wwPDB X-ray Structure Validation Summary Report (i)

Nov 13, 2023 – 10:45 AM JST

PDB ID	:	5WXU
Title	:	11S globulin from Wrightia tinctoria reveals auxin binding site
Authors	:	Kumar, P.; Kesari, P.; Dhindwal, S.; Kumar, P.
Deposited on	:	2017-01-09
Resolution	:	1.70 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 (i) 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 (i)) were used in the production of this report:

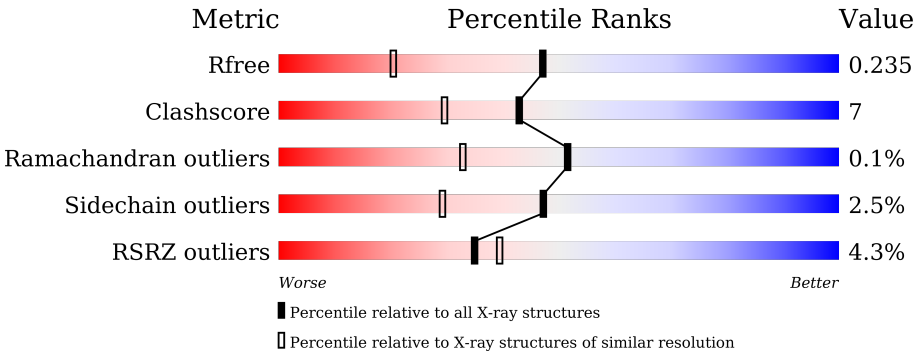
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 1.70 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}	130704	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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	479	2% 73% 9% • 17%
1	B	479	4% 71% 11% • 16%
1	C	479	4% 71% 10% • 17%
1	D	479	4% 71% 11% • 17%
1	E	479	4% 72% 10% • 17%
1	F	479	4% 71% 11% • 17%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	PO4	B	501	-	X	-	-
2	PO4	C	506	-	-	-	X
3	FLC	A	503	-	X	X	-
3	FLC	B	504	-	X	-	-
3	FLC	C	501	-	X	X	-
3	FLC	D	502	-	X	-	-
3	FLC	E	504	-	X	-	-
3	FLC	F	501	-	X	-	-
4	GOL	B	503	-	X	-	-
6	PEG	D	505	-	-	X	-
6	PEG	E	506	-	-	X	-
6	PEG	F	505	-	-	X	-

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 21977 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.

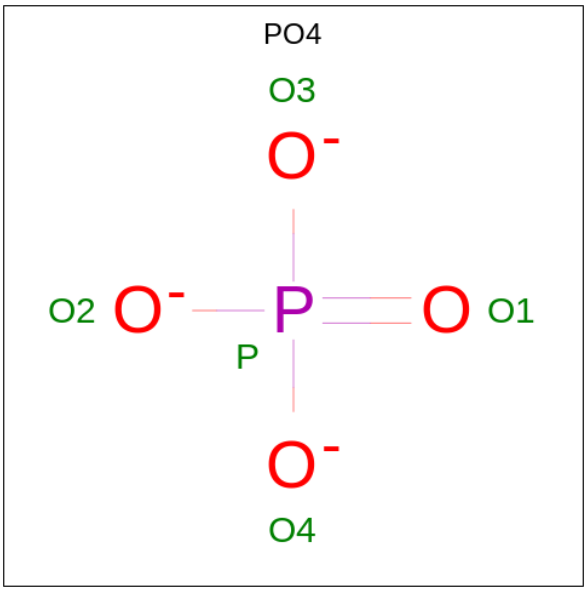
- Molecule 1 is a protein called 11S globulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	399	Total	C	N	O	S	0	20	0
			3360	2102	620	631	7			
1	B	400	Total	C	N	O	S	0	12	0
			3281	2060	600	614	7			
1	C	397	Total	C	N	O	S	0	9	0
			3240	2035	595	603	7			
1	D	396	Total	C	N	O	S	0	4	0
			3192	2006	584	595	7			
1	E	397	Total	C	N	O	S	0	6	0
			3221	2020	590	604	7			
1	F	398	Total	C	N	O	S	0	10	0
			3264	2047	599	610	8			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	147	GLN	ARG	conflict	UNP A0A162EGL7
A	459	ASP	GLY	conflict	UNP A0A162EGL7
B	147	GLN	ARG	conflict	UNP A0A162EGL7
B	459	ASP	GLY	conflict	UNP A0A162EGL7
C	147	GLN	ARG	conflict	UNP A0A162EGL7
C	459	ASP	GLY	conflict	UNP A0A162EGL7
D	147	GLN	ARG	conflict	UNP A0A162EGL7
D	459	ASP	GLY	conflict	UNP A0A162EGL7
E	147	GLN	ARG	conflict	UNP A0A162EGL7
E	459	ASP	GLY	conflict	UNP A0A162EGL7
F	147	GLN	ARG	conflict	UNP A0A162EGL7
F	459	ASP	GLY	conflict	UNP A0A162EGL7

- Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O P 5 4 1	0	0
2	A	1	Total O P 5 4 1	0	0
2	B	1	Total O P 5 4 1	0	0
2	B	1	Total O P 5 4 1	0	0
2	B	1	Total O P 5 4 1	0	0
2	C	1	Total O P 5 4 1	0	0
2	C	1	Total O P 5 4 1	0	0
2	C	1	Total O P 5 4 1	0	0
2	D	1	Total O P 5 4 1	0	0
2	D	1	Total O P 5 4 1	0	0
2	D	1	Total O P 5 4 1	0	0
2	E	1	Total O P 5 4 1	0	0
2	E	1	Total O P 5 4 1	0	0
2	E	1	Total O P 5 4 1	0	0

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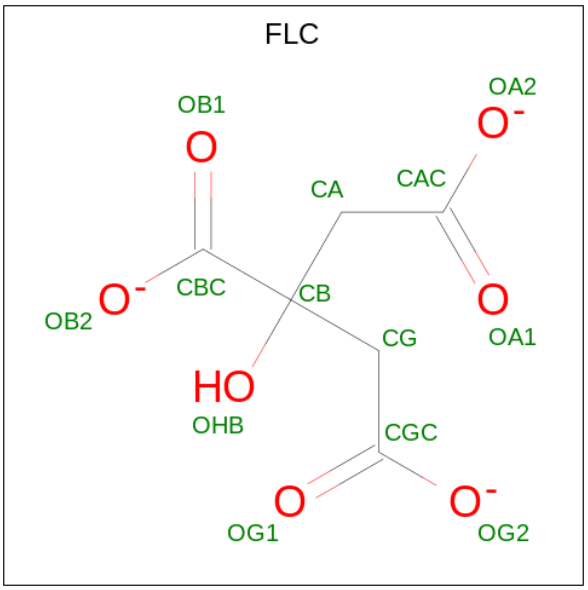
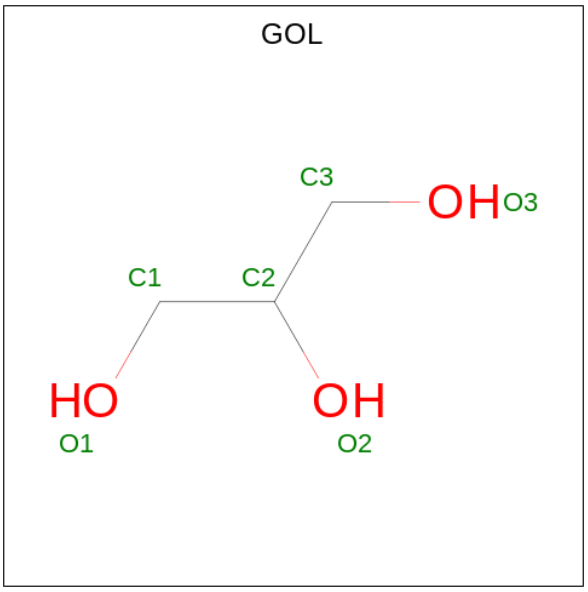
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	E	1	Total O P 5 4 1	0	0
2	F	1	Total O P 5 4 1	0	0
2	F	1	Total O P 5 4 1	0	0
2	F	1	Total O P 5 4 1	0	0

- Molecule 3 is CITRATE ANION (three-letter code: FLC) (formula: $C_6H_5O_7$).



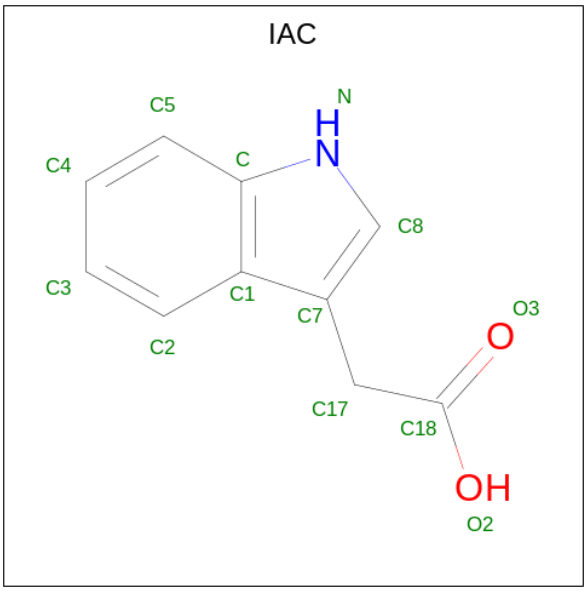
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 13 6 7	0	0
3	B	1	Total C O 13 6 7	0	0
3	C	1	Total C O 13 6 7	0	0
3	D	1	Total C O 13 6 7	0	0
3	E	1	Total C O 13 6 7	0	0
3	F	1	Total C O 13 6 7	0	0

