



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 10:12 pm GMT

PDB ID : 4J8D
Title : Middle domain of Hsc70-interacting protein, crystal form II
Authors : Li, Z.; Bracher, A.
Deposited on : 2013-02-14
Resolution : 2.80 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
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

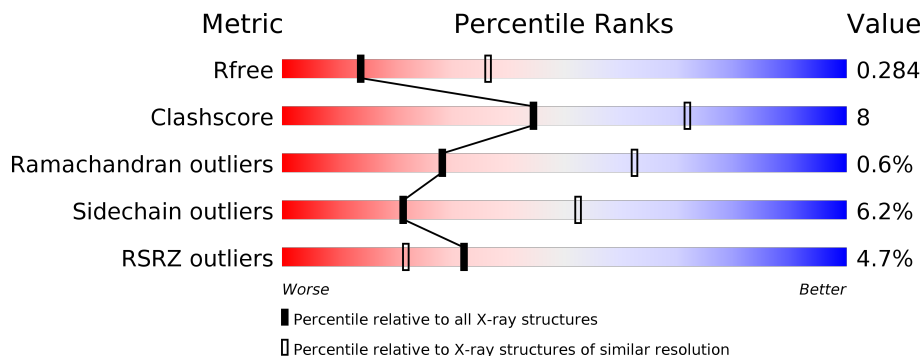
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	100719	2583 (2.80-2.80)
Clashscore	112137	3033 (2.80-2.80)
Ramachandran outliers	110173	2983 (2.80-2.80)
Sidechain outliers	110143	2985 (2.80-2.80)
RSRZ outliers	101464	2610 (2.80-2.80)

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	175	<div> <div>5%</div> <div> <div></div> <div>74%</div> <div>17%</div> <div>• 8%</div> </div> </div>
1	B	175	<div> <div>2%</div> <div> <div></div> <div>72%</div> <div>17%</div> <div>• 9%</div> </div> </div>
1	C	175	<div> <div>7%</div> <div> <div></div> <div>71%</div> <div>21%</div> <div>9%</div> </div> </div>
1	D	175	<div> <div>3%</div> <div> <div></div> <div>74%</div> <div>18%</div> <div>• 7%</div> </div> </div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 4884 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 Hsc70-interacting protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	161	Total	C	N	O	S	0	0	0
			1225	756	222	241	6			
1	B	159	Total	C	N	O	S	0	0	0
			1206	745	218	237	6			
1	C	160	Total	C	N	O	S	0	0	0
			1216	751	221	238	6			
1	D	162	Total	C	N	O	S	0	0	0
			1237	767	225	239	6			

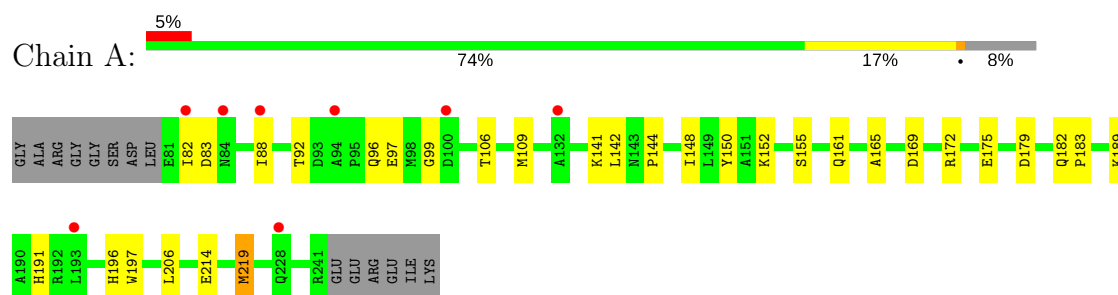
There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	73	GLY	-	EXPRESSION TAG	UNP P50503
A	74	ALA	-	EXPRESSION TAG	UNP P50503
A	75	ARG	-	EXPRESSION TAG	UNP P50503
A	76	GLY	-	EXPRESSION TAG	UNP P50503
A	77	GLY	-	EXPRESSION TAG	UNP P50503
B	73	GLY	-	EXPRESSION TAG	UNP P50503
B	74	ALA	-	EXPRESSION TAG	UNP P50503
B	75	ARG	-	EXPRESSION TAG	UNP P50503
B	76	GLY	-	EXPRESSION TAG	UNP P50503
B	77	GLY	-	EXPRESSION TAG	UNP P50503
C	73	GLY	-	EXPRESSION TAG	UNP P50503
C	74	ALA	-	EXPRESSION TAG	UNP P50503
C	75	ARG	-	EXPRESSION TAG	UNP P50503
C	76	GLY	-	EXPRESSION TAG	UNP P50503
C	77	GLY	-	EXPRESSION TAG	UNP P50503
D	73	GLY	-	EXPRESSION TAG	UNP P50503
D	74	ALA	-	EXPRESSION TAG	UNP P50503
D	75	ARG	-	EXPRESSION TAG	UNP P50503
D	76	GLY	-	EXPRESSION TAG	UNP P50503
D	77	GLY	-	EXPRESSION TAG	UNP P50503

