Full wwPDB X-ray Structure Validation Report ⓘ

Jun 15, 2024 – 04:45 PM EDT

PDB ID	:	2P63
Title	:	Suprafacial orientation of the SCFCdc4 dimer accommodates multiple geometries for substrate ubiquitination
Authors	:	Orlicky, S.; Neculai, D.; Ceccarelli, D.
Deposited on	:	2007-03-16
Resolution	:	2.67 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
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

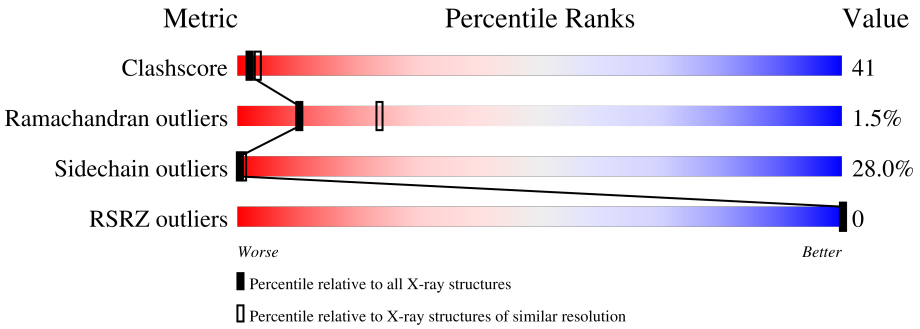
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 2.67 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))
Clashscore	141614	4210 (2.70-2.66)
Ramachandran outliers	138981	4141 (2.70-2.66)
Sidechain outliers	138945	4141 (2.70-2.66)
RSRZ outliers	127900	3780 (2.70-2.66)

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 of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	56	30% 48% 14% 7%
1	B	56	25% 39% 25% • 9%
1	C	56	41% 38% 16% 5%
1	D	56	32% 45% 14% 9%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 1742 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 Cell division control protein 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	52	Total	C	N	O	Se	0	0	0
			419	266	72	80	1			
1	B	51	Total	C	N	O	Se	0	1	0
			425	270	74	80	1			
1	C	53	Total	C	N	O	Se	0	1	0
			434	275	75	83	1			
1	D	51	Total	C	N	O	Se	0	1	0
			427	271	74	81	1			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	218	GLY	-	CLONING ARTIFACT	UNP P07834
A	219	ALA	-	CLONING ARTIFACT	UNP P07834
A	220	MSE	-	CLONING ARTIFACT	UNP P07834
A	221	GLY	-	CLONING ARTIFACT	UNP P07834
A	254	MSE	-	MODIFIED RESIDUE	UNP P07834
B	218	GLY	-	CLONING ARTIFACT	UNP P07834
B	219	ALA	-	CLONING ARTIFACT	UNP P07834
B	220	MSE	-	CLONING ARTIFACT	UNP P07834
B	221	GLY	-	CLONING ARTIFACT	UNP P07834
B	254	MSE	-	MODIFIED RESIDUE	UNP P07834
C	218	GLY	-	CLONING ARTIFACT	UNP P07834
C	219	ALA	-	CLONING ARTIFACT	UNP P07834
C	220	MSE	-	CLONING ARTIFACT	UNP P07834
C	221	GLY	-	CLONING ARTIFACT	UNP P07834
C	254	MSE	-	MODIFIED RESIDUE	UNP P07834
D	218	GLY	-	CLONING ARTIFACT	UNP P07834
D	219	ALA	-	CLONING ARTIFACT	UNP P07834
D	220	MSE	-	CLONING ARTIFACT	UNP P07834
D	221	GLY	-	CLONING ARTIFACT	UNP P07834
D	254	MSE	-	MODIFIED RESIDUE	UNP P07834

- Molecule 2 is water.