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



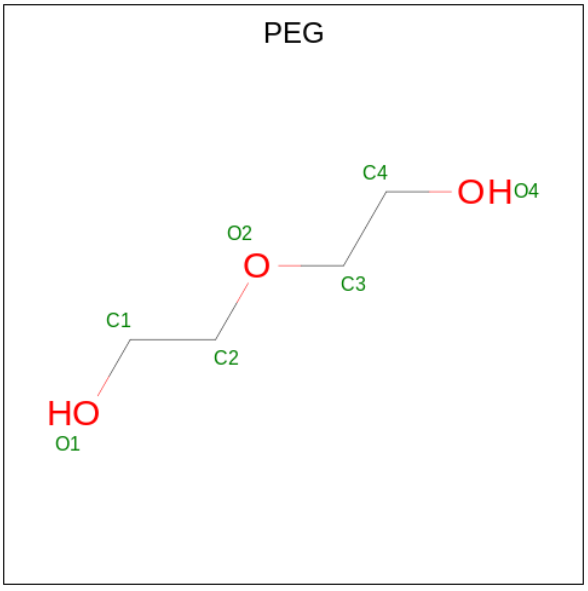
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 6 3 3	0	0
4	A	1	Total C O 6 3 3	0	0
4	A	1	Total C O 6 3 3	0	0
4	B	1	Total C O 6 3 3	0	0
4	B	1	Total C O 6 3 3	0	0
4	C	1	Total C O 6 3 3	0	0
4	C	1	Total C O 6 3 3	0	0
4	E	1	Total C O 6 3 3	0	0
4	F	1	Total C O 6 3 3	0	0

- Molecule 5 is 1H-INDOL-3-YLACETIC ACID (three-letter code: IAC) (formula: $C_{10}H_9NO_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	1
			26	20	2	4		
5	B	1	Total	C	N	O	0	1
			26	20	2	4		
5	D	1	Total	C	N	O	0	1
			26	20	2	4		

- Molecule 6 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	D	1	Total	C	O	0	0
			7	4	3		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	E	1	Total C O 7 4 3	0	0
6	F	1	Total C O 7 4 3	0	0

- Molecule 7 is water.

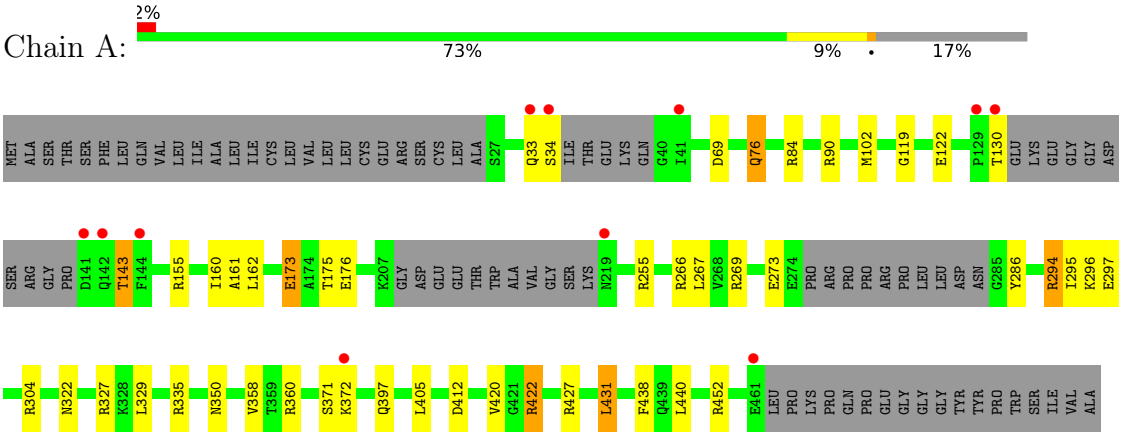
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	388	Total O 388 388	0	0
7	B	346	Total O 346 346	0	0
7	C	327	Total O 327 327	0	0
7	D	339	Total O 339 339	0	0
7	E	352	Total O 352 352	0	0
7	F	346	Total O 346 346	0	0

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.

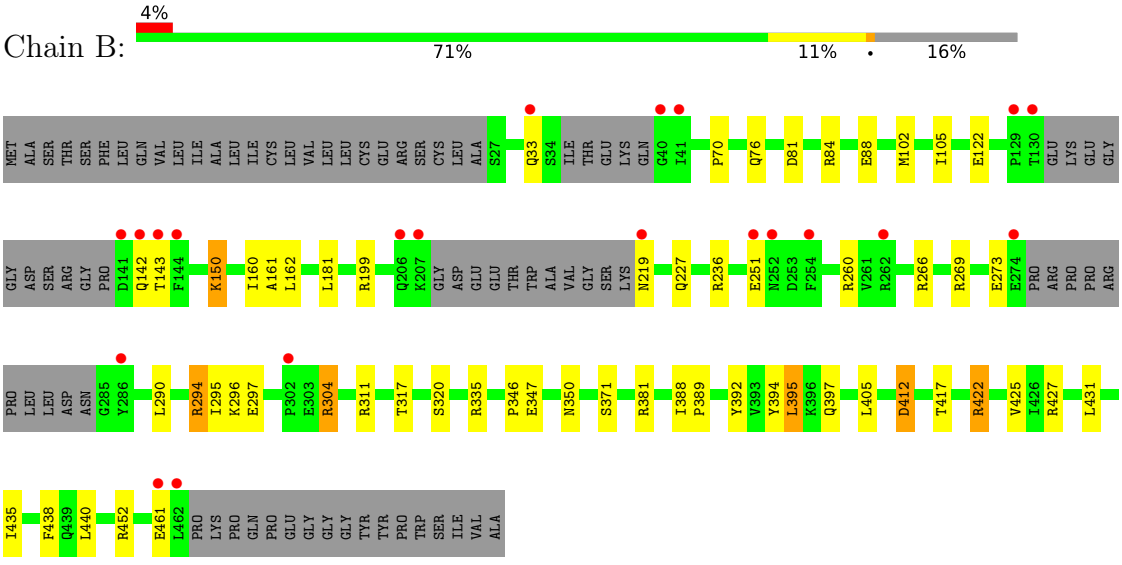
• Molecule 1: 11S globulin

Chain A:



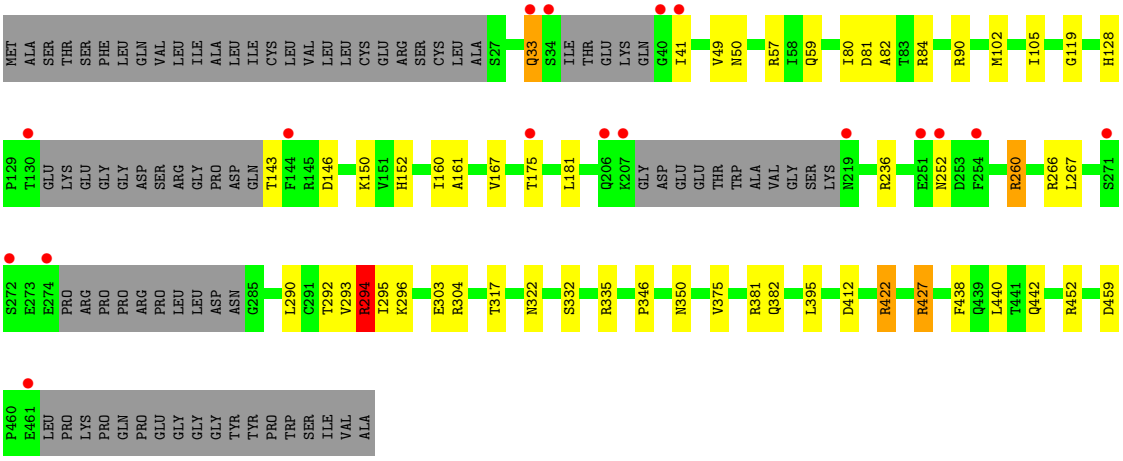
• Molecule 1: 11S globulin

Chain B:



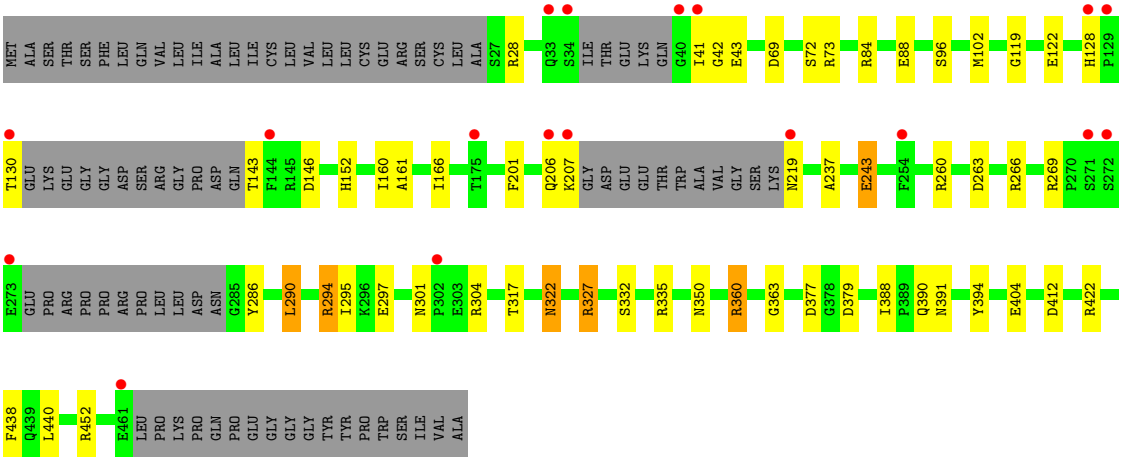
• Molecule 1: 11S globulin

Chain C:



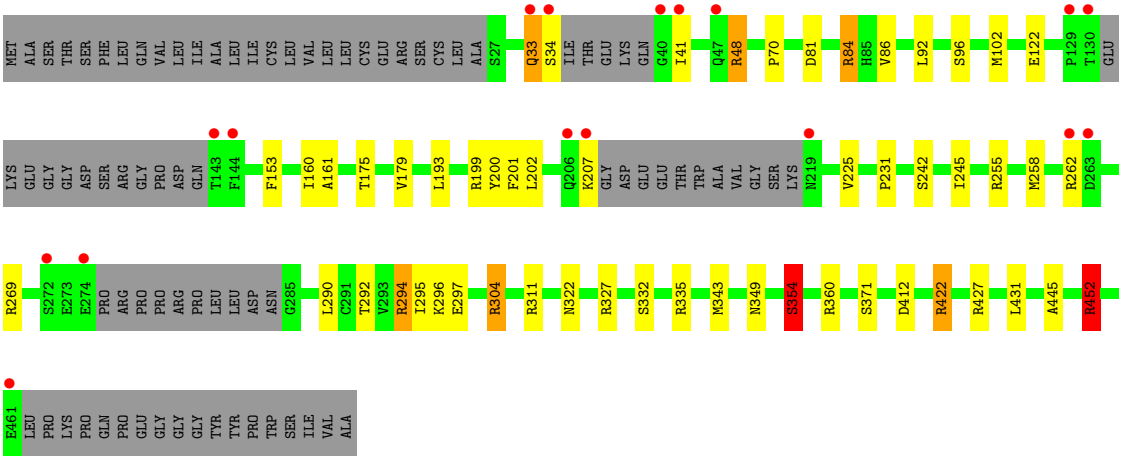
• Molecule 1: 11S globulin

Chain D:



