Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:39 PM GMT

PDB ID	:	3UC4
Title	:	The crystal structure of Snf1-related kinase 2.6
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Deposited on	:	2011-10-26
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 ⓘ symbol.

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

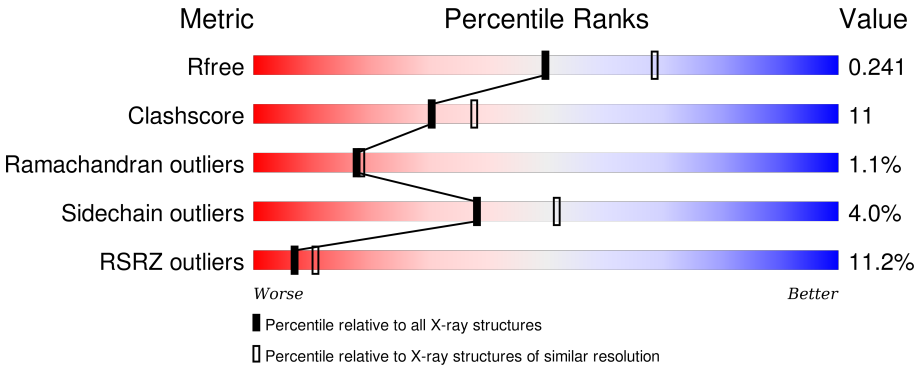
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	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	362	7% 57% 22% • 19%
1	B	362	11% 57% 18% • 23%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4711 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 SRK2E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	295	Total	C	N	O	S	0	0	0
			2369	1508	411	436	14			
1	B	277	Total	C	N	O	S	0	0	0
			2227	1426	387	401	13			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	59	ALA	ASP	ENGINEERED MUTATION	UNP Q940H6
A	60	ALA	GLU	ENGINEERED MUTATION	UNP Q940H6
B	59	ALA	ASP	ENGINEERED MUTATION	UNP Q940H6
B	60	ALA	GLU	ENGINEERED MUTATION	UNP Q940H6

- Molecule 2 is water.

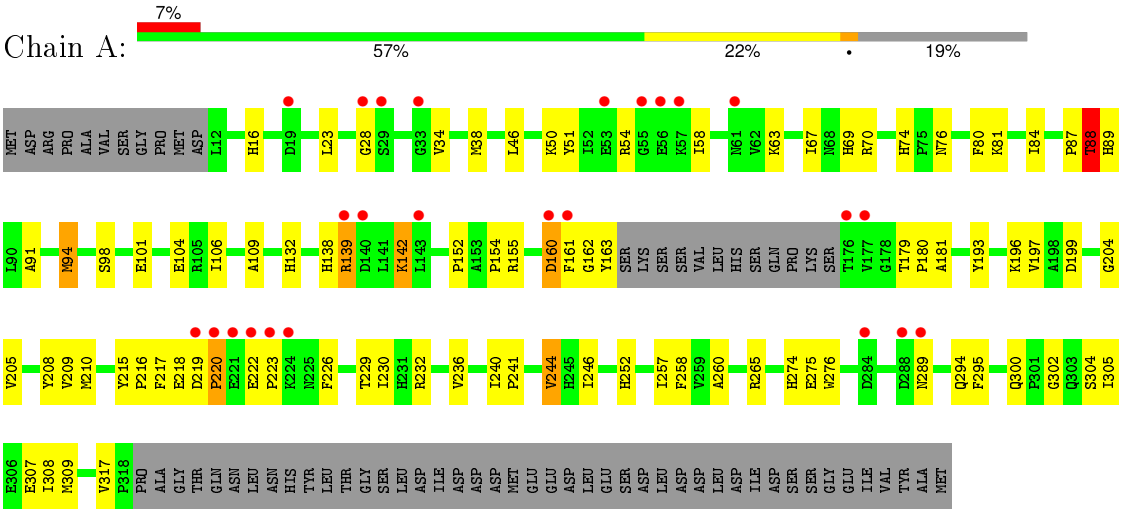
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	56	Total	O	0	0
			56	56		
2	B	59	Total	O	0	0
			59	59		

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.

