Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2016 – 02:54 PM EDT

PDB ID	:	5D93
Title	:	Oxidoreductase Fragment of Mouse QSOX1 in Complex with a FAb Fragment from a Mouse QSOX1-Specific Antibody
Authors	:	Grossman, I.; Fass, D.
Deposited on	:	2015-08-18
Resolution	:	2.20 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:

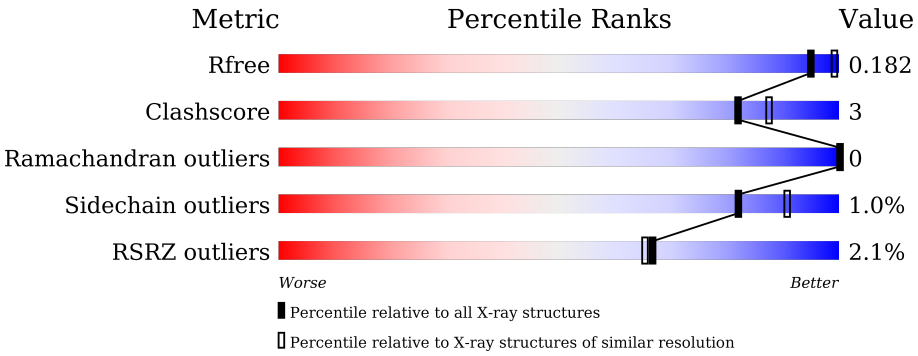
MolProbity	:	4.02b-467
Mogul	:	unknown
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20027107
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0122
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20027107

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 2.20 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	3774 (2.20-2.20)
Clashscore	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)
RSRZ outliers	91569	3781 (2.20-2.20)

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	244	2% 85% 12%
1	D	244	3% 83% 13%
2	C	218	3% 88% 7% 5%
2	F	218	2% 94% 5%
3	B	213	2% 95%
3	E	213	% 98%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10907 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 Sulfhydryl oxidase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	240	Total	C	N	O	S	0	0	0
			1868	1190	319	351	8			
1	D	235	Total	C	N	O	S	0	0	0
			1828	1168	311	342	7			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	32	GLY	-	expression tag	UNP Q8BND5
A	33	SER	-	expression tag	UNP Q8BND5
A	34	HIS	-	expression tag	UNP Q8BND5
A	35	MET	-	expression tag	UNP Q8BND5
D	32	GLY	-	expression tag	UNP Q8BND5
D	33	SER	-	expression tag	UNP Q8BND5
D	34	HIS	-	expression tag	UNP Q8BND5
D	35	MET	-	expression tag	UNP Q8BND5

- Molecule 2 is a protein called Heavy Chain of Fab Fragment from a Mouse QSOX1-Specific Antibody.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	207	Total	C	N	O	S	0	0	0
			1578	1009	255	309	5			
2	F	216	Total	C	N	O	S	0	0	0
			1638	1043	266	324	5			

- Molecule 3 is a protein called Light Chain of Fab Fragment from a Mouse QSOX1-Specific Antibody.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	B	212	Total	C	N	O	S	0	0	0
			1622	1018	268	329	7			

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	212	Total	C	N	O	S	0	0	0
			1622	1018	268	329	7			