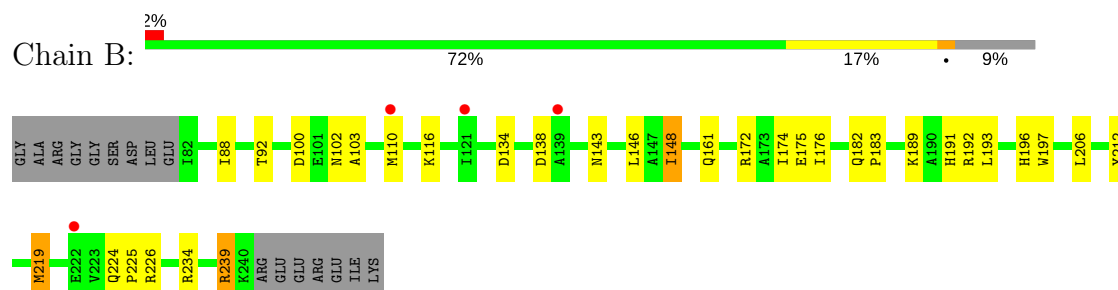
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

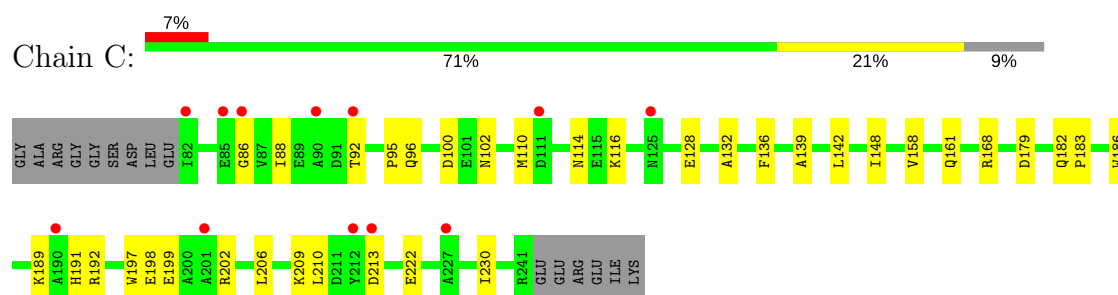
- Molecule 1: Hsc70-interacting protein



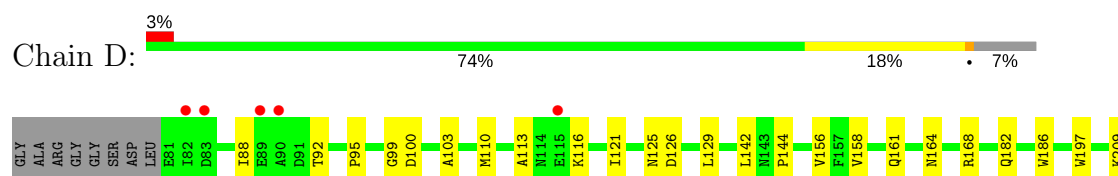
- Molecule 1: Hsc70-interacting protein



- Molecule 1: Hsc70-interacting protein



- Molecule 1: Hsc70-interacting protein





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	57.29Å 127.00Å 57.31Å 90.00° 105.93° 90.00°	Depositor
Resolution (Å)	20.00 – 2.80 43.04 – 2.80	Depositor EDS
% Data completeness (in resolution range)	98.4 (20.00-2.80) 98.5 (43.04-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.84 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.246 , 0.299 0.244 , 0.284	Depositor DCC
R_{free} test set	982 reflections (5.37%)	DCC
Wilson B-factor (Å ²)	36.5	Xtriage
Anisotropy	1.047	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 7.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.388 for l,-k,h	Xtriage
Reported twinning fraction	0.594 for H, K, L 0.406 for L, -K, H	Depositor
Outliers	0 of 19227 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	4884	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 32.05 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.0018e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.35	0/1242	0.54	1/1680 (0.1%)
1	B	0.35	0/1222	0.55	0/1653
1	C	0.35	0/1233	0.51	0/1668
1	D	0.36	0/1255	0.52	0/1696
All	All	0.35	0/4952	0.53	1/6697 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	206	LEU	CA-CB-CG	5.10	127.03	115.30

There are no chirality outliers.

There are no planarity outliers.

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	1225	0	1171	17	0
1	B	1206	0	1158	22	0
1	C	1216	0	1165	18	0
1	D	1237	0	1194	19	0
All	All	4884	0	4688	72	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 8.