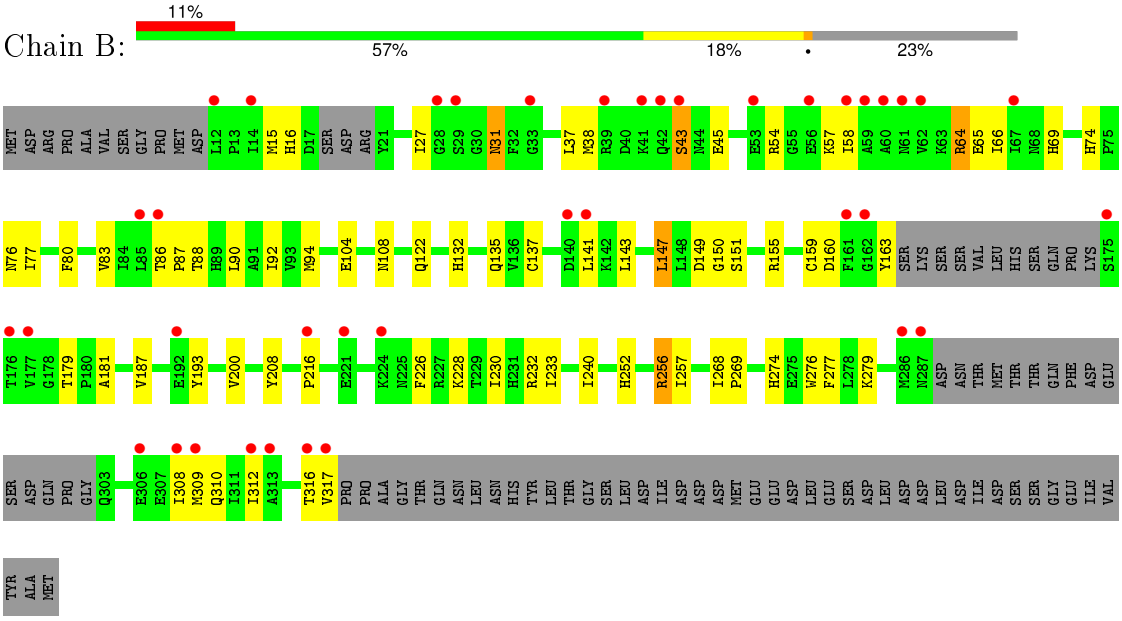
- Molecule 1: Serine/threonine-protein kinase SRK2E

Chain A:



- Molecule 1: Serine/threonine-protein kinase SRK2E

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	76.11Å 171.54Å 116.24Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.85 – 2.30 29.56 – 2.28	Depositor EDS
% Data completeness (in resolution range)	99.9 (29.85-2.30) 99.2 (29.56-2.28)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.73 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.5.0072	Depositor
R, R_{free}	0.221 , 0.246 0.221 , 0.241	Depositor DCC
R_{free} test set	2454 reflections (7.74%)	DCC
Wilson B-factor (Å^2)	36.7	Xtriage
Anisotropy	0.154	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 44.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Outliers	0 of 34808 reflections	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	4711	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 4.44% 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

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	0.57	0/2422	0.61	0/3279
1	B	0.60	0/2275	0.62	0/3075
All	All	0.59	0/4697	0.62	0/6354

There are no bond length outliers.

There are no bond angle outliers.

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	2369	0	2354	58	0
1	B	2227	0	2234	44	0
2	A	56	0	0	2	0
2	B	59	0	0	2	0
All	All	4711	0	4588	101	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 11.

