCC
R_{free} test set	804 reflections (5.24%)	DCC
Wilson B-factor (Å^2)	34.0	Xtriage
Anisotropy	0.047	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 54.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Outliers	0 of 16247 reflections	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	2263	wwPDB-VP
Average B, all atoms (Å^2)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.22% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: H52

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	1.25	1/2220 (0.0%)	1.03	8/2999 (0.3%)

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	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1288	GLU	CD-OE1	-5.84	1.19	1.25

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	1187	SER	CB-CA-C	-11.94	87.41	110.10
1	A	1183	GLN	CB-CA-C	11.55	133.50	110.40
1	A	1275	ASP	CB-CG-OD1	6.62	124.26	118.30
1	A	1135	ASP	CB-CG-OD1	5.74	123.46	118.30
1	A	1204	GLY	N-CA-C	-5.60	99.09	113.10
1	A	1035	GLY	N-CA-C	5.39	126.58	113.10
1	A	1215	ASP	CB-CG-OD1	5.16	122.94	118.30
1	A	1119	ASP	CB-CG-OD1	5.00	122.81	118.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1022	ALA	Peptide
1	A	1034	LYS	Peptide
1	A	1188	VAL	Peptide

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	2165	0	2165	143	0
2	A	44	0	42	29	0
3	A	54	0	0	0	0
All	All	2263	0	2207	168	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 38.