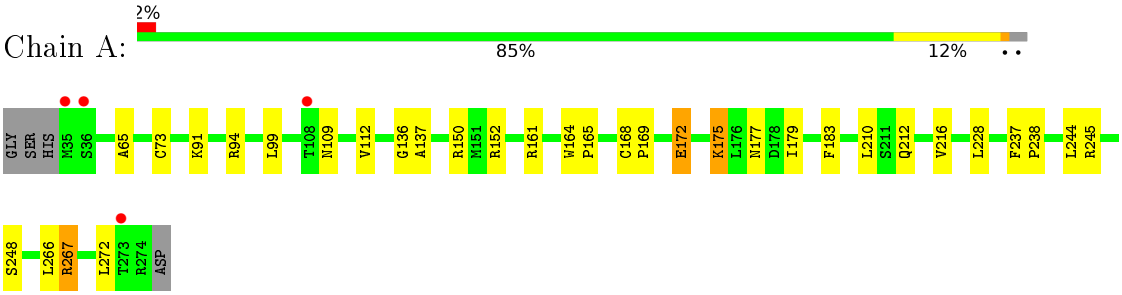
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	153	Total	O	0	0
			153	153		
4	C	120	Total	O	0	0
			120	120		
4	B	126	Total	O	0	0
			126	126		
4	D	85	Total	O	0	0
			85	85		
4	F	138	Total	O	0	0
			138	138		
4	E	129	Total	O	0	0
			129	129		

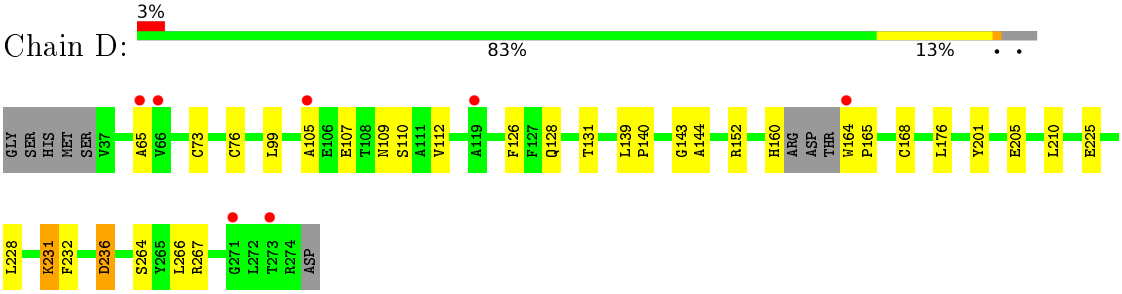
3 Residue-property plots

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.

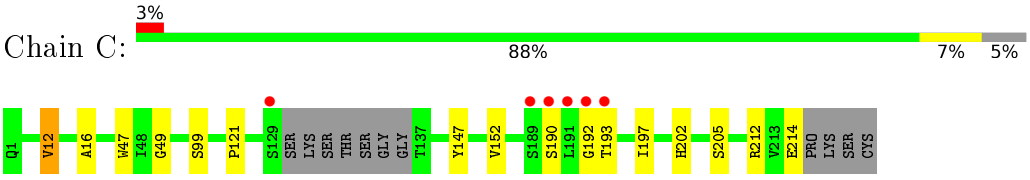
- Molecule 1: Sulfhydryl oxidase 1



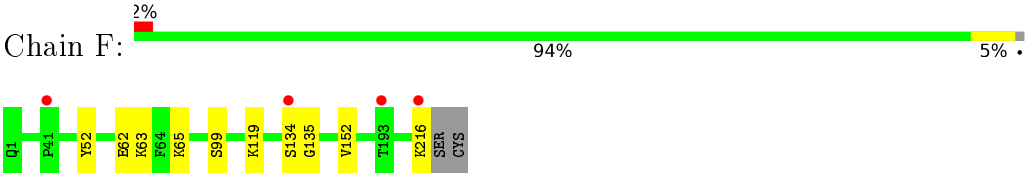
- Molecule 1: Sulfhydryl oxidase 1



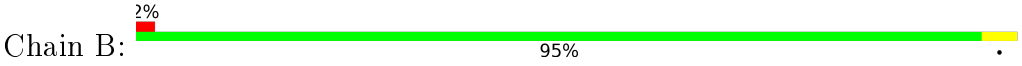
- Molecule 2: Heavy Chain of Fab Fragment from a Mouse QSOX1-Specific Antibody