All (101) 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:179:THR:HG22	1:A:181:ALA:H	1.41	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:74:HIS:HD2	1:A:76:ASN:H	1.36	0.72
1:B:86:THR:HG22	1:B:88:THR:H	1.55	0.71
1:B:27:ILE:HD13	1:B:37:LEU:HD11	1.72	0.71
1:A:28:GLY:HA2	1:A:34:VAL:HA	1.71	0.70
1:B:308:ILE:O	1:B:312:ILE:HD13	1.92	0.69
1:A:81:LYS:NZ	1:A:300:GLN:HE22	1.92	0.68
1:A:74:HIS:CD2	1:A:76:ASN:H	2.11	0.67
1:B:274:HIS:HD2	1:B:276:TRP:H	1.42	0.66
1:A:81:LYS:HZ1	1:A:300:GLN:HE22	1.45	0.64
1:B:252:HIS:ND1	1:B:274:HIS:HE1	1.96	0.62
1:A:226:PHE:O	1:A:230:ILE:HG12	2.00	0.61
1:A:180:PRO:HG2	1:A:229:THR:HG21	1.83	0.60
1:B:54:ARG:HH12	1:B:317:VAL:HB	1.67	0.59
1:A:81:LYS:NZ	1:A:300:GLN:NE2	2.51	0.59
1:A:132:HIS:HE1	1:A:199:ASP:OD2	1.85	0.59
1:B:27:ILE:CD1	1:B:37:LEU:HD11	2.33	0.58
1:A:87:PRO:O	1:A:88:THR:HG23	2.04	0.58
1:A:252:HIS:ND1	1:A:274:HIS:HE1	2.01	0.58
1:B:15:MET:HE2	1:B:16:HIS:H	1.69	0.57
1:B:274:HIS:CD2	1:B:276:TRP:H	2.21	0.57
1:A:132:HIS:HD2	2:A:415:HOH:O	1.88	0.56
1:A:138:HIS:NE2	1:A:196:LYS:NZ	2.53	0.56
1:B:58:ILE:HB	1:B:316:THR:HG22	1.88	0.55
1:A:289:ASN:HD22	1:A:295:PHE:H	1.52	0.55
1:A:305:ILE:O	1:A:309:MET:HG2	2.07	0.55
1:A:205:VAL:O	1:A:209:VAL:HG23	2.08	0.54
1:B:31:ASN:N	1:B:31:ASN:HD22	2.06	0.54
1:A:54:ARG:HH21	1:A:87:PRO:HA	1.72	0.53
1:A:179:THR:HG23	1:A:218:GLU:OE2	2.07	0.53
1:B:43:SER:HB2	1:B:45:GLU:OE1	2.07	0.53
1:A:304:SER:OG	1:A:307:GLU:HG3	2.09	0.52
1:B:69:HIS:CD2	1:B:80:PHE:HB2	2.45	0.52
1:A:67:ILE:HD11	1:A:309:MET:SD	2.50	0.51
1:A:240:ILE:HD13	1:A:246:ILE:HD12	1.92	0.51
1:A:217:PHE:O	1:A:232:ARG:HD2	2.11	0.51
1:A:152:PRO:O	1:A:154:PRO:HD3	2.11	0.50
1:B:309:MET:HE3	2:B:404:HOH:O	2.12	0.50
1:A:161:PHE:HB2	1:A:163:TYR:CE1	2.46	0.50
1:B:58:ILE:HG22	1:B:58:ILE:O	2.12	0.49
1:A:160:ASP:N	1:A:160:ASP:OD1	2.46	0.48
1:A:54:ARG:HD2	1:A:317:VAL:O	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:241:PRO:HG2	1:A:244:VAL:HG12	1.95	0.47
1:B:86:THR:HG23	1:B:87:PRO:HD2	1.96	0.47
1:A:132:HIS:HB3	1:A:196:LYS:HE3	1.95	0.47
1:A:222:GLU:HB2	1:A:223:PRO:HD3	1.95	0.47
1:A:236:VAL:HG11	1:A:258:PHE:O	2.15	0.47
1:B:187:VAL:HG22	1:B:193:TYR:CZ	2.50	0.47
1:A:209:VAL:HG21	1:A:215:TYR:CE2	2.49	0.47
1:A:240:ILE:HG21	1:A:246:ILE:HD12	1.97	0.47
1:A:236:VAL:CG2	1:A:260:ALA:HB2	2.45	0.47
1:A:139:ARG:HA	1:A:139:ARG:HH11	1.79	0.47
