W O R L D W I D E
wwPDB
PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 01:03 PM GMT

PDB ID	:	3SMH
Title	:	Crystal structure of major peanut allergen Ara h 1
Authors	:	Cabanos, C.S.; Mikami, B.; Maruyama, N.
Deposited on	:	2011-06-28
Resolution	:	2.43 Å(reported)

The following versions of software and data (see references ⓘ) 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 2.43 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.
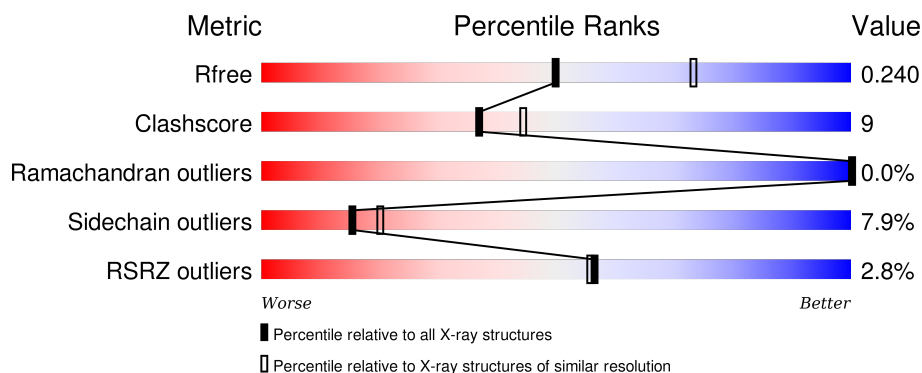
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1003 (2.46-2.42)
Clashscore	102246	1071 (2.46-2.42)
Ramachandran outliers	100387	1065 (2.46-2.42)
Sidechain outliers	100360	1065 (2.46-2.42)
RSRZ outliers	91569	1005 (2.46-2.42)

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	418	2% — 68% / 19% / • / 11%
1	B	418	% — 65% / 20% / • / 13%
1	C	418	2% — 67% / 20% / • / 11%
1	D	418	% — 67% / 19% / • / 11%
1	E	418	4% — 65% / 20% / • / 13%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	418	

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 17950 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 Allergen Ara h 1, clone P41B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	373	Total 2982	C 1859	N 553	O 564	S 6	0	0	0
1	B	365	Total 2910	C 1820	N 537	O 547	S 6	0	0	0
1	C	370	Total 2949	C 1841	N 546	O 556	S 6	0	0	0
1	D	373	Total 2965	C 1851	N 551	O 557	S 6	0	0	0
1	E	365	Total 2901	C 1812	N 532	O 551	S 6	0	0	0
1	F	364	Total 2906	C 1817	N 538	O 545	S 6	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	275	VAL	MET	CONFLICT	UNP P43238
B	275	VAL	MET	CONFLICT	UNP P43238
C	275	VAL	MET	CONFLICT	UNP P43238
D	275	VAL	MET	CONFLICT	UNP P43238
E	275	VAL	MET	CONFLICT	UNP P43238
F	275	VAL	MET	CONFLICT	UNP P43238

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	63	Total 63	O 63	0	0
2	B	47	Total 47	O 47	0	0
2	C	59	Total 59	O 59	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	D	85	Total 85	O 85	0	0
2	E	36	Total 36	O 36	0	0
2	F	47	Total 47	O 47	0	0