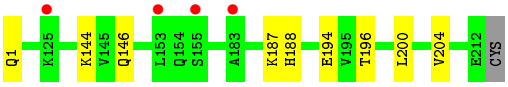


- Molecule 2: Heavy Chain of Fab Fragment from a Mouse QSOX1-Specific Antibody



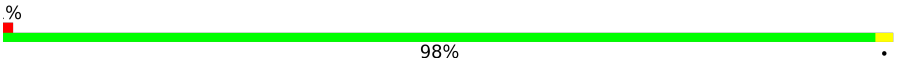
- Molecule 3: Light Chain of Fab Fragment from a Mouse QSOX1-Specific Antibody

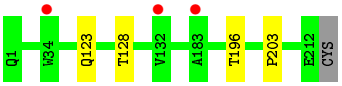




• Molecule 3: Light Chain of Fab Fragment from a Mouse QSOX1-Specific Antibody

Chain E:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	65.54Å 112.72Å 193.42Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	23.20 – 2.20 23.20 – 2.20	Depositor EDS
% Data completeness (in resolution range)	98.9 (23.20-2.20) 98.9 (23.20-2.20)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$< I/\sigma(I) >$ [1]	2.27 (at 2.19Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, R_{free}	0.174 , 0.236 0.173 , 0.182	Depositor DCC
R_{free} test set	3628 reflections (5.00%)	DCC
Wilson B-factor (Å^2)	30.0	Xtriage
Anisotropy	0.352	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 27.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Outliers	0 of 72580 reflections	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	10907	wwPDB-VP
Average B, all atoms (Å^2)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.80% 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	0.43	0/1915	0.60	2/2613 (0.1%)
1	D	0.40	0/1874	0.52	0/2557
2	C	0.43	0/1622	0.55	0/2215
2	F	0.42	0/1684	0.56	0/2298
3	B	0.40	0/1662	0.54	0/2259
3	E	0.41	0/1662	0.52	0/2259
All	All	0.42	0/10419	0.55	2/14201 (0.0%)

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
2	C	0	1
2	F	0	1
All	All	0	2

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	161	ARG	NE-CZ-NH2	-5.66	117.47	120.30
1	A	150	ARG	NE-CZ-NH2	-5.50	117.55	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	99	SER	Peptide
2	F	99	SER	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	1868	0	1818	21	0
1	D	1828	0	1781	23	0
2	C	1578	0	1524	8	0
2	F	1638	0	1592	6	0
3	B	1622	0	1565	5	0
3	E	1622	0	1565	2	0
4	A	153	0	0	5	5
4	B	126	0	0	0	2
4	C	120	0	0	0	2
4	D	85	0	0	2	1
4	E	129	0	0	0	0
4	F	138	0	0	3	0
All	All	10907	0	9845	63	5

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 3.