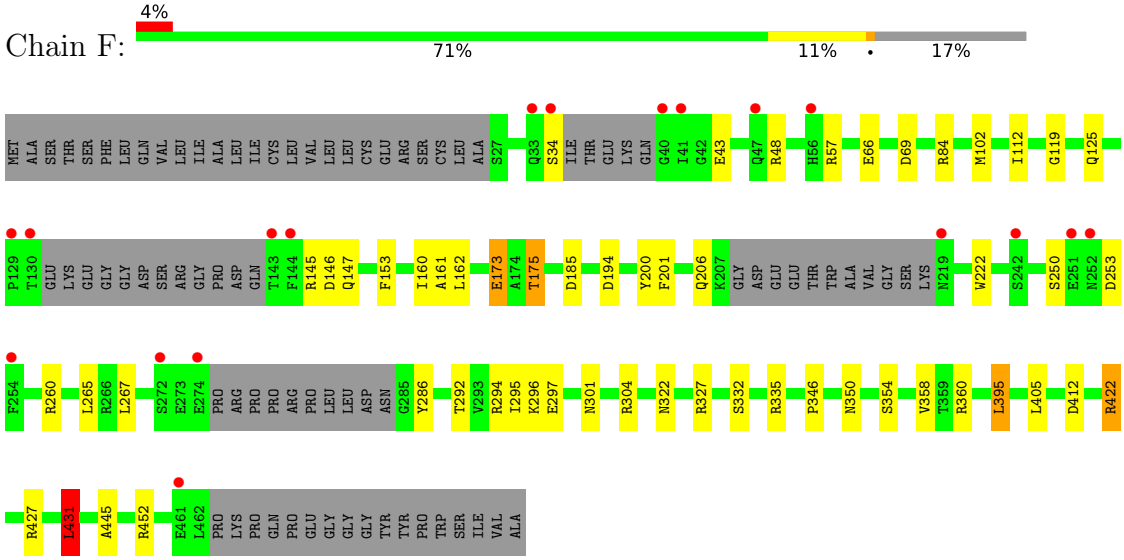
• Molecule 1: 11S globulin

Chain E:



• Molecule 1: 11S globulin

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	111.21Å 114.24Å 202.48Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	101.24 – 1.70 31.42 – 1.70	Depositor EDS
% Data completeness (in resolution range)	94.2 (101.24-1.70) 94.3 (31.42-1.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	2.57 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.174 , 0.227 0.185 , 0.235	Depositor DCC
R_{free} test set	13201 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å^2)	21.1	Xtriage
Anisotropy	0.445	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 46.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.35$	Xtriage
Estimated twinning fraction	0.009 for k,h,-l	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	21977	wwPDB-VP
Average B, all atoms (Å^2)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.71% 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

Bond lengths and bond angles in the following residue types are not validated in this section: IAC, FLC, PO4, GOL, PEG

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	1.00	1/3425 (0.0%)	1.08	13/4641 (0.3%)
1	B	1.02	1/3360 (0.0%)	1.11	21/4556 (0.5%)
1	C	1.01	3/3316 (0.1%)	1.12	16/4495 (0.4%)
1	D	1.03	4/3259 (0.1%)	1.09	10/4420 (0.2%)
1	E	1.01	4/3285 (0.1%)	1.12	14/4454 (0.3%)
1	F	1.04	4/3328 (0.1%)	1.08	14/4512 (0.3%)
All	All	1.02	17/19973 (0.1%)	1.10	88/27078 (0.3%)

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	332	SER	CB-OG	-9.16	1.30	1.42
1	B	122	GLU	CD-OE2	7.75	1.34	1.25
1	D	122	GLU	CD-OE2	6.91	1.33	1.25
1	F	175	THR	CB-CG2	-6.62	1.30	1.52
1	D	332	SER	CB-OG	-6.61	1.33	1.42