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: Allergen Ara h 1, clone P41B
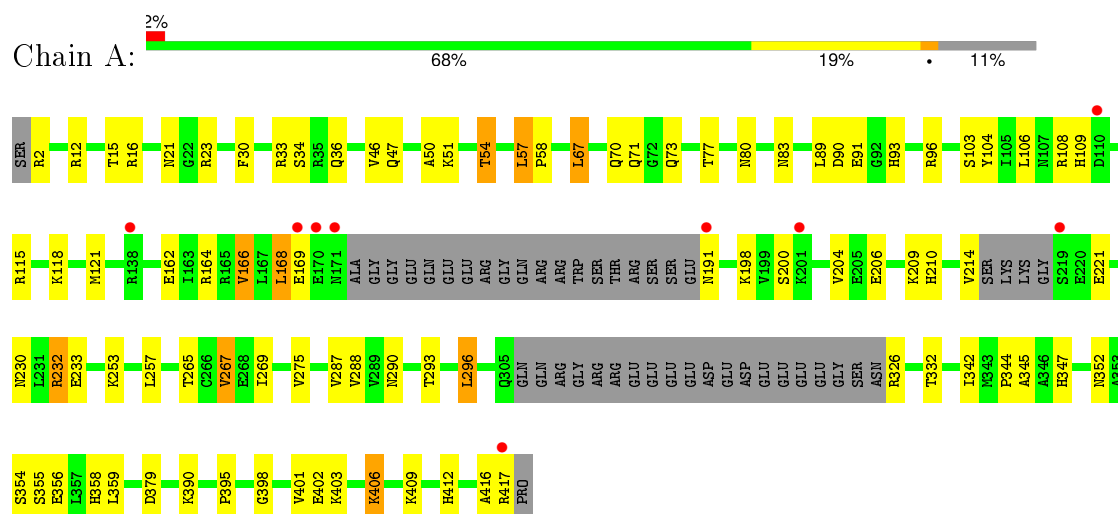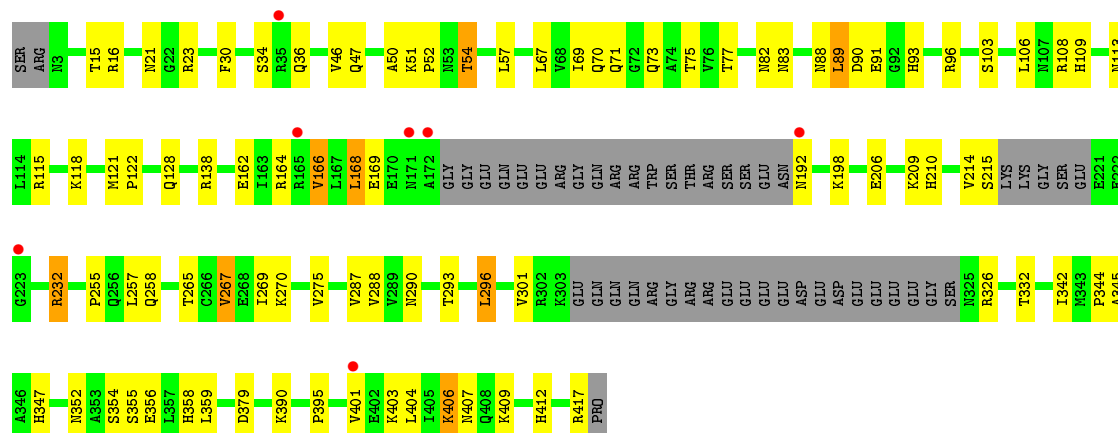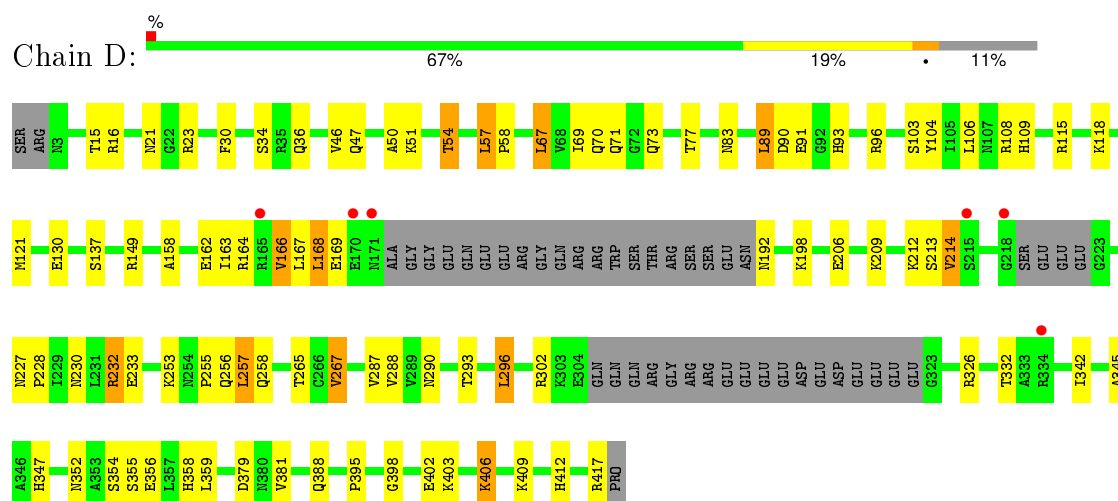
- Molecule 1: Allergen Ara h 1, clone P41B