All (72) 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:B:189:LYS:NZ	1:B:219:MET:HG3	1.90	0.85
1:B:239:ARG:HG3	1:B:239:ARG:HH11	1.47	0.79
1:A:189:LYS:NZ	1:A:219:MET:HG3	2.02	0.75
1:D:164:ASN:HB3	1:D:168:ARG:HH21	1.63	0.63
1:A:189:LYS:HZ1	1:A:219:MET:HG3	1.64	0.62
1:C:116:LYS:HB3	1:C:139:ALA:HB2	1.82	0.62
1:B:224:GLN:HB2	1:B:225:PRO:HD3	1.82	0.61
1:D:95:PRO:HA	1:D:168:ARG:NH1	2.16	0.61
1:B:189:LYS:NZ	1:B:219:MET:CG	2.64	0.60
1:D:197:TRP:CZ3	1:D:226:ARG:HD3	2.35	0.60
1:C:191:HIS:CD2	1:C:199:GLU:HB3	2.36	0.60
1:A:88:ILE:HD13	1:A:161:GLN:HB3	1.87	0.57
1:A:97:GLU:HG2	1:A:141:LYS:HD2	1.86	0.56
1:B:191:HIS:ND1	1:B:196:HIS:HD2	2.03	0.56
1:C:88:ILE:HD13	1:C:161:GLN:HB3	1.87	0.56
1:B:189:LYS:HZ1	1:B:219:MET:HG3	1.70	0.55
1:C:86:GLY:HA3	1:C:192:ARG:HH12	1.72	0.55
1:A:189:LYS:HZ2	1:A:219:MET:HG3	1.72	0.55
1:B:146:LEU:HG	1:B:148:ILE:HG13	1.88	0.55
1:C:158:VAL:HG11	1:C:189:LYS:HD2	1.89	0.54
1:B:189:LYS:HZ3	1:B:219:MET:HG3	1.71	0.54
1:B:88:ILE:HD13	1:B:161:GLN:HB3	1.91	0.53
1:A:99:GLY:HA3	1:A:144:PRO:HB3	1.90	0.52
1:B:189:LYS:NZ	1:B:219:MET:SD	2.82	0.52
1:C:148:ILE:H	1:C:148:ILE:HD12	1.74	0.52
1:D:222:GLU:O	1:D:226:ARG:NH1	2.41	0.52
1:C:102:ASN:HA	1:D:235:ARG:HG3	1.92	0.51
1:A:189:LYS:HZ2	1:A:219:MET:CG	2.24	0.51
1:B:172:ARG:HG3	1:B:172:ARG:O	2.11	0.51
1:D:182:GLN:O	1:D:186:TRP:HD1	1.95	0.50
1:C:198:GLU:O	1:C:202:ARG:HG3	2.11	0.49
1:A:96:GLN:NE2	1:A:165:ALA:O	2.45	0.49
1:D:121:ILE:O	1:D:125:ASN:ND2	2.44	0.49
1:C:179:ASP:O	1:D:209:LYS:HD2	2.12	0.49
1:C:197:TRP:HD1	1:C:230:ILE:HD12	1.77	0.48
1:D:158:VAL:O	1:D:161:GLN:N	2.40	0.48
1:D:182:GLN:O	1:D:186:TRP:CD1	2.67	0.47
1:A:150:TYR:CE1	1:A:172:ARG:HG2	2.49	0.47
1:B:88:ILE:HG12	1:B:193:LEU:HD22	1.96	0.47
