wwPDB X-ray Structure Validation Summary Report (i)

Jun 24, 2024 – 12:04 PM EDT

PDB ID	:	5OTB
Title	:	Structure of caprine serum albumin in P1 space group
Authors	:	Talaj, J.A.; Bujacz, A.; Bujacz, G.
Deposited on	:	2017-08-21
Resolution	:	2.50 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:

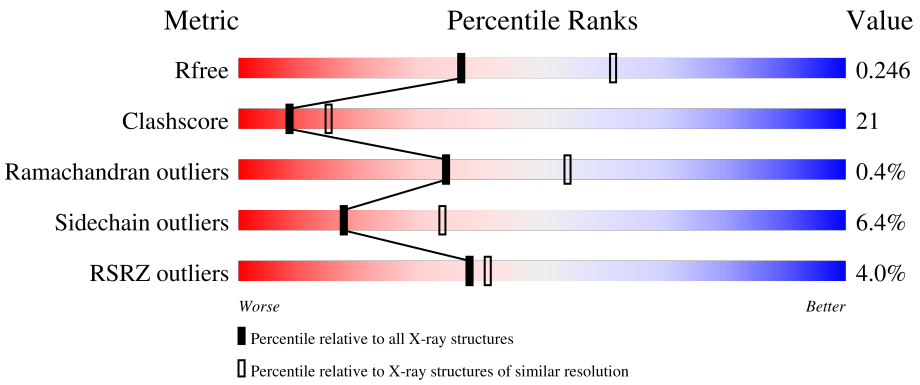
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (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 2.50 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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	583	3% 58% 38% ·
1	B	583	5% 58% 40% ·
1	C	583	5% 60% 36% ·
1	D	583	3% 61% 36% ·

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
3	PRO	A	602	-	-	X	-
3	PRO	B	602	-	-	X	-
3	PRO	D	602	-	-	X	-

2 Entry composition (i)

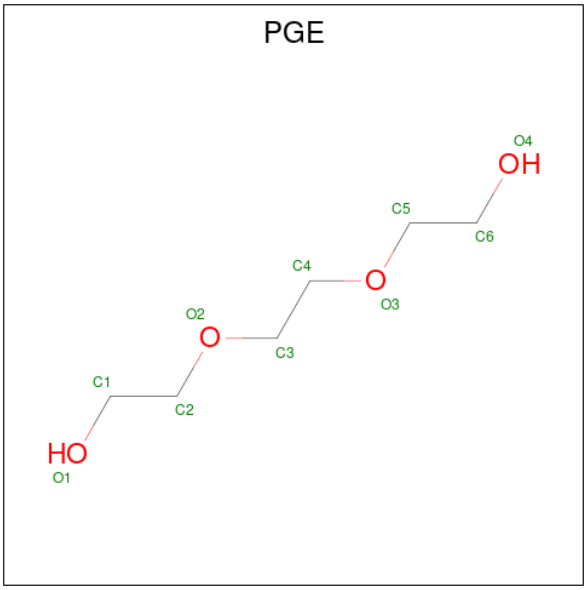
There are 5 unique types of molecules in this entry. The entry contains 19131 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Albumin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	581	4628	2922	777	890	39	0	0	0
1	B	581	4627	2922	777	889	39	0	0	0
1	C	581	4628	2922	777	890	39	0	0	0
1	D	581	4634	2927	778	890	39	0	1	0

- Molecule 2 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: $C_6H_{14}O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	10	6	4	0	0
2	B	1	10	6	4	0	0

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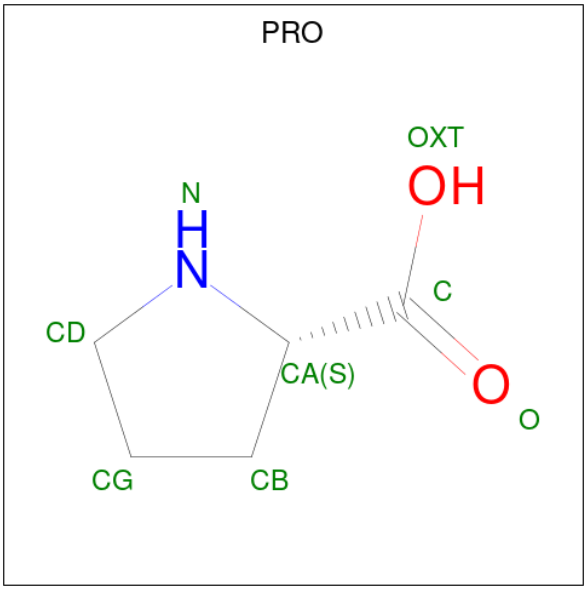
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	C	1	10	6	4	0	0