The worst 5 of 88 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	452	ARG	NE-CZ-NH2	-9.64	115.48	120.30
1	E	335	ARG	NE-CZ-NH1	9.29	124.94	120.30
1	C	452	ARG	NE-CZ-NH2	-9.14	115.73	120.30
1	F	260	ARG	NE-CZ-NH2	-9.06	115.77	120.30
1	E	294[A]	ARG	NE-CZ-NH1	-8.96	115.82	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	3360	0	3297	40	0
1	B	3281	0	3247	39	0
1	C	3240	0	3207	54	0
1	D	3192	0	3155	43	0
1	E	3221	0	3168	47	0
1	F	3264	0	3218	47	0
2	A	10	0	0	0	0
2	B	15	0	0	0	0
2	C	15	0	0	0	0
2	D	15	0	0	0	0
2	E	20	0	0	0	0
2	F	15	0	0	0	0
3	A	13	0	5	4	0
3	B	13	0	5	2	0
3	C	13	0	5	5	0
3	D	13	0	5	3	0
3	E	13	0	5	2	0
3	F	13	0	5	3	0
4	A	18	0	24	2	0
4	B	12	0	16	0	0
4	C	12	0	16	0	0
4	E	6	0	8	0	0
4	F	6	0	8	0	0
5	A	26	0	16	8	0
5	B	26	0	16	8	0
5	D	26	0	16	5	0
6	D	7	0	10	10	0
6	E	7	0	10	7	0
6	F	7	0	10	12	0
7	A	388	0	0	8	3
7	B	346	0	0	7	0
7	C	327	0	0	14	0
7	D	339	0	0	15	3
7	E	352	0	0	12	3
7	F	346	0	0	10	1
All	All	21977	0	19472	266	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 7.

The worst 5 of 266 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:C:57[A]:ARG:HH21	1:C:59[A]:GLN:NE2	1.01	1.48
1:C:57[A]:ARG:NH2	1:C:59[A]:GLN:HE22	1.08	1.47
1:B:294[A]:ARG:NH2	1:B:297:GLU:OE1	1.75	1.20
1:E:84:ARG:HD2	7:E:747:HOH:O	1.53	1.04
1:C:57[A]:ARG:NH2	1:C:59[A]:GLN:NE2	1.79	1.01

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)
7:D:746:HOH:O	7:E:883:HOH:O[4_556]	1.46	0.74
7:A:868:HOH:O	7:F:750:HOH:O[3_545]	1.58	0.62
7:D:858:HOH:O	7:E:883:HOH:O[4_556]	1.94	0.26
7:A:898:HOH:O	7:E:651:HOH:O[2_454]	2.08	0.12
7:A:898:HOH:O	7:D:601:HOH:O[2_454]	2.17	0.03

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	409/479 (85%)	393 (96%)	16 (4%)	0	100 100
1	B	402/479 (84%)	385 (96%)	16 (4%)	1 (0%)	47 30
1	C	396/479 (83%)	384 (97%)	12 (3%)	0	100 100
1	D	390/479 (81%)	378 (97%)	12 (3%)	0	100 100
1	E	393/479 (82%)	378 (96%)	13 (3%)	2 (0%)	29 13
1	F	398/479 (83%)	382 (96%)	16 (4%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	2388/2874 (83%)	2300 (96%)	85 (4%)	3 (0%)	51 33

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	41	ILE
1	B	33	GLN
1	E	193	LEU

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	369/416 (89%)	360 (98%)	9 (2%)	49 31
1	B	362/416 (87%)	354 (98%)	8 (2%)	52 34
1	C	356/416 (86%)	344 (97%)	12 (3%)	37 18
1	D	350/416 (84%)	340 (97%)	10 (3%)	42 23
1	E	353/416 (85%)	343 (97%)	10 (3%)	43 25
1	F	358/416 (86%)	351 (98%)	7 (2%)	55 38
All	All	2148/2496 (86%)	2092 (97%)	56 (3%)	47 28

5 of 56 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	427[B]	ARG
1	F	431	LEU
1	D	269	ARG
1	F	354	SER
1	F	34	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	382	GLN
1	D	128	HIS
1	D	223	ASN
1	B	76	GLN
1	A	232	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