All (63) 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:136:GLY:O	4:A:301:HOH:O	2.02	0.77
2:C:212:ARG:NH2	2:C:214:GLU:OE2	2.21	0.72
2:C:197:ILE:HG12	2:C:212:ARG:HG2	1.75	0.68
1:D:65:ALA:HB3	1:D:99:LEU:HD22	1.75	0.67
1:A:172:GLU:OE1	4:A:302:HOH:O	2.15	0.64
1:A:210:LEU:HD22	1:A:216:VAL:HG11	1.82	0.60
1:D:126:PHE:HB2	1:D:139:LEU:HD11	1.84	0.59
1:A:65:ALA:HB3	1:A:99:LEU:HD22	1.85	0.58
1:A:172:GLU:OE2	4:A:303:HOH:O	2.17	0.57
1:A:183:PHE:O	1:A:245:ARG:NH2	2.38	0.57
3:E:196:THR:HG22	3:E:203:PRO:HG3	1.89	0.55
2:F:119:LYS:NZ	4:F:307:HOH:O	2.39	0.55
2:F:62:GLU:OE2	2:F:65:LYS:NZ	2.27	0.55
1:D:267:ARG:NH1	4:D:306:HOH:O	2.40	0.54
1:D:236:ASP:N	1:D:236:ASP:OD1	2.40	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:144:LYS:HB3	3:B:196:THR:HB	1.90	0.53
1:A:137:ALA:HA	4:A:301:HOH:O	2.09	0.52
1:D:107:GLU:O	1:D:110:SER:OG	2.22	0.52
3:B:1:GLN:N	3:B:1:GLN:CD	2.64	0.50
1:D:109:ASN:O	1:D:112:VAL:HG12	2.11	0.50
1:A:210:LEU:HD11	1:A:266:LEU:HB2	1.94	0.49
1:D:201:TYR:O	1:D:205:GLU:HG2	2.12	0.49
1:D:210:LEU:HD11	1:D:266:LEU:HB3	1.95	0.49
1:A:94:ARG:O	1:A:212:GLN:NE2	2.44	0.48
1:D:143:GLY:HA3	2:F:52:TYR:CD2	2.48	0.48
2:C:12:VAL:HG13	2:C:16:ALA:HB3	1.96	0.47
1:A:175:LYS:HG3	1:A:177:ASN:ND2	2.28	0.47
1:D:176:LEU:N	1:D:228:LEU:HD11	2.29	0.47
1:A:152:ARG:HA	1:A:152:ARG:HD3	1.69	0.47
2:F:134:SER:N	2:F:135:GLY:HA3	2.28	0.47
2:F:63:LYS:NZ	4:F:312:HOH:O	2.47	0.47
1:D:105:ALA:HA	4:D:320:HOH:O	2.15	0.46
3:B:187:LYS:HG3	3:B:188:HIS:CE1	2.51	0.46
1:D:128:GLN:O	1:D:131:THR:OG1	2.22	0.45
1:A:91:LYS:HB3	1:A:91:LYS:HE2	1.79	0.45
1:A:168:CYS:HA	1:A:169:PRO:HD3	1.80	0.45
1:A:179:ILE:HD12	1:A:228:LEU:CD2	2.47	0.45
1:D:152:ARG:HA	1:D:152:ARG:HD3	1.76	0.45
1:D:210:LEU:HD11	1:D:266:LEU:CB	2.47	0.44
2:C:121:PRO:HB3	2:C:147:TYR:HB3	1.99	0.44
1:A:244:LEU:HD12	1:A:248:SER:HB2	1.98	0.44
1:A:237:PHE:HA	1:A:238:PRO:HA	1.83	0.44
1:D:73:CYS:HG	1:D:76:CYS:HG	1.64	0.43
3:E:123:GLN:HG2	3:E:128:THR:O	2.18	0.43
2:C:152:VAL:HG12	2:C:202:HIS:HB2	2.00	0.43
1:A:164:TRP:HA	1:A:165:PRO:HD3	1.91	0.43
1:A:91:LYS:HG3	1:A:94:ARG:NH2	2.34	0.43
1:D:225:GLU:HG2	1:D:228:LEU:HD22	2.00	0.43
1:A:267:ARG:NH2	4:A:315:HOH:O	2.51	0.43
1:D:231:LYS:HE2	1:D:232:PHE:CE1	2.54	0.43
1:D:165:PRO:HG2	1:D:168:CYS:CB	2.49	0.43
2:C:205:SER:HB2	1:D:264:SER:HB3	2.00	0.43
1:A:228:LEU:HA	1:A:228:LEU:HD23	1.81	0.42
3:B:146:GLN:HB3	3:B:194:GLU:HB3	2.02	0.41
2:C:47:TRP:CZ2	2:C:49:GLY:HA2	2.54	0.41
2:C:190:SER:C	2:C:192:GLY:H	2.24	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:63:LYS:NZ	4:F:310:HOH:O	2.46	0.41
3:B:200:LEU:HD13	3:B:204:VAL:HG23	2.03	0.41
1:D:160:HIS:HB2	1:D:164:TRP:CE3	2.56	0.41
1:D:205:GLU:HG2	1:D:205:GLU:H	1.72	0.41
1:D:176:LEU:CA	1:D:228:LEU:HD11	2.52	0.40
1:A:109:ASN:O	1:A:112:VAL:HG22	2.21	0.40
1:D:140:PRO:HB2	1:D:144:ALA:HB2	2.04	0.40