1:B:226:PHE:O	1:B:230:ILE:HG12	2.15	0.47
1:A:109:ALA:HB1	2:A:412:HOH:O	2.15	0.47
1:A:197:VAL:HG12	1:A:265:ARG:NH2	2.30	0.46
1:A:88:THR:HB	1:A:89:HIS:ND1	2.30	0.46
1:B:94:MET:HE1	1:B:163:TYR:CE1	2.51	0.46
1:A:142:LYS:NZ	1:A:142:LYS:HB3	2.30	0.46
1:A:241:PRO:HG2	1:A:244:VAL:CG1	2.45	0.46
1:B:64:ARG:H	1:B:64:ARG:HD3	1.79	0.46
1:A:50:LYS:CD	1:A:163:TYR:HB2	2.45	0.46
1:A:219:ASP:CG	1:A:223:PRO:HG2	2.36	0.46
1:B:122:GLN:HA	1:B:277:PHE:CE1	2.50	0.46
1:A:81:LYS:HG2	1:A:94:MET:HA	1.98	0.46
1:B:83:VAL:HG13	1:B:90:LEU:HD11	1.98	0.46
1:A:240:ILE:HG22	1:A:244:VAL:HG13	1.98	0.46
1:B:15:MET:CE	1:B:16:HIS:H	2.29	0.45
1:A:84:ILE:HB	1:A:91:ALA:HB3	1.98	0.45
1:B:228:LYS:HE2	1:B:232:ARG:NH2	2.32	0.45
1:B:92:ILE:HD13	1:B:163:TYR:CE2	2.52	0.45
1:B:135:GLN:HE22	1:B:141:LEU:HD13	1.81	0.45
1:B:149:ASP:OD1	1:B:155:ARG:HB3	2.18	0.44
1:B:74:HIS:HB3	1:B:77:ILE:HD12	1.99	0.44
1:A:208:TYR:CE2	1:A:216:PRO:HA	2.53	0.44
1:A:139:ARG:NE	1:A:193:TYR:OH	2.51	0.44
1:A:16:HIS:HE1	1:A:51:TYR:OH	2.00	0.43
1:B:147:LEU:HD22	1:B:159:CYS:SG	2.58	0.43
1:A:219:ASP:O	1:A:220:PRO:C	2.57	0.43
1:A:274:HIS:HD2	1:A:276:TRP:H	1.65	0.42
1:B:181:ALA:HA	1:B:233:ILE:HD11	2.01	0.42
1:A:98:SER:O	1:B:108:ASN:HB3	2.19	0.42
1:B:252:HIS:CD2	1:B:256:ARG:NH2	2.87	0.42
1:B:208:TYR:CE1	1:B:240:ILE:HD13	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:141:LEU:O	1:B:143:LEU:HD22	2.20	0.42
1:B:104:GLU:HB2	2:B:403:HOH:O	2.20	0.41
1:B:66:ILE:HG23	1:B:80:PHE:CE1	2.56	0.41
1:A:70:ARG:HD2	1:A:308:ILE:CD1	2.50	0.41
1:A:106:ILE:HD11	1:A:210:MET:HG2	2.01	0.41
1:B:279:LYS:HB2	1:B:279:LYS:NZ	2.36	0.41
1:B:74:HIS:CD2	1:B:76:ASN:H	2.39	0.41
1:A:101:GLU:HB2	1:A:104:GLU:HG2	2.01	0.41
1:A:204:GLY:HA3	1:A:257:ILE:HG21	2.03	0.41
1:A:63:LYS:O	1:A:67:ILE:HG12	2.21	0.41
1:B:150:GLY:O	1:B:151:SER:C	2.60	0.41
1:B:200:VAL:HG12	1:B:257:ILE:HG23	2.03	0.41
1:B:15:MET:HE1	1:B:38:MET:SD	2.61	0.40
1:B:268:ILE:N	1:B:269:PRO:HD2	2.36	0.40
1:B:208:TYR:CE2	1:B:216:PRO:HA	2.56	0.40
1:B:141:LEU:HD11	1:B:160:ASP:OD2	2.21	0.40
1:A:38:MET:O	1:A:46:LEU:HD12	2.22	0.40
1:A:69:HIS:CD2	1:A:80:PHE:HB2	2.57	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	291/362 (80%)	267 (92%)	19 (6%)	5 (2%)	11 10
1	B	269/362 (74%)	244 (91%)	24 (9%)	1 (0%)	39 48
All	All	560/724 (77%)	511 (91%)	43 (8%)	6 (1%)	17 18