- Molecule 3 is PROLINE (three-letter code: PRO) (formula: $C_5H_9NO_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	8	5	1	2	0	0
			Total	C	N	O		
3	A	1	8	5	1	2	0	0
			Total	C	N	O		
3	B	1	8	5	1	2	0	0
			Total	C	N	O		
3	B	1	8	5	1	2	0	0
			Total	C	N	O		
3	C	1	8	5	1	2	0	0
			Total	C	N	O		
3	C	1	8	5	1	2	0	0
			Total	C	N	O		
3	C	1	8	5	1	2	0	0
			Total	C	N	O		
3	D	1	8	5	1	2	0	0
			Total	C	N	O		
3	D	1	8	5	1	2	0	0
			Total	C	N	O		
3	D	1	8	5	1	2	0	0

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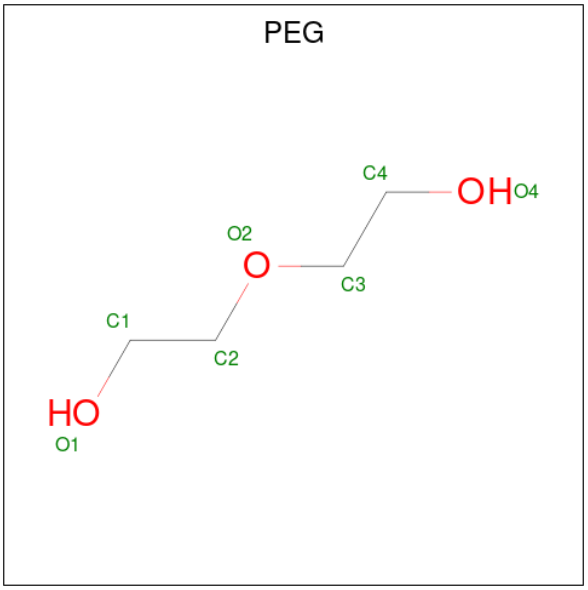
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	D	1	8	5	1	2	0	0

- Molecule 4 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



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

- Molecule 5 is water.