- Molecule 1: Allergen Ara h 1, clone P41B

- Molecule 1: Allergen Ara h 1, clone P41B
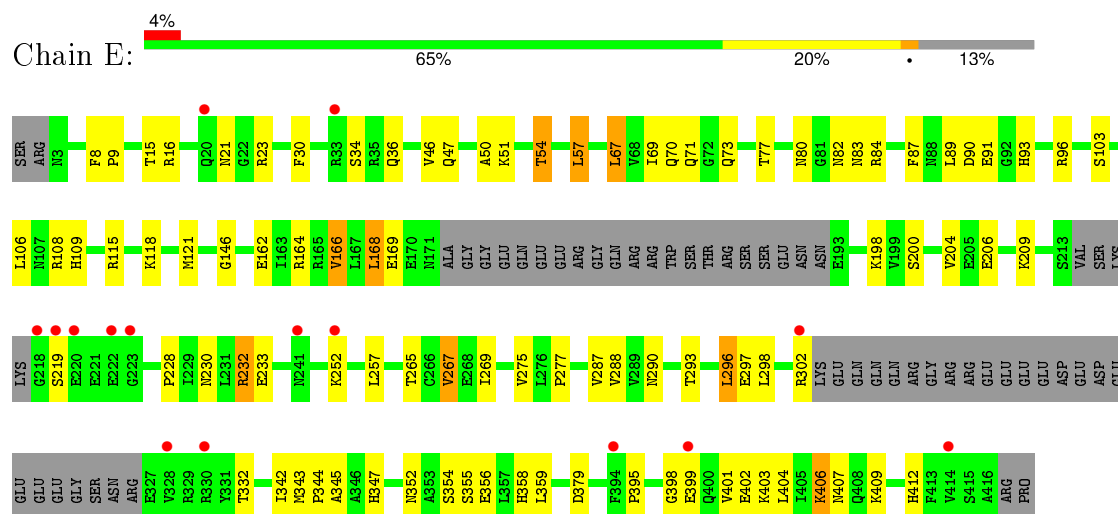
Chain D:

67%	19%	11%

- Molecule 1: Allergen Ara h 1, clone P41B

Chain E:

65%	20%	13%

- Molecule 1: Allergen Ara h 1, clone P41B

Chain F:

67%	18%	13%

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	156.49Å 89.01Å 158.97Å 90.00° 107.15° 90.00°	Depositor
Resolution (Å)	15.00 – 2.43 49.20 – 2.43	Depositor EDS
% Data completeness (in resolution range)	98.3 (15.00-2.43) 98.3 (49.20-2.43)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$<I/\sigma(I)>$ [1]	6.35 (at 2.42Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.4_486)	Depositor
R, R_{free}	0.202 , 0.244 0.195 , 0.240	Depositor DCC
R_{free} test set	3876 reflections (5.03%)	DCC
Wilson B-factor (Å^2)	39.2	Xtriage
Anisotropy	0.754	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 45.0	EDS
Estimated twinning fraction	0.017 for 1/2*h-3/2*k,-1/2*h-1/2*k,-1/2*h +1/2*k-l 0.018 for 1/2*h+3/2*k,1/2*h-1/2*k,-1/2*h- 1/2*k-l	Xtriage
L-test for twinning[2]	$<|L|>=0.48$, $<L^2>=0.31$	Xtriage
Outliers	1 of 77091 reflections (0.001%)	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	17950	wwPDB-VP
Average B, all atoms (Å^2)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.13% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: CSD

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	0.42	0/3023	0.56	0/4072
1	B	0.41	0/2951	0.88	6/3977 (0.2%)
1	C	0.41	0/2990	0.56	0/4029
1	D	0.42	0/3006	0.75	3/4047 (0.1%)
1	E	0.41	0/2942	0.57	0/3965
1	F	0.41	0/2947	0.56	0/3970
All	All	0.41	0/17859	0.66	9/24060 (0.0%)

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	149	ARG	NE-CZ-NH1	-21.52	109.54	120.30
1	B	35	ARG	NE-CZ-NH1	-21.03	109.79	120.30
1	D	149	ARG	NE-CZ-NH2	20.62	130.61	120.30
1	B	35	ARG	NE-CZ-NH2	20.39	130.49	120.30
1	B	165	ARG	NE-CZ-NH1	-20.22	110.19	120.30

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	2982	0	2955	71	0
1	B	2910	0	2892	57	0
1	C	2949	0	2927	58	0
1	D	2965	0	2949	60	0
1	E	2901	0	2864	57	0
1	F	2906	0	2890	66	0
2	A	63	0	0	0	0
2	B	47	0	0	3	0
2	C	59	0	0	3	0
2	D	85	0	0	5	0
2	E	36	0	0	2	0
2	F	47	0	0	1	0
All	All	17950	0	17477	328	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 9.