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	57	LYS
1	A	88	THR
1	A	58	ILE
1	A	220	PRO
1	A	302	GLY
1	A	162	GLY

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	260/320 (81%)	250 (96%)	10 (4%)	40	54
1	B	243/320 (76%)	233 (96%)	10 (4%)	37	50
All	All	503/640 (79%)	483 (96%)	20 (4%)	38	52

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	23	LEU
1	A	88	THR
1	A	94	MET
1	A	139	ARG
1	A	142	LYS
1	A	155	ARG
1	A	160	ASP
1	A	244	VAL
1	A	275	GLU
1	A	294	GLN
1	B	31	ASN
1	B	43	SER
1	B	64	ARG
1	B	65	GLU
1	B	132	HIS
1	B	137	CYS
1	B	147	LEU
1	B	179	THR

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Mol	Chain	Res	Type
1	B	256	ARG
1	B	310	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	16	HIS
1	A	42	GLN
1	A	44	ASN
1	A	74	HIS
1	A	76	ASN
1	A	122	GLN
1	A	132	HIS
1	A	235	ASN
1	A	274	HIS
1	A	289	ASN
1	A	294	GLN
1	A	300	GLN
1	B	69	HIS
1	B	74	HIS
1	B	76	ASN
1	B	89	HIS
1	B	122	GLN
1	B	132	HIS
1	B	135	GLN
1	B	235	ASN
1	B	274	HIS

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

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	295/362 (81%)	0.45	25 (8%) 13 19	16, 44, 81, 100	0
1	B	277/362 (76%)	0.65	39 (14%) 4 6	15, 45, 111, 122	0
All	All	572/724 (79%)	0.55	64 (11%) 7 10	15, 45, 99, 122	0

All (64) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	221	GLU	7.3
1	A	176	THR	6.9
1	B	42	GLN	6.1
1	B	176	THR	6.0
1	A	220	PRO	6.0
1	A	177	VAL	5.9
1	A	29	SER	5.7
1	B	162	GLY	5.4
1	A	222	GLU	5.2
1	A	56	GLU	4.9
1	B	177	VAL	4.6
1	B	175	SER	4.3
1	B	85	LEU	4.3
1	B	61	ASN	4.3
1	A	57	LYS	4.2
1	B	306	GLU	4.0
1	B	58	ILE	3.8
1	B	56	GLU	3.8
1	B	29	SER	3.8
1	B	317	VAL	3.7
1	B	43	SER	3.7
1	B	309	MET	3.5
1	B	316	THR	3.5
1	B	59	ALA	3.5

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Mol	Chain	Res	Type	RSRZ
1	B	221	GLU	3.4
1	B	60	ALA	3.4
1	B	28	GLY	3.4
1	A	139	ARG	3.3
1	B	287	ASN	3.3
1	B	62	VAL	3.2
1	A	33	GLY	3.2
1	A	224	LYS	3.0
1	B	41	LYS	3.0
1	A	53	GLU	3.0
1	B	86	THR	3.0
1	B	12	LEU	2.9
1	A	61	ASN	2.9
1	B	53	GLU	2.9
1	B	308	ILE	2.9
1	A	289	ASN	2.8
1	B	161	PHE	2.7
1	A	284	ASP	2.7
1	B	33	GLY	2.7
1	B	286	MET	2.6
1	B	39	ARG	2.5
1	B	140	ASP	2.5
1	B	313	ALA	2.5
1	A	219	ASP	2.5
1	A	143	LEU	2.5
1	B	312	ILE	2.4
1	A	160	ASP	2.4
1	B	224	LYS	2.4
1	B	67	ILE	2.4
1	A	140	ASP	2.3
1	A	161	PHE	2.3
1	A	28	GLY	2.2
1	A	19	ASP	2.2
1	A	223	PRO	2.2
1	B	216	PRO	2.2
1	A	55	GLY	2.1
1	B	141	LEU	2.1
1	B	14	ILE	2.1
1	B	192	GLU	2.0
1	A	288	ASP	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)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.