All (168) 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:A:1301:H52:H2M2	2:A:1301:H52:C25	1.49	1.41
1:A:1098:HIS:CE1	2:A:1302:H52:H2M1	1.55	1.38
1:A:1066:THR:CA	1:A:1069:ILE:HG13	1.52	1.38
1:A:1025:GLU:O	1:A:1046:VAL:CG1	1.69	1.36
1:A:1066:THR:N	1:A:1069:ILE:HG13	1.40	1.32
1:A:1066:THR:N	1:A:1069:ILE:CG1	1.98	1.24
2:A:1302:H52:C26	2:A:1302:H52:H2M2	1.66	1.21
2:A:1301:H52:C2M	2:A:1301:H52:H251	1.71	1.20
2:A:1302:H52:H261	2:A:1302:H52:C2M	1.62	1.18
1:A:1191:LEU:H	1:A:1191:LEU:HD23	0.99	1.16
1:A:1191:LEU:N	1:A:1191:LEU:HD23	1.61	1.14
2:A:1302:H52:H6	2:A:1302:H52:C22	1.72	1.14
1:A:1153:ARG:NH1	1:A:1182:GLN:HG3	1.63	1.13
1:A:1025:GLU:O	1:A:1046:VAL:HG12	1.32	1.11
1:A:1029:GLU:C	1:A:1030:LYS:HD2	1.72	1.10
2:A:1301:H52:H6	2:A:1301:H52:H22	1.11	1.10
1:A:1153:ARG:NH1	1:A:1182:GLN:HB2	1.67	1.10
1:A:1066:THR:N	1:A:1069:ILE:CD1	2.16	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1098:HIS:HE1	2:A:1302:H52:C2M	1.66	1.08
1:A:1034:LYS:O	1:A:1038:GLY:O	1.76	1.04
1:A:1025:GLU:O	1:A:1046:VAL:HG13	1.57	1.02
2:A:1302:H52:H22	2:A:1302:H52:C6	1.90	1.01
2:A:1301:H52:H6	2:A:1301:H52:C22	1.92	1.00
2:A:1302:H52:H22	2:A:1302:H52:H6	1.01	1.00
1:A:1021:LEU:O	1:A:1097:MET:HG2	1.62	1.00
1:A:1153:ARG:HH12	1:A:1182:GLN:HB2	1.20	1.00
1:A:1077:ARG:NH2	1:A:1179:GLY:O	1.97	0.98
2:A:1301:H52:H22	2:A:1301:H52:C6	1.95	0.96
1:A:1153:ARG:NH1	1:A:1182:GLN:CG	2.28	0.96
1:A:1066:THR:C	1:A:1069:ILE:HG13	1.87	0.94
1:A:1153:ARG:NH1	1:A:1182:GLN:CB	2.30	0.94
1:A:1098:HIS:HE1	2:A:1302:H52:H2M1	0.77	0.93
1:A:1044:ARG:HG3	1:A:1045:LEU:N	1.84	0.93
1:A:1191:LEU:N	1:A:1191:LEU:CD2	2.30	0.92
1:A:1098:HIS:CE1	2:A:1302:H52:C2M	2.45	0.91
1:A:1087:HIS:HD2	1:A:1089:ASN:H	1.15	0.91
1:A:1066:THR:N	1:A:1069:ILE:HD11	1.84	0.91
2:A:1301:H52:O2	2:A:1301:H52:HM2	1.71	0.90
1:A:1185:VAL:O	1:A:1185:VAL:HG12	1.69	0.90
1:A:1067:GLU:H	1:A:1067:GLU:CD	1.62	0.90
1:A:1153:ARG:CZ	1:A:1182:GLN:HG3	2.02	0.89
1:A:1153:ARG:HH12	1:A:1182:GLN:CB	1.86	0.89
1:A:1066:THR:CA	1:A:1069:ILE:CG1	2.44	0.88
1:A:1207:GLU:HG2	1:A:1208:GLU:N	1.85	0.88
1:A:1207:GLU:HG2	1:A:1208:GLU:H	1.38	0.86
1:A:1187:SER:O	1:A:1210:TYR:HD1	1.58	0.86
1:A:1034:LYS:CG	1:A:1035:GLY:HA2	2.06	0.86
1:A:1067:GLU:CD	1:A:1067:GLU:N	2.29	0.85
1:A:1021:LEU:H	1:A:1021:LEU:HD12	1.39	0.85
1:A:1029:GLU:C	1:A:1030:LYS:CD	2.43	0.85
2:A:1302:H52:HM2	2:A:1302:H52:O2	1.77	0.84
2:A:1301:H52:H2M2	2:A:1301:H52:H251	0.84	0.83
1:A:1153:ARG:HD3	1:A:1180:LEU:O	1.78	0.83
1:A:1153:ARG:NH2	1:A:1187:SER:CB	2.42	0.82
2:A:1301:H52:O2	2:A:1301:H52:CM	2.30	0.80
1:A:1153:ARG:HH22	1:A:1187:SER:HB2	1.45	0.80
1:A:1185:VAL:O	1:A:1185:VAL:CG1	2.29	0.80