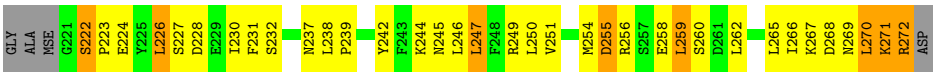
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	13	Total O 13 13	0	0
2	B	5	Total O 5 5	0	0
2	C	14	Total O 14 14	0	0
2	D	5	Total O 5 5	0	0

3 Residue-property plots (i)

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

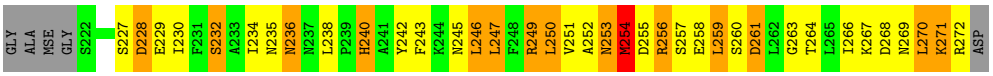
• Molecule 1: Cell division control protein 4

Chain A:



• Molecule 1: Cell division control protein 4

Chain B:

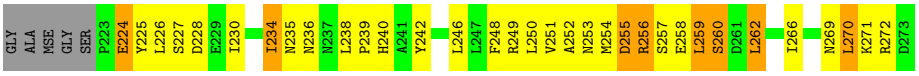


• Molecule 1: Cell division control protein 4

Chain C:

• Molecule 1: Cell division control protein 4

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α, β, γ	37.82Å 37.82Å 298.12Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.69 – 2.67 32.55 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.1 (49.69-2.67) 92.3 (32.55-2.50)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.03	Depositor
$< I/\sigma(I) >$ [1]	4.50 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.220 , 0.279 0.196 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	36.2	Xtriage
Anisotropy	0.727	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 137.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.56$, $< L^2 > = 0.41$	Xtriage
Estimated twinning fraction	0.257 for h,-h-k,-l	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	1742	wwPDB-VP
Average B, all atoms (Å^2)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.11% 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, 0.333 respectively for untwinned datasets, and 0.375, 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	0.29	0/425	0.80	0/571
1	B	0.25	0/432	0.73	0/581
1	C	0.28	0/444	0.78	0/597
1	D	0.27	0/434	0.74	0/583
All	All	0.27	0/1735	0.76	0/2332

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	419	0	416	48	0
1	B	425	0	419	49	0
1	C	434	0	427	31	0
1	D	427	0	419	38	0
2	A	13	0	0	1	0
2	B	5	0	0	2	0
2	C	14	0	0	1	0
2	D	5	0	0	1	0
All	All	1742	0	1681	139	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 41.