All (5) 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)
4:A:301:HOH:O	4:B:306:HOH:O[4_475]	1.71	0.49
4:A:444:HOH:O	4:C:301:HOH:O[4_475]	1.77	0.43
4:A:304:HOH:O	4:C:352:HOH:O[4_475]	1.86	0.34
4:A:425:HOH:O	4:D:334:HOH:O[2_474]	2.04	0.16
4:A:444:HOH:O	4:B:355:HOH:O[4_475]	2.05	0.15

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	238/244 (98%)	233 (98%)	5 (2%)	0	100	100
1	D	231/244 (95%)	223 (96%)	8 (4%)	0	100	100
2	C	203/218 (93%)	194 (96%)	9 (4%)	0	100	100
2	F	214/218 (98%)	206 (96%)	8 (4%)	0	100	100
3	B	210/213 (99%)	203 (97%)	7 (3%)	0	100	100
3	E	210/213 (99%)	203 (97%)	7 (3%)	0	100	100
All	All	1306/1350 (97%)	1262 (97%)	44 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	203/207 (98%)	198 (98%)	5 (2%)	55 67
1	D	198/207 (96%)	196 (99%)	2 (1%)	82 91
2	C	175/186 (94%)	173 (99%)	2 (1%)	80 89
2	F	184/186 (99%)	182 (99%)	2 (1%)	80 89
3	B	184/185 (100%)	184 (100%)	0	100 100
3	E	184/185 (100%)	184 (100%)	0	100 100
All	All	1128/1156 (98%)	1117 (99%)	11 (1%)	82 91

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	73	CYS
1	A	172	GLU
1	A	175	LYS
1	A	267	ARG
1	A	272	LEU
2	C	12	VAL
2	C	193	THR
1	D	231	LYS
1	D	236	ASP
2	F	152	VAL
2	F	216	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	117	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 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	240/244 (98%)	-0.29	4 (1%)	73	72	21, 29, 43, 52	0
1	D	235/244 (96%)	-0.05	7 (2%)	54	53	24, 35, 55, 63	0
2	C	207/218 (94%)	-0.21	6 (2%)	55	54	19, 30, 56, 77	0
2	F	216/218 (99%)	-0.44	4 (1%)	70	68	21, 28, 45, 59	0
3	B	212/213 (99%)	-0.29	4 (1%)	70	68	19, 31, 53, 60	0
3	E	212/213 (99%)	-0.24	3 (1%)	78	77	24, 31, 45, 57	0
All	All	1322/1350 (97%)	-0.25	28 (2%)	67	65	19, 30, 51, 77	0

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	193	THR	6.5
2	C	129	SER	4.9
1	D	164	TRP	4.5
1	D	66	VAL	3.8
2	C	192	GLY	3.7
3	B	125	LYS	3.5
2	F	134	SER	3.3
2	C	189	SER	3.2
3	E	132	VAL	3.0
1	D	271	GLY	3.0
2	C	190	SER	3.0
3	B	153	LEU	2.9
1	A	36	SER	2.8
1	A	108	THR	2.8
3	E	183	ALA	2.6
2	C	191	LEU	2.6
1	D	65	ALA	2.5
1	A	273	THR	2.5
1	A	35	MET	2.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
3	E	34	TRP	2.4
3	B	183	ALA	2.3
2	F	216	LYS	2.3
1	D	273	THR	2.1
1	D	119	ALA	2.1
2	F	41	PRO	2.0
2	F	193	THR	2.0
3	B	155	SER	2.0
1	D	105	ALA	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.