1:A:1025:GLU:C	1:A:1046:VAL:CG1	2.51	0.79
1:A:1058:ILE:CG2	1:A:1058:ILE:O	2.30	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1070:GLU:CA	1:A:1070:GLU:OE2	2.29	0.78
1:A:1078:GLU:O	1:A:1082:MET:HG2	1.83	0.78
1:A:1034:LYS:HG3	1:A:1035:GLY:HA2	1.66	0.78
1:A:1070:GLU:HA	1:A:1070:GLU:OE2	1.83	0.78
1:A:1152:HIS:O	1:A:1153:ARG:HB2	1.83	0.77
1:A:1151:VAL:O	1:A:1181:SER:CB	2.32	0.77
2:A:1302:H52:H252	2:A:1302:H52:O1	1.85	0.77
1:A:1030:LYS:CD	1:A:1030:LYS:N	2.48	0.77
1:A:1021:LEU:HD12	1:A:1021:LEU:N	2.02	0.75
1:A:1034:LYS:HG3	1:A:1035:GLY:CA	2.16	0.75
1:A:1066:THR:HA	1:A:1069:ILE:HG13	1.65	0.74
1:A:1184:SER:O	1:A:1186:HIS:CE1	2.40	0.74
1:A:1021:LEU:O	1:A:1097:MET:CG	2.36	0.73
1:A:1087:HIS:CD2	1:A:1089:ASN:H	2.02	0.73
1:A:1187:SER:O	1:A:1210:TYR:CD1	2.42	0.72
1:A:1029:GLU:HB3	1:A:1030:LYS:CD	2.20	0.72
2:A:1302:H52:S5	2:A:1302:H52:H252	2.29	0.72
1:A:1029:GLU:HB3	1:A:1030:LYS:HD2	1.72	0.72
1:A:1153:ARG:NH2	1:A:1187:SER:HB2	2.04	0.71
1:A:1034:LYS:HG2	1:A:1035:GLY:HA2	1.69	0.71
2:A:1302:H52:H261	2:A:1302:H52:H2M2	0.79	0.71
1:A:1029:GLU:CB	1:A:1030:LYS:HD2	2.21	0.70
1:A:1151:VAL:O	1:A:1181:SER:HB2	1.91	0.70
1:A:1066:THR:O	1:A:1069:ILE:N	2.25	0.69
1:A:1044:ARG:HG3	1:A:1045:LEU:H	1.55	0.69
1:A:1029:GLU:CB	1:A:1030:LYS:CD	2.71	0.68
1:A:1029:GLU:HB3	1:A:1030:LYS:CE	2.24	0.67
1:A:1185:VAL:O	1:A:1186:HIS:ND1	2.27	0.67
1:A:1152:HIS:HA	1:A:1181:SER:HB3	1.76	0.67
1:A:1058:ILE:HG22	1:A:1058:ILE:O	1.95	0.66
1:A:1067:GLU:OE2	1:A:1067:GLU:N	2.29	0.65
1:A:1022:ALA:N	1:A:1025:GLU:OE2	2.28	0.65
1:A:1066:THR:OG1	1:A:1067:GLU:N	2.30	0.65
1:A:1153:ARG:NH2	1:A:1187:SER:HB3	2.12	0.65
1:A:1067:GLU:OE2	1:A:1068:MET:N	2.29	0.64
1:A:1151:VAL:O	1:A:1181:SER:HB3	1.96	0.64
1:A:1070:GLU:N	1:A:1070:GLU:OE2	2.30	0.64
1:A:1030:LYS:HD3	1:A:1030:LYS:N	2.12	0.63
2:A:1302:H52:CM	2:A:1302:H52:O2	2.47	0.62
1:A:1044:ARG:HD3	1:A:1049:LYS:O	2.00	0.61
1:A:1100:PRO:HD2	1:A:1102:ARG:HH21	1.66	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1097:MET:HB2	1:A:1102:ARG:HB2	1.83	0.60
1:A:1078:GLU:O	1:A:1082:MET:CG	2.49	0.60
2:A:1302:H52:H6	2:A:1302:H52:C23	2.30	0.60
1:A:1029:GLU:CA	1:A:1030:LYS:HD2	2.30	0.60
1:A:1153:ARG:HH22	1:A:1187:SER:CB	2.07	0.59
1:A:1044:ARG:CG	1:A:1045:LEU:N	2.64	0.59
1:A:1205:ALA:O	1:A:1206:GLU:HG2	2.03	0.59
1:A:1066:THR:OG1	1:A:1067:GLU:OE1	2.22	0.58
1:A:1208:GLU:O	1:A:1208:GLU:HG3	2.04	0.57
1:A:1021:LEU:HB3	1:A:1025:GLU:HG3	1.87	0.57
1:A:1204:GLY:O	1:A:1248:ARG:NH2	2.36	0.57
1:A:1184:SER:O	1:A:1186:HIS:NE2	2.37	0.57
1:A:1066:THR:OG1	1:A:1067:GLU:CD	2.43	0.56
1:A:1058:ILE:HG23	1:A:1058:ILE:O	2.05	0.56
2:A:1302:H52:C26	2:A:1302:H52:C2M	2.33	0.56