All (139) 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:266:ILE:HG23	1:B:259:LEU:HG	1.48	0.95
1:B:254:MSE:SE	1:B:259:LEU:HD13	2.17	0.94
1:B:269:ASN:HA	1:B:272:ARG:HB2	1.50	0.93
1:B:255:ASP:HB2	1:B:258:GLU:HG3	1.56	0.87
1:C:256:ARG:HH11	1:C:256:ARG:HB3	1.49	0.76
1:A:255:ASP:O	1:A:259:LEU:HD22	1.87	0.75
1:A:254:MSE:HA	1:A:258:GLU:OE2	1.88	0.74
1:D:262:LEU:O	1:D:266:ILE:HD12	1.88	0.73
1:C:226:LEU:HA	2:C:7:HOH:O	1.88	0.73
1:A:254:MSE:SE	1:A:262:LEU:CD2	2.88	0.72
1:B:243:PHE:O	1:B:246:LEU:HB2	1.89	0.72
1:A:254:MSE:SE	1:A:262:LEU:HD23	2.40	0.71
1:C:230:ILE:O	1:C:234:ILE:HG13	1.93	0.68
1:A:226:LEU:HB3	1:B:249:ARG:NH2	2.09	0.67
1:B:268:ASP:OD1	1:D:228:ASP:HB2	1.97	0.64
1:A:262:LEU:HG	1:B:266:ILE:HD11	1.81	0.63
1:A:247:LEU:O	1:A:251:VAL:HG23	1.99	0.62
1:B:266:ILE:O	1:B:270:LEU:HD22	2.00	0.62
1:C:235:ASN:O	1:C:238:LEU:HB2	2.01	0.61
1:A:251:VAL:HA	1:A:254:MSE:HE3	1.82	0.61
1:A:254:MSE:SE	1:A:262:LEU:HD22	2.52	0.59
1:B:232:SER:O	1:B:236:ASN:HB2	2.01	0.59
1:C:273:ASP:HB3	1:D:256:ARG:HH12	1.67	0.59
1:B:253:ASN:HD22	1:B:253:ASN:N	2.00	0.59
1:C:262:LEU:HG	1:C:266:ILE:HD12	1.84	0.59
1:A:266:ILE:HG12	1:B:259:LEU:HD11	1.84	0.58
1:A:238:LEU:CD2	1:A:239:PRO:HD2	2.33	0.58
1:B:238:LEU:HD23	1:B:242:TYR:CD1	2.39	0.58
1:A:255:ASP:H	1:A:258:GLU:HG3	1.67	0.57
1:C:255:ASP:OD2	1:C:257:SER:HB3	2.03	0.57
1:B:247:LEU:O	1:B:251:VAL:HG23	2.05	0.57
1:A:238:LEU:HD23	1:A:239:PRO:HD2	1.86	0.57
1:A:227:SER:OG	1:A:230:ILE:HG13	2.05	0.57
1:C:267:LYS:O	1:C:270:LEU:HB2	2.06	0.56
1:C:272:ARG:O	1:C:272:ARG:HG3	2.04	0.56
1:C:266:ILE:HD11	1:D:262:LEU:HD21	1.87	0.56
1:C:247:LEU:O	1:C:251:VAL:HG23	2.07	0.55
1:B:249:ARG:O	1:B:252:ALA:HB3	2.06	0.55
1:D:235:ASN:HA	1:D:238:LEU:HD12	1.90	0.54
1:A:246:LEU:HD21	1:B:246:LEU:HD13	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:254:MSE:SE	1:B:259:LEU:CD1	3.01	0.54
1:D:227:SER:OG	1:D:230:ILE:HG13	2.09	0.54
1:B:268:ASP:O	1:B:271:LYS:HG2	2.07	0.53
1:B:269:ASN:ND2	1:B:272:ARG:HD2	2.24	0.53
1:D:254:MSE:SE	1:D:259:LEU:HD12	2.59	0.52
1:A:226:LEU:HD11	1:A:230:ILE:HG22	1.90	0.52
1:A:226:LEU:HB3	1:B:249:ARG:HH22	1.73	0.52
1:A:238:LEU:HD13	1:A:242:TYR:CD2	2.45	0.52
1:A:254:MSE:CE	1:B:247:LEU:HD21	2.39	0.52
1:D:249:ARG:O	1:D:252:ALA:HB3	2.10	0.51
1:A:247:LEU:HD13	1:A:251:VAL:CG2	2.41	0.51
1:A:267:LYS:O	1:A:271:LYS:HG2	2.11	0.50
1:D:251:VAL:HG13	1:D:259:LEU:HD11	1.91	0.50
1:D:239:PRO:HD2	1:D:242:TYR:CB	2.41	0.50
1:D:256:ARG:O	1:D:260:SER:OG	2.30	0.50
1:B:264:THR:HG22	1:D:225:TYR:HE2	1.77	0.50
1:B:271:LYS:O	1:B:272:ARG:O	2.30	0.50
1:B:228:ASP:OD2	1:D:272:ARG:NH2	2.41	0.50
1:C:272:ARG:O	1:C:273:ASP:O	2.30	0.49
1:A:254:MSE:HB3	1:A:258:GLU:HB2	1.92	0.49
1:A:268:ASP:O	1:A:271:LYS:HG2	2.13	0.49
1:A:270:LEU:HD12	1:B:256:ARG:HD3	1.93	0.49
1:A:254:MSE:HE2	1:B:247:LEU:HD21	1.94	0.49
1:C:265:LEU:HD12	1:C:269:ASN:HD22	1.77	0.48
1:A:246:LEU:O	1:A:250:LEU:HG	2.13	0.48
1:A:245:ASN:HB3	1:A:249:ARG:NH2	2.29	0.48
1:B:255:ASP:HB2	1:B:258:GLU:CG	2.38	0.48
1:A:271:LYS:O	1:A:272:ARG:O	2.32	0.48
1:C:270:LEU:HD13	1:C:270:LEU:HA	1.72	0.48
1:C:226:LEU:HD22	1:C:230:ILE:HG21	1.96	0.47
1:C:271:LYS:O	1:C:271:LYS:HG2	2.13	0.47
1:D:224:GLU:HG3	2:D:20:HOH:O	2.14	0.47