42 ligands 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	$\#\|Z\| > 2$
2	PO4	C	505	-	4,4,4	1.28	0	6,6,6	2.03	3 (50%)
2	PO4	E	502	-	4,4,4	1.29	0	6,6,6	1.07	1 (16%)
6	PEG	E	506	-	6,6,6	0.85	0	5,5,5	1.18	0
3	FLC	F	501	-	12,12,12	1.84	3 (25%)	17,17,17	5.92	11 (64%)
2	PO4	D	501	-	4,4,4	0.76	0	6,6,6	1.70	2 (33%)
2	PO4	E	507	-	4,4,4	0.78	0	6,6,6	0.59	0
3	FLC	E	504	-	12,12,12	1.40	2 (16%)	17,17,17	4.92	13 (76%)
5	IAC	B	506[B]	-	13,14,14	1.46	2 (15%)	14,19,19	1.06	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
6	PEG	D	505	-	6,6,6	0.96	0	5,5,5	1.92	3 (60%)
2	PO4	B	501	-	4,4,4	2.32	1 (25%)	6,6,6	2.46	3 (50%)
2	PO4	B	502	-	4,4,4	0.91	0	6,6,6	1.69	1 (16%)
5	IAC	B	506[A]	-	13,14,14	1.34	1 (7%)	14,19,19	1.53	3 (21%)
3	FLC	A	503	-	12,12,12	1.67	3 (25%)	17,17,17	4.81	12 (70%)
3	FLC	D	502	-	12,12,12	1.59	2 (16%)	17,17,17	4.41	9 (52%)
2	PO4	D	504	-	4,4,4	0.72	0	6,6,6	0.76	0
4	GOL	B	507	-	5,5,5	0.88	0	5,5,5	0.66	0
2	PO4	A	501	-	4,4,4	1.32	1 (25%)	6,6,6	1.30	0
2	PO4	F	504	-	4,4,4	1.10	0	6,6,6	1.57	1 (16%)
5	IAC	A	507[B]	-	13,14,14	1.49	1 (7%)	14,19,19	1.06	1 (7%)
2	PO4	A	502	-	4,4,4	0.41	0	6,6,6	1.30	1 (16%)
4	GOL	A	506	-	5,5,5	0.50	0	5,5,5	0.36	0
2	PO4	F	502	-	4,4,4	1.03	0	6,6,6	1.33	0
2	PO4	E	505	-	4,4,4	0.71	0	6,6,6	1.10	1 (16%)
4	GOL	B	503	-	5,5,5	1.63	2 (40%)	5,5,5	1.72	2 (40%)
5	IAC	A	507[A]	-	13,14,14	1.60	2 (15%)	14,19,19	1.31	2 (14%)
5	IAC	D	506[B]	-	13,14,14	1.43	2 (15%)	14,19,19	1.12	1 (7%)
4	GOL	E	503	-	5,5,5	0.54	0	5,5,5	0.63	0
2	PO4	F	503	-	4,4,4	0.91	0	6,6,6	1.90	2 (33%)
4	GOL	A	504	-	5,5,5	0.38	0	5,5,5	0.46	0
5	IAC	D	506[A]	-	13,14,14	1.49	2 (15%)	14,19,19	1.20	2 (14%)
4	GOL	F	506	-	5,5,5	0.85	0	5,5,5	0.78	0
2	PO4	E	501	-	4,4,4	1.22	1 (25%)	6,6,6	1.59	1 (16%)
2	PO4	D	503	-	4,4,4	0.86	0	6,6,6	0.39	0
3	FLC	B	504	-	12,12,12	1.96	5 (41%)	17,17,17	5.42	10 (58%)
3	FLC	C	501	-	12,12,12	1.75	1 (8%)	17,17,17	4.66	12 (70%)
4	GOL	A	505	-	5,5,5	0.66	0	5,5,5	0.54	0
4	GOL	C	502	-	5,5,5	0.63	0	5,5,5	0.75	0
4	GOL	C	503	-	5,5,5	0.59	0	5,5,5	0.82	0
2	PO4	B	505	-	4,4,4	0.96	0	6,6,6	2.02	2 (33%)
2	PO4	C	504	-	4,4,4	0.91	0	6,6,6	1.14	0
2	PO4	C	506	-	4,4,4	0.85	0	6,6,6	0.34	0
6	PEG	F	505	-	6,6,6	1.08	1 (16%)	5,5,5	2.15	2 (40%)

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
6	PEG	E	506	-	-	3/4/4/4	-
3	FLC	F	501	-	-	11/16/16/16	-
5	IAC	B	506[B]	-	-	2/4/4/4	0/2/2/2
3	FLC	E	504	-	-	9/16/16/16	-
6	PEG	D	505	-	-	2/4/4/4	-
5	IAC	B	506[A]	-	-	2/4/4/4	0/2/2/2
3	FLC	D	502	-	-	10/16/16/16	-
3	FLC	A	503	-	-	14/16/16/16	-
4	GOL	B	507	-	-	2/4/4/4	-
5	IAC	A	507[B]	-	-	0/4/4/4	0/2/2/2
4	GOL	A	506	-	-	2/4/4/4	-
4	GOL	B	503	-	-	4/4/4/4	-
5	IAC	A	507[A]	-	-	2/4/4/4	0/2/2/2
5	IAC	D	506[B]	-	-	0/4/4/4	0/2/2/2
4	GOL	E	503	-	-	3/4/4/4	-
4	GOL	A	504	-	-	1/4/4/4	-
5	IAC	D	506[A]	-	-	0/4/4/4	0/2/2/2
4	GOL	F	506	-	-	2/4/4/4	-
3	FLC	B	504	-	-	9/16/16/16	-
3	FLC	C	501	-	-	9/16/16/16	-
4	GOL	A	505	-	-	4/4/4/4	-
4	GOL	C	502	-	-	2/4/4/4	-
4	GOL	C	503	-	-	4/4/4/4	-
6	PEG	F	505	-	-	1/4/4/4	-

The worst 5 of 32 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	PO4	P-O1	4.57	1.61	1.50
3	C	501	FLC	OHB-CB	4.24	1.51	1.43
3	D	502	FLC	OHB-CB	3.92	1.50	1.43
3	F	501	FLC	CG-CB	3.55	1.58	1.53
3	A	503	FLC	CG-CB	-3.26	1.49	1.53

The worst 5 of 101 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	F	501	FLC	OHB-CB-CBC	-16.00	86.40	108.86
3	B	504	FLC	OHB-CB-CBC	-12.71	91.02	108.86
3	E	504	FLC	OHB-CB-CBC	-12.62	91.15	108.86
3	B	504	FLC	OHB-CB-CG	-12.41	80.36	109.40
3	A	503	FLC	CG-CB-CA	10.50	136.57	109.16

There are no chirality outliers.

5 of 98 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	503	FLC	CA-CB-CBC-OB1
3	A	503	FLC	CA-CB-CBC-OB2
3	A	503	FLC	OHB-CB-CBC-OB1
3	A	503	FLC	OHB-CB-CBC-OB2
3	A	503	FLC	CA-CB-CG-CGC

There are no ring outliers.