1:A:1021:LEU:CB	1:A:1025:GLU:HG3	2.36	0.56
1:A:1029:GLU:O	1:A:1030:LYS:HD2	2.03	0.55
1:A:1152:HIS:CA	1:A:1181:SER:HB3	2.37	0.55
1:A:1204:GLY:C	1:A:1248:ARG:HH21	2.10	0.54
1:A:1100:PRO:HB2	1:A:1101:PRO:CD	2.38	0.53
1:A:1034:LYS:CG	1:A:1035:GLY:CA	2.79	0.53
1:A:1207:GLU:CG	1:A:1208:GLU:H	2.15	0.53
2:A:1301:H52:C2M	2:A:1301:H52:C25	2.30	0.52
1:A:1206:GLU:HG3	1:A:1248:ARG:HH22	1.75	0.51
1:A:1100:PRO:HB2	1:A:1101:PRO:HD2	1.92	0.51
1:A:1156:ARG:HG3	1:A:1158:PRO:HD2	1.91	0.51
1:A:1068:MET:HG3	1:A:1068:MET:O	2.10	0.51
1:A:1184:SER:O	1:A:1186:HIS:CD2	2.65	0.50
2:A:1302:H52:S5	2:A:1302:H52:CM	2.99	0.50
1:A:1066:THR:O	1:A:1069:ILE:HG13	2.11	0.50
2:A:1301:H52:C6	2:A:1301:H52:C22	2.64	0.49
1:A:1021:LEU:HD22	1:A:1026:ILE:HD11	1.95	0.49
1:A:1097:MET:SD	1:A:1102:ARG:NH1	2.85	0.49
1:A:1066:THR:OG1	1:A:1067:GLU:HG3	2.13	0.49
1:A:1152:HIS:O	1:A:1181:SER:HB3	2.12	0.49
1:A:1048:ASP:C	1:A:1048:ASP:OD1	2.50	0.49
2:A:1302:H52:HM3	2:A:1302:H52:O1	2.13	0.48
1:A:1069:ILE:C	1:A:1070:GLU:OE2	2.51	0.48
1:A:1021:LEU:HD11	1:A:1095:GLY:HA3	1.96	0.48
1:A:1203:ILE:HG13	1:A:1204:GLY:H	1.79	0.48
1:A:1289:LEU:HA	1:A:1292:LEU:HD22	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1187:SER:O	1:A:1210:TYR:HB2	2.15	0.46
1:A:1058:ILE:HD12	1:A:1058:ILE:HA	1.72	0.46
1:A:1100:PRO:CB	1:A:1101:PRO:CD	2.93	0.46
1:A:1190:GLY:HA3	1:A:1191:LEU:HD23	1.97	0.46
1:A:1045:LEU:O	1:A:1049:LYS:N	2.49	0.46
1:A:1044:ARG:HD3	1:A:1049:LYS:C	2.36	0.46
1:A:1037:PHE:HB2	1:A:1057:LEU:HD12	1.98	0.45
1:A:1082:MET:HG2	1:A:1082:MET:H	1.53	0.45
1:A:1066:THR:HA	1:A:1069:ILE:CG1	2.34	0.45
1:A:1066:THR:O	1:A:1069:ILE:CB	2.65	0.45
1:A:1152:HIS:C	1:A:1181:SER:HB3	2.38	0.45
1:A:1077:ARG:NH2	1:A:1180:LEU:HA	2.32	0.44
1:A:1027:GLU:CD	1:A:1046:VAL:HB	2.38	0.44
1:A:1153:ARG:HH21	1:A:1187:SER:CB	2.26	0.44
1:A:1182:GLN:HB3	1:A:1182:GLN:HE21	1.54	0.43
1:A:1187:SER:OG	1:A:1188:VAL:N	2.46	0.43
2:A:1302:H52:C22	2:A:1302:H52:C6	2.58	0.43
1:A:1066:THR:OG1	1:A:1067:GLU:CG	2.67	0.43
1:A:1203:ILE:H	1:A:1203:ILE:HG12	1.71	0.43
1:A:1045:LEU:O	1:A:1049:LYS:HA	2.19	0.42
1:A:1153:ARG:HH11	1:A:1182:GLN:HB2	1.71	0.42
1:A:1034:LYS:CG	1:A:1035:GLY:N	2.82	0.42
1:A:1066:THR:C	1:A:1069:ILE:H	2.22	0.41
1:A:1147:ASN:HA	1:A:1148:PRO:HA	1.87	0.41
1:A:1207:GLU:CG	1:A:1208:GLU:N	2.64	0.41
1:A:1027:GLU:OE1	1:A:1046:VAL:CG1	2.69	0.40
1:A:1209:SER:O	1:A:1210:TYR:HB2	2.22	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	266/287 (93%)	253 (95%)	13 (5%)	0	100 100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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	240/253 (95%)	202 (84%)	38 (16%)	3 3