1:B:182:GLN:HB2	1:B:183:PRO:HD3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:132:ALA:O	1:C:136:PHE:CD2	2.68	0.47
1:A:82:ILE:CG2	1:A:197:TRP:HE1	2.28	0.46
1:D:99:GLY:HA3	1:D:144:PRO:HB3	1.98	0.46
1:D:129:LEU:HB3	1:D:156:VAL:CG1	2.45	0.46
1:A:152:LYS:O	1:A:155:SER:HB3	2.16	0.46
1:A:182:GLN:HB2	1:A:183:PRO:HD3	1.97	0.46
1:B:100:ASP:HB3	1:B:103:ALA:HB2	1.97	0.46
1:B:110:MET:HG3	1:B:143:ASN:ND2	2.31	0.45
1:D:224:GLN:HB2	1:D:225:PRO:HD3	1.99	0.45
1:A:197:TRP:HA	1:A:197:TRP:CE3	2.51	0.44
1:C:182:GLN:N	1:C:183:PRO:HD2	2.31	0.44
1:D:100:ASP:HB2	1:D:103:ALA:HB2	1.99	0.44
1:B:239:ARG:HG3	1:B:239:ARG:NH1	2.23	0.44
1:A:197:TRP:HE3	1:A:197:TRP:HA	1.82	0.44
1:A:191:HIS:ND1	1:A:196:HIS:HD2	2.15	0.44
1:B:197:TRP:CG	1:B:226:ARG:HB3	2.53	0.43
1:B:224:GLN:CB	1:B:225:PRO:HD3	2.47	0.43
1:D:113:ALA:HB2	1:D:142:LEU:HB2	2.00	0.43
1:A:172:ARG:HG3	1:A:172:ARG:O	2.17	0.43
1:C:100:ASP:C	1:C:102:ASN:H	2.21	0.42
1:A:106:THR:OG1	1:A:109:MET:HG3	2.20	0.42
1:B:116:LYS:HD3	1:B:138:ASP:HB3	2.01	0.42
1:C:182:GLN:O	1:C:186:TRP:HD1	2.03	0.42
1:B:174:ILE:O	1:B:176:ILE:N	2.53	0.41
1:B:192:ARG:HG2	1:B:219:MET:CE	2.50	0.41
1:B:191:HIS:ND1	1:B:196:HIS:CD2	2.86	0.41
1:C:210:LEU:HD22	1:D:209:LYS:HD3	2.02	0.41
1:C:206:LEU:HD12	1:D:210:LEU:HD21	2.02	0.41
1:C:95:PRO:HA	1:C:168:ARG:NH1	2.36	0.41
1:D:88:ILE:HD13	1:D:161:GLN:HB3	2.02	0.41
1:C:96:GLN:OE1	1:C:168:ARG:NH1	2.54	0.40
1:D:240:LYS:C	1:D:242:GLU:H	2.25	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	159/175 (91%)	139 (87%)	19 (12%)	1 (1%)	28	62
1	B	157/175 (90%)	141 (90%)	14 (9%)	2 (1%)	14	41
1	C	158/175 (90%)	153 (97%)	5 (3%)	0	100	100
1	D	160/175 (91%)	153 (96%)	6 (4%)	1 (1%)	28	62
All	All	634/700 (91%)	586 (92%)	44 (7%)	4 (1%)	28	62