16 monomers are involved in 60 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	E	506	PEG	7	0
3	F	501	FLC	3	0
3	E	504	FLC	2	0
5	B	506[B]	IAC	4	0
6	D	505	PEG	10	0
5	B	506[A]	IAC	4	0
3	A	503	FLC	4	0
3	D	502	FLC	3	0
5	A	507[B]	IAC	3	0
4	A	506	GOL	2	0
5	A	507[A]	IAC	5	0
5	D	506[B]	IAC	3	0
5	D	506[A]	IAC	2	0
3	B	504	FLC	2	0
3	C	501	FLC	5	0
6	F	505	PEG	12	0

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

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	399/479 (83%)	-0.08	11 (2%)	53	57	14, 21, 42, 69	0
1	B	400/479 (83%)	0.00	21 (5%)	26	29	15, 23, 50, 85	0
1	C	397/479 (82%)	0.01	17 (4%)	35	39	15, 24, 47, 75	0
1	D	396/479 (82%)	0.01	18 (4%)	33	37	15, 23, 42, 98	0
1	E	397/479 (82%)	-0.04	17 (4%)	35	39	15, 23, 49, 75	0
1	F	398/479 (83%)	-0.05	18 (4%)	33	37	15, 22, 47, 77	0
All	All	2387/2874 (83%)	-0.02	102 (4%)	35	39	14, 23, 46, 98	0

The worst 5 of 102 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	40	GLY	10.2
1	D	130	THR	7.9
1	B	130	THR	7.4
1	A	41	ILE	6.8
1	D	144	PHE	6.7

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 (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. The B-factors column lists the minimum, median, 95^{th} 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	B-factors(Å^2)	Q<0.9
2	PO4	E	507	5/5	0.42	0.31	76,78,99,101	0
4	GOL	A	506	6/6	0.49	0.27	49,61,63,67	0
4	GOL	B	503	6/6	0.55	0.24	40,55,58,58	0
2	PO4	D	503	5/5	0.56	0.39	100,101,114,121	0
3	FLC	F	501	13/13	0.64	0.32	37,55,63,78	0
2	PO4	C	506	5/5	0.65	0.53	101,107,122,124	0
3	FLC	C	501	13/13	0.70	0.28	33,51,67,67	0
3	FLC	B	504	13/13	0.70	0.34	36,57,68,79	0
3	FLC	D	502	13/13	0.72	0.27	31,51,68,74	0
4	GOL	C	502	6/6	0.73	0.25	37,56,59,67	0
2	PO4	D	504	5/5	0.75	0.21	89,98,102,102	0
3	FLC	E	504	13/13	0.76	0.32	44,66,83,95	0
6	PEG	E	506	7/7	0.76	0.17	28,38,44,46	0
4	GOL	F	506	6/6	0.77	0.24	39,52,54,55	0
3	FLC	A	503	13/13	0.77	0.29	33,59,82,87	0
4	GOL	B	507	6/6	0.79	0.27	34,49,51,51	0
2	PO4	E	505	5/5	0.79	0.25	68,86,92,93	0
4	GOL	A	505	6/6	0.80	0.17	45,51,60,62	0
4	GOL	E	503	6/6	0.84	0.14	47,50,53,54	0
4	GOL	C	503	6/6	0.85	0.23	43,54,66,73	0
6	PEG	D	505	7/7	0.85	0.17	35,36,44,44	0
4	GOL	A	504	6/6	0.85	0.13	35,47,50,52	0
6	PEG	F	505	7/7	0.86	0.14	28,34,41,42	0
2	PO4	B	501	5/5	0.92	0.11	26,35,45,48	0
2	PO4	C	505	5/5	0.94	0.13	33,42,48,50	0
2	PO4	E	501	5/5	0.95	0.08	32,39,45,51	0
5	IAC	B	506[A]	13/13	0.95	0.12	21,23,25,26	13
5	IAC	B	506[B]	13/13	0.95	0.12	21,21,22,22	13
5	IAC	A	507[B]	13/13	0.96	0.12	23,24,29,32	13
2	PO4	F	504	5/5	0.96	0.20	45,46,54,55	0
2	PO4	D	501	5/5	0.96	0.08	34,35,46,46	0
2	PO4	A	501	5/5	0.96	0.08	30,33,37,37	0
2	PO4	F	503	5/5	0.96	0.08	34,42,44,45	0
5	IAC	A	507[A]	13/13	0.96	0.12	20,21,24,29	13
5	IAC	D	506[B]	13/13	0.97	0.10	19,20,23,23	13
2	PO4	B	505	5/5	0.97	0.17	37,38,45,52	0
2	PO4	B	502	5/5	0.97	0.20	30,32,40,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	IAC	D	506[A]	13/13	0.97	0.10	20,20,22,26	13
2	PO4	F	502	5/5	0.98	0.18	35,37,47,47	0
2	PO4	A	502	5/5	0.98	0.14	34,34,41,43	0
2	PO4	C	504	5/5	0.98	0.15	35,36,47,48	0
2	PO4	E	502	5/5	0.99	0.17	35,39,44,47	0

6.5 Other polymers (i)

There are no such residues in this entry.