The worst 5 of 328 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:253:LYS:CG	1:F:233:GLU:HG3	1.93	0.99
1:A:209:LYS:HE3	1:A:210:HIS:CE1	1.97	0.98
1:A:417:ARG:HH11	1:A:417:ARG:HA	1.25	0.97
1:A:2:ARG:HG2	1:A:12:ARG:HH12	1.30	0.97
1:A:253:LYS:HG3	1:F:233:GLU:CG	2.01	0.91

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	364/418 (87%)	351 (96%)	13 (4%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	356/418 (85%)	343 (96%)	13 (4%)	0	100	100
1	C	361/418 (86%)	349 (97%)	12 (3%)	0	100	100
1	D	364/418 (87%)	352 (97%)	12 (3%)	0	100	100
1	E	356/418 (85%)	342 (96%)	13 (4%)	1 (0%)	46	56
1	F	355/418 (85%)	340 (96%)	15 (4%)	0	100	100
All	All	2156/2508 (86%)	2077 (96%)	78 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	219	SER

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	326/364 (90%)	300 (92%)	26 (8%)	15	19
1	B	318/364 (87%)	293 (92%)	25 (8%)	15	20
1	C	322/364 (88%)	297 (92%)	25 (8%)	16	20
1	D	323/364 (89%)	296 (92%)	27 (8%)	14	16
1	E	316/364 (87%)	293 (93%)	23 (7%)	17	23
1	F	317/364 (87%)	292 (92%)	25 (8%)	15	20
All	All	1922/2184 (88%)	1771 (92%)	151 (8%)	15	20

5 of 151 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	287	VAL
1	D	106	LEU
1	F	257	LEU
1	C	296	LEU
1	D	15	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 108 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	352	ASN
1	D	88	ASN
1	F	93	HIS
1	C	368	ASN
1	D	32	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)

6 non-standard protein/DNA/RNA residues 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	$\#|Z| > 2$
1	CSD	A	266	1	3,7,8	0.94	0	3,8,10	1.38	0
1	CSD	B	266	1	3,7,8	0.83	0	3,8,10	1.71	1 (33%)
1	CSD	C	266	1	3,7,8	0.71	0	3,8,10	1.25	0
1	CSD	D	266	1	3,7,8	0.76	0	3,8,10	1.63	1 (33%)
1	CSD	E	266	1	3,7,8	0.67	0	3,8,10	1.55	1 (33%)
1	CSD	F	266	1	3,7,8	0.72	0	3,8,10	2.22	1 (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
1	CSD	A	266	1	-	0/2/6/8	0/0/0/0
1	CSD	B	266	1	-	0/2/6/8	0/0/0/0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	CSD	C	266	1	-	0/2/6/8	0/0/0/0
1	CSD	D	266	1	-	0/2/6/8	0/0/0/0
1	CSD	E	266	1	-	0/2/6/8	0/0/0/0
1	CSD	F	266	1	-	0/2/6/8	0/0/0/0

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	E	266	CSD	OD1-SG-CB	2.20	109.07	105.40
1	D	266	CSD	OD1-SG-CB	2.36	109.33	105.40
1	B	266	CSD	OD1-SG-CB	2.41	109.42	105.40
1	F	266	CSD	OD1-SG-CB	3.47	111.18	105.40

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	372/418 (88%)	-0.08	9 (2%)	62	61	26, 42, 75, 120	0
1	B	364/418 (87%)	-0.05	6 (1%)	74	74	28, 43, 71, 96	0
1	C	369/418 (88%)	-0.10	7 (1%)	70	69	25, 42, 72, 95	0
1	D	372/418 (88%)	-0.01	6 (1%)	74	74	26, 41, 69, 93	0
1	E	364/418 (87%)	0.18	15 (4%)	41	40	29, 44, 73, 122	0
1	F	363/418 (86%)	0.11	19 (5%)	31	30	28, 44, 72, 97	0
All	All	2204/2508 (87%)	0.01	62 (2%)	56	56	25, 43, 72, 122	0

The worst 5 of 62 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	220	GLU	4.4
1	D	171	ASN	4.1
1	E	399	GLU	3.9
1	E	219	SER	3.6
1	F	201	LYS	3.6

6.2 Non-standard residues in protein, DNA, RNA chains (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, 95th 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
1	CSD	D	266	8/9	0.88	0.14	-	27,36,58,72	0
1	CSD	F	266	8/9	0.94	0.12	-	35,38,53,75	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
1	CSD	E	266	8/9	0.92	0.14	-	34,39,61,78	0
1	CSD	B	266	8/9	0.84	0.15	-	30,40,57,71	0
1	CSD	A	266	8/9	0.93	0.12	-	27,35,59,73	0
1	CSD	C	266	8/9	0.93	0.15	-	33,37,59,71	0

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.