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	175	GLU
1	A	175	GLU
1	B	212	TYR
1	D	241	ARG

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	118/139 (85%)	110 (93%)	8 (7%)	18	47
1	B	116/139 (84%)	108 (93%)	8 (7%)	18	46
1	C	117/139 (84%)	109 (93%)	8 (7%)	18	47
1	D	119/139 (86%)	114 (96%)	5 (4%)	34	68
All	All	470/556 (84%)	441 (94%)	29 (6%)	21	52

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	83	ASP
1	A	92	THR

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Mol	Chain	Res	Type
1	A	142	LEU
1	A	148	ILE
1	A	169	ASP
1	A	179	ASP
1	A	214	GLU
1	A	219	MET
1	B	92	THR
1	B	102	ASN
1	B	134	ASP
1	B	148	ILE
1	B	206	LEU
1	B	219	MET
1	B	234	ARG
1	B	239	ARG
1	C	92	THR
1	C	110	MET
1	C	114	ASN
1	C	128	GLU
1	C	142	LEU
1	C	209	LYS
1	C	213	ASP
1	C	222	GLU
1	D	92	THR
1	D	110	MET
1	D	116	LYS
1	D	126	ASP
1	D	222	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	125	ASN
1	A	196	HIS
1	B	125	ASN
1	B	196	HIS
1	C	125	ASN
1	C	191	HIS
1	D	161	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	161/175 (92%)	0.50	8 (4%)	30 20	22, 33, 59, 71	0
1	B	159/175 (90%)	0.48	4 (2%)	58 47	22, 33, 59, 71	0
1	C	160/175 (91%)	0.50	12 (7%)	15 8	23, 34, 59, 71	0
1	D	162/175 (92%)	0.44	6 (3%)	42 31	23, 34, 59, 72	0
All	All	642/700 (91%)	0.48	30 (4%)	32 22	22, 34, 62, 72	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	90	ALA	5.5
1	A	193	LEU	3.6
1	C	201	ALA	3.5
1	A	132	ALA	3.4
1	A	84	ASN	3.1
1	C	90	ALA	3.0
1	B	110	MET	2.9
1	C	82	ILE	2.8
1	D	82	ILE	2.7
1	C	190	ALA	2.6
1	C	86	GLY	2.5
1	A	100	ASP	2.4
1	C	85	GLU	2.4
1	A	88	ILE	2.4
1	B	139	ALA	2.4
1	C	111	ASP	2.3
1	D	89	GLU	2.3
1	A	82	ILE	2.3
1	D	115	GLU	2.3
1	B	222	GLU	2.3
1	C	212	TYR	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	228	GLN	2.1
1	B	121	ILE	2.1
1	C	227	ALA	2.1
1	C	125	ASN	2.1
1	C	213	ASP	2.1
1	D	83	ASP	2.0
1	D	225	PRO	2.0
1	A	94	ALA	2.0
1	C	92	THR	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.