1:C:244:LYS:O	1:C:248:PHE:HD1	1.97	0.47
1:C:226:LEU:HD22	1:C:230:ILE:CG2	2.45	0.46
1:A:245:ASN:HB3	1:A:249:ARG:HH21	1.81	0.46
1:B:263:GLY:HA2	2:B:37:HOH:O	2.15	0.46
1:A:262:LEU:HG	1:B:266:ILE:CD1	2.45	0.46
1:B:252:ALA:C	1:B:253:ASN:HD22	2.19	0.46
1:A:247:LEU:HD22	1:A:247:LEU:HA	1.70	0.45
1:B:243:PHE:HA	1:B:246:LEU:HB2	1.97	0.45
1:C:259:LEU:HB3	1:D:270:LEU:CD2	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:272:ARG:HD3	1:D:272:ARG:HA	1.70	0.45
1:C:249:ARG:NH2	1:D:226:LEU:O	2.50	0.45
1:D:254:MSE:SE	1:D:259:LEU:CD1	3.15	0.45
1:D:254:MSE:HG2	1:D:259:LEU:HD13	1.99	0.45
1:D:250:LEU:O	1:D:253:ASN:N	2.50	0.45
1:A:265:LEU:O	1:A:269:ASN:ND2	2.50	0.45
1:C:273:ASP:OD2	1:C:273:ASP:N	2.50	0.45
1:A:255:ASP:OD2	1:A:256:ARG:N	2.50	0.45
1:B:272:ARG:NH2	1:D:225:TYR:OH	2.50	0.45
1:A:224:GLU:OE1	1:B:240[B]:HIS:NE2	2.50	0.45
1:D:255:ASP:N	1:D:258:GLU:OE2	2.50	0.45
1:A:228:ASP:O	1:A:231:PHE:HB3	2.17	0.44
1:B:261:ASP:OD2	1:D:225:TYR:N	2.50	0.44
1:D:272:ARG:HH11	1:D:272:ARG:HG2	1.82	0.44
1:C:244:LYS:HZ3	1:D:224:GLU:H	1.64	0.44
1:C:256:ARG:HH11	1:C:256:ARG:CB	2.25	0.44
1:D:239:PRO:HD2	1:D:242:TYR:HB2	1.98	0.44
1:A:245:ASN:OD1	1:A:249:ARG:NH2	2.50	0.44
1:A:245:ASN:O	1:A:249:ARG:HB2	2.17	0.44
1:A:271:LYS:HG2	1:A:271:LYS:H	1.39	0.44
1:D:235:ASN:OD1	1:D:238:LEU:HD12	2.17	0.44
1:B:256:ARG:O	1:B:260:SER:OG	2.30	0.44
1:C:249:ARG:O	1:C:253:ASN:ND2	2.50	0.44
1:B:271:LYS:HB3	1:B:271:LYS:HE3	1.38	0.43
1:A:268:ASP:HB3	1:A:272:ARG:HE	1.83	0.43
1:B:249:ARG:O	1:B:253:ASN:ND2	2.51	0.43
1:B:243:PHE:HA	1:B:246:LEU:HG	2.00	0.43
1:D:226:LEU:HD23	1:D:226:LEU:HA	1.91	0.43
1:D:227:SER:OG	1:D:230:ILE:N	2.50	0.43
1:B:251:VAL:HA	1:B:254:MSE:SE	2.69	0.43
1:C:249:ARG:NH1	1:D:228:ASP:OD1	2.50	0.43
1:D:256:ARG:HA	1:D:259:LEU:HB2	2.00	0.43
1:A:237:ASN:HB3	2:A:27:HOH:O	2.18	0.43
1:D:234:ILE:HG22	1:D:235:ASN:N	2.33	0.43
1:C:242:TYR:HA	1:D:226:LEU:HD12	2.01	0.43
1:C:266:ILE:HD11	1:D:262:LEU:CD2	2.49	0.43
1:B:257:SER:O	1:B:261:ASP:HB2	2.19	0.42
1:B:247:LEU:HD13	1:B:247:LEU:HA	1.85	0.42
1:A:251:VAL:CA	1:A:254:MSE:HE3	2.48	0.42
1:A:259:LEU:HD12	1:A:259:LEU:HA	1.91	0.42
1:B:234:ILE:HG22	1:B:235:ASN:N	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:222:SER:HA	1:A:223:PRO:HD2	1.65	0.42
1:D:257:SER:OG	1:D:258:GLU:N	2.52	0.42
1:A:266:ILE:HG12	1:B:259:LEU:CD1	2.49	0.41
1:A:268:ASP:O	1:A:272:ARG:HG2	2.19	0.41
1:D:272:ARG:HG2	1:D:272:ARG:NH1	2.34	0.41
1:A:269:ASN:HA	1:A:272:ARG:HG3	2.02	0.41
1:B:246:LEU:CD2	1:B:250:LEU:HD21	2.50	0.41
1:B:259:LEU:HD12	1:B:259:LEU:HA	1.75	0.41
1:B:264:THR:HG22	1:D:225:TYR:CE2	2.55	0.41
1:C:234:ILE:HG22	1:C:234:ILE:O	2.20	0.41
1:C:246:LEU:O	1:C:250:LEU:HG	2.20	0.41
1:B:272:ARG:NH2	1:D:228:ASP:OD1	2.50	0.40
1:B:245:ASN:HB2	2:B:19:HOH:O	2.20	0.40
1:C:242:TYR:HD2	1:C:243:PHE:CD1	2.38	0.40
1:A:250:LEU:C	1:A:254:MSE:HE3	2.42	0.40
1:B:249:ARG:O	1:B:252:ALA:N	2.54	0.40
1:C:247:LEU:HD23	1:C:247:LEU:HA	1.82	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	50/56 (89%)	44 (88%)	6 (12%)	0	100 100
1	B	50/56 (89%)	46 (92%)	2 (4%)	2 (4%)	3 5
1	C	52/56 (93%)	46 (88%)	6 (12%)	0	100 100
1	D	50/56 (89%)	37 (74%)	12 (24%)	1 (2%)	7 17
All	All	202/224 (90%)	173 (86%)	26 (13%)	3 (2%)	10 23