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1021	LEU
1	A	1023	ASP
1	A	1025	GLU
1	A	1027	GLU
1	A	1030	LYS
1	A	1034	LYS
1	A	1039	LEU
1	A	1044	ARG
1	A	1046	VAL
1	A	1058	ILE
1	A	1067	GLU
1	A	1069	ILE
1	A	1070	GLU
1	A	1071	LYS
1	A	1074	GLU
1	A	1105	MET
1	A	1118	LEU
1	A	1125	LYS
1	A	1132	LEU
1	A	1147	ASN
1	A	1174	LYS
1	A	1177	ASP
1	A	1180	LEU

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Mol	Chain	Res	Type
1	A	1182	GLN
1	A	1184	SER
1	A	1189	SER
1	A	1191	LEU
1	A	1192	LEU
1	A	1194	ASN
1	A	1196	GLN
1	A	1203	ILE
1	A	1209	SER
1	A	1225	THR
1	A	1243	PHE
1	A	1272	TRP
1	A	1277	LYS
1	A	1278	LYS
1	A	1292	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1087	HIS
1	A	1098	HIS
1	A	1182	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

2 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	H52	A	1301	-	20,24,24	4.47	9 (45%)	24,35,35	1.73	7 (29%)
2	H52	A	1302	-	20,24,24	3.94	8 (40%)	24,35,35	3.02	8 (33%)

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
2	H52	A	1301	-	-	0/12/24/24	0/2/3/3
2	H52	A	1302	-	-	0/12/24/24	0/2/3/3

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1301	H52	C5-S5	-13.31	1.56	1.77
2	A	1302	H52	C5-S5	-12.61	1.58	1.77
2	A	1301	H52	S5-N21	-11.91	1.45	1.63
2	A	1302	H52	S5-N21	-8.35	1.50	1.63
2	A	1302	H52	O1-S5	-4.17	1.38	1.43
2	A	1302	H52	C27-N21	-4.09	1.43	1.47
2	A	1302	H52	O2-S5	-3.91	1.38	1.43
2	A	1301	H52	O1-S5	-3.45	1.39	1.43
2	A	1301	H52	C27-N21	-3.29	1.44	1.47
2	A	1301	H52	O2-S5	-3.08	1.39	1.43
2	A	1301	H52	C1-C9	-2.02	1.37	1.41
2	A	1302	H52	C8-C9	-2.00	1.37	1.41
2	A	1301	H52	C10-C9	2.34	1.47	1.42
2	A	1302	H52	C4-C10	2.39	1.48	1.44
2	A	1301	H52	C4-C10	3.05	1.49	1.44
2	A	1302	H52	C5-C10	3.76	1.49	1.43
2	A	1301	H52	C5-C10	4.94	1.50	1.43

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	1302	H52	O2-S5-O1	-11.92	98.91	119.47
2	A	1301	H52	O2-S5-O1	-4.65	111.44	119.47
2	A	1302	H52	C27-C26-C25	-4.01	104.82	113.81
2	A	1302	H52	C4-C3-N2	-2.92	121.37	124.77
2	A	1301	H52	O2-S5-N21	-2.66	101.33	106.97
2	A	1301	H52	C4-C3-N2	-2.57	121.77	124.77
2	A	1302	H52	C10-C5-S5	2.04	125.24	121.83
2	A	1302	H52	C5-C10-C9	2.08	118.46	116.28
2	A	1301	H52	O1-S5-C5	2.10	112.40	107.92
2	A	1301	H52	C10-C5-S5	2.10	125.34	121.83
2	A	1302	H52	C1-C9-C10	2.25	119.46	117.39
2	A	1301	H52	C1-C9-C10	2.34	119.55	117.39
2	A	1301	H52	O2-S5-C5	2.45	113.16	107.92
2	A	1302	H52	O1-S5-C5	2.92	114.14	107.92
2	A	1302	H52	O1-S5-N21	3.39	114.18	106.97

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 29 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1301	H52	10	0
2	A	1302	H52	19	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^{th} 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	269/287 (93%)	0.39	31 (11%) 6 10	17, 33, 112, 175	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1191	LEU	12.9
1	A	1205	ALA	10.4
1	A	1190	GLY	9.9
1	A	1184	SER	8.4
1	A	1181	SER	6.5
1	A	1185	VAL	6.4
1	A	1193	GLY	5.8
1	A	1208	GLU	4.5
1	A	1035	GLY	3.9
1	A	1207	GLU	3.8
1	A	1021	LEU	3.8
1	A	1186	HIS	3.6
1	A	1068	MET	3.6
1	A	1179	GLY	3.6
1	A	1067	GLU	3.4
1	A	1183	GLN	3.4
1	A	1206	GLU	3.2
1	A	1192	LEU	3.0
1	A	1258	GLU	3.0
1	A	1039	LEU	2.7
1	A	1026	ILE	2.7
1	A	1025	GLU	2.7
1	A	1204	GLY	2.6
1	A	1182	GLN	2.6
1	A	1066	THR	2.6
1	A	1210	TYR	2.5
1	A	1180	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	1037	PHE	2.3
1	A	1209	SER	2.2
1	A	1074	GLU	2.1
1	A	1057	LEU	2.0

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

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

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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^{th} 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(Å^2)	Q<0.9
2	H52	A	1302	22/22	0.87	0.32	4.74	24,33,36,37	0
2	H52	A	1301	22/22	0.90	0.32	2.25	24,33,36,37	0

6.5 Other polymers (i)

There are no such residues in this entry.