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	254	MSE
1	B	228	ASP
1	D	234	ILE

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	47/47 (100%)	36 (77%)	11 (23%)	1	1
1	B	48/47 (102%)	29 (60%)	19 (40%)	0	0
1	C	49/47 (104%)	38 (78%)	11 (22%)	1	2
1	D	48/47 (102%)	34 (71%)	14 (29%)	0	0
All	All	192/188 (102%)	137 (71%)	55 (29%)	0	1

All (55) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	222	SER
1	A	226	LEU
1	A	232	SER
1	A	244	LYS
1	A	247	LEU
1	A	255	ASP
1	A	259	LEU
1	A	260	SER
1	A	270	LEU
1	A	271	LYS
1	A	272	ARG
1	B	227	SER
1	B	229	GLU
1	B	230	ILE
1	B	232	SER
1	B	236	ASN
1	B	240[A]	HIS
1	B	240[B]	HIS
1	B	246	LEU

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Mol	Chain	Res	Type
1	B	247	LEU
1	B	249	ARG
1	B	250	LEU
1	B	253	ASN
1	B	254	MSE
1	B	256	ARG
1	B	259	LEU
1	B	261	ASP
1	B	267	LYS
1	B	270	LEU
1	B	271	LYS
1	C	222	SER
1	C	244	LYS
1	C	246	LEU
1	C	247	LEU
1	C	249	ARG
1	C	256	ARG
1	C	259	LEU
1	C	260	SER
1	C	270	LEU
1	C	271	LYS
1	C	272	ARG
1	D	224	GLU
1	D	236	ASN
1	D	240[A]	HIS
1	D	240[B]	HIS
1	D	246	LEU
1	D	248	PHE
1	D	255	ASP
1	D	256	ARG
1	D	259	LEU
1	D	260	SER
1	D	262	LEU
1	D	269	ASN
1	D	270	LEU
1	D	271	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	269	ASN
1	B	253	ASN

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Mol	Chain	Res	Type
1	B	269	ASN
1	C	269	ASN
1	D	236	ASN
1	D	269	ASN

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 monosaccharides 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	51/56 (91%)	-0.50	0	100	100	28, 47, 68, 76	0
1	B	50/56 (89%)	-0.30	0	100	100	35, 56, 89, 93	0
1	C	52/56 (92%)	-0.48	0	100	100	29, 48, 66, 88	0
1	D	50/56 (89%)	-0.32	0	100	100	30, 52, 82, 109	0
All	All	203/224 (90%)	-0.40	0	100	100	28, 51, 80, 109	0

There are no RSRZ outliers to report.

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

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

6.3 Carbohydrates

There are no monosaccharides in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.