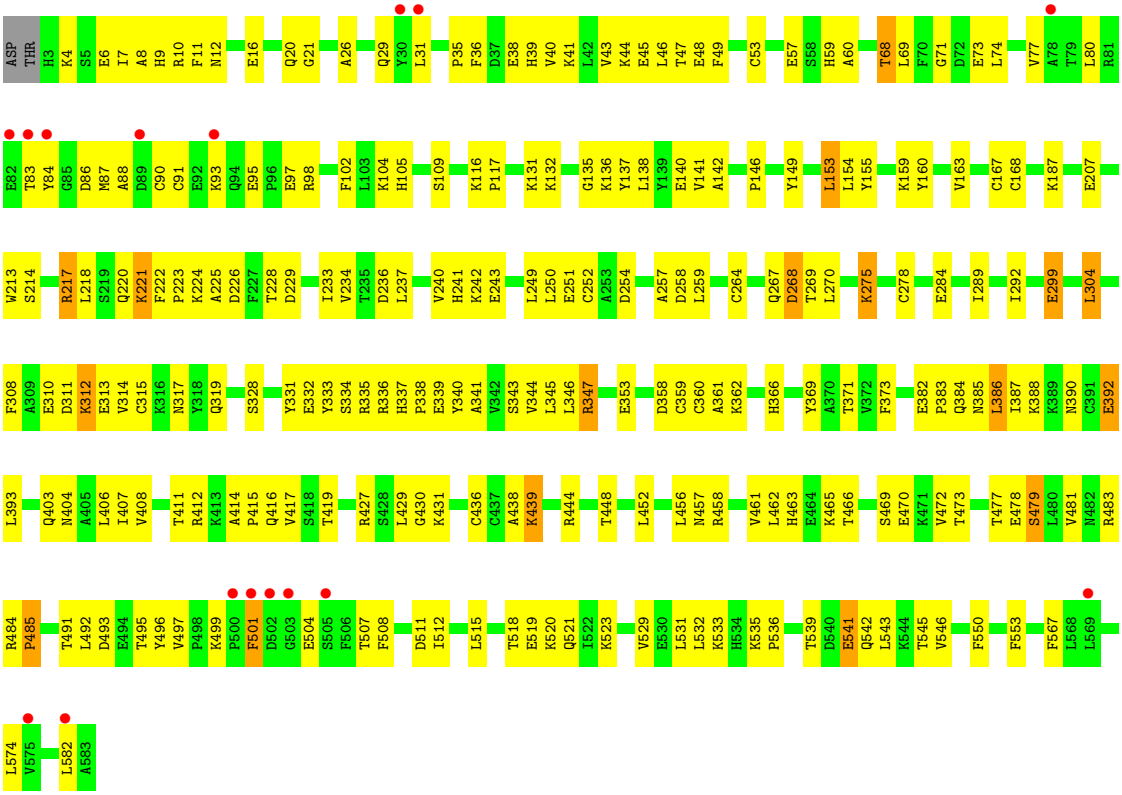
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	108	108	108	0	0
5	B	124	124	124	0	0
5	C	124	124	124	0	0
5	D	126	126	126	0	0

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.

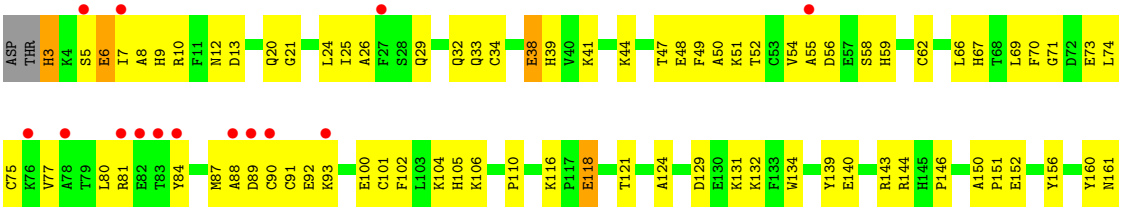
- Molecule 1: Albumin

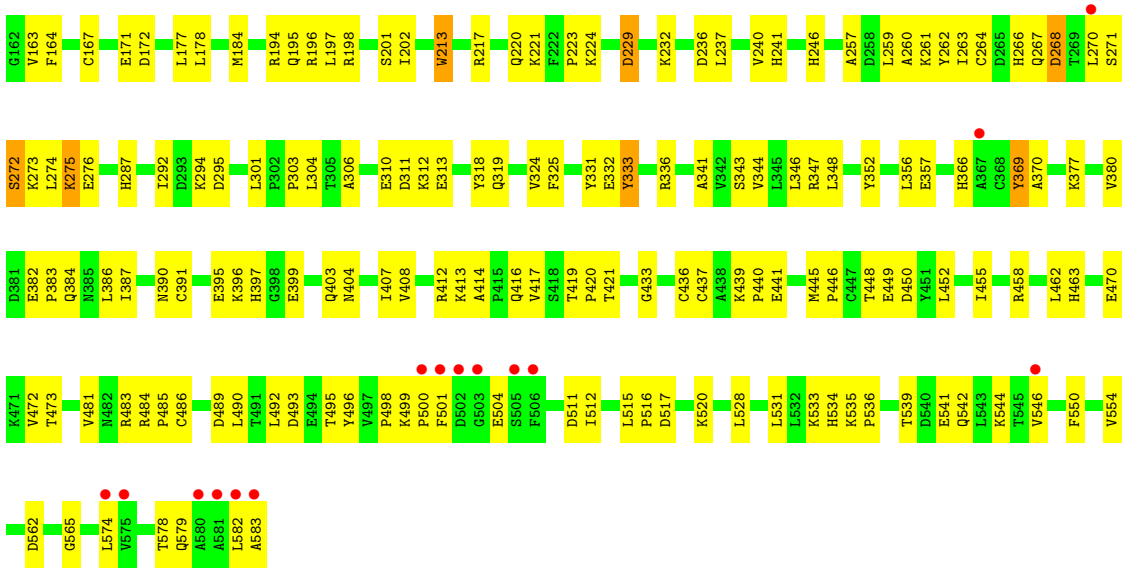
Chain A:



- Molecule 1: Albumin

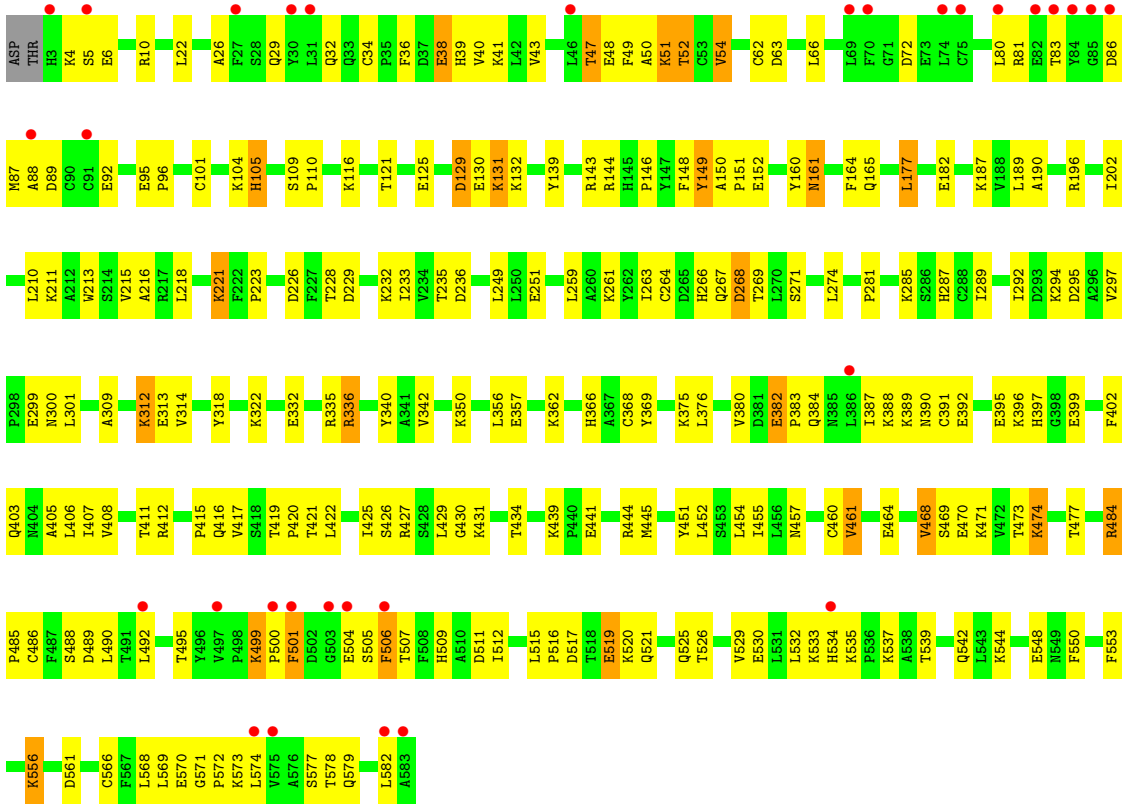
Chain B:





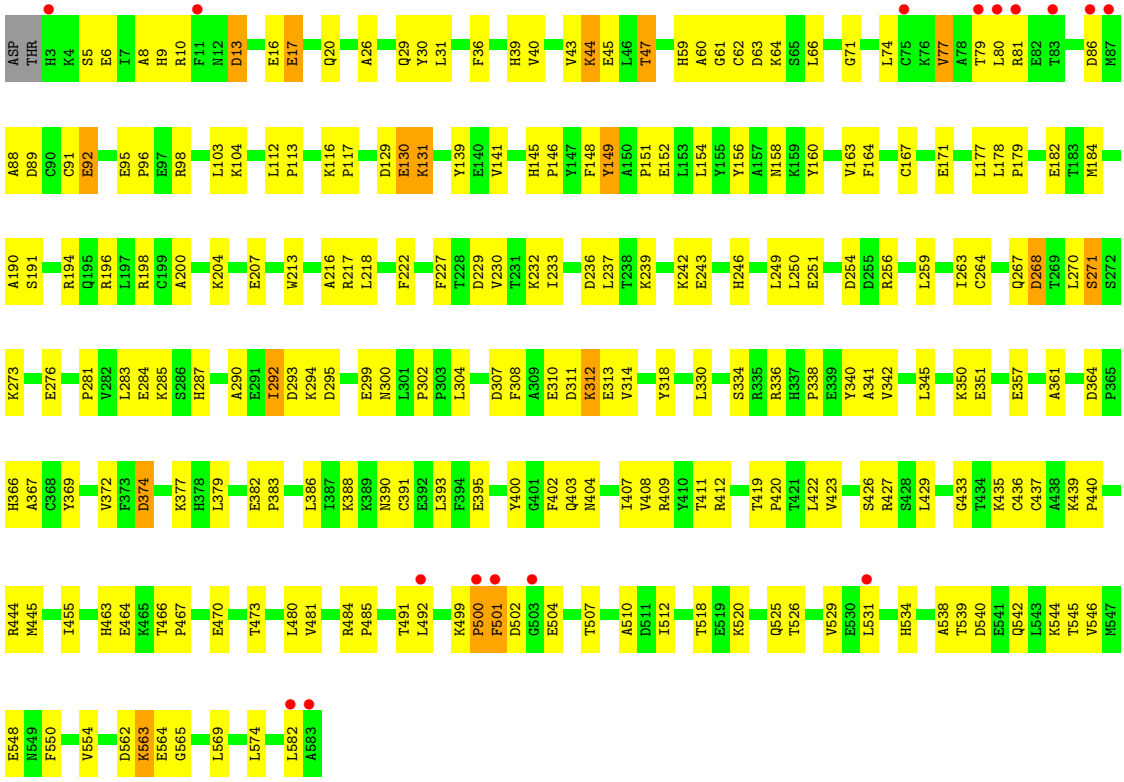
- Molecule 1: Albumin

Chain C:



- Molecule 1: Albumin

Chain D:


ASP THR H3 K4 S5 E6 I7 A8 H9 R10 F11 N12 D13 E16 E17 Q20 A26 Q29 Y30 L31 F36 H39 V40 V43 K44 E45 L46 T47 H59 A60 G61 C62 D63 K64 S65 L66 G71 L74 C75 K76 V77 A78 T79 L80 R81 E82 T83 D86 M87
A88 D89 C90 C91 E92 E95 P96 E97 R98 L103 K104 L112 P113 K116 P117 D129 E130 K131 Y139 E140 V141 H145 P146 Y147 F148 Y149 A150 P151 E152 L153 L154 Y155 Y156 A157 N158 K159 Y160 V163 F164 C167 E171 L177 L178 P179 E182 T183 M184
A190 S191 R194 Q195 R196 L197 R198 C199 A200 K204 E207 W213 A216 R217 L218 F222 F227 T228 D229 V230 T231 K232 I233 D236 L237 T238 K239 K242 E243 H246 L249 L250 E251 D254 D255 R256 L259 I263 C264 Q267 D268 T269 L270 S271 S272
K273 E276 P281 V282 L283 E284 K285 S286 H287 A290 E291 I292 D293 K294 D295 E299 N300 L301 P302 P303 L304 D307 F308 A309 E310 D311 K312 E313 V314 Y318 L330 S334 R335 R336 H337 P338 E339 Y340 A341 V342 L345 K350 E351 E357 A361 D364 P365
H366 A367 C368 Y369 V372 F373 D374 K377 H378 L379 E382 P383 L386 I387 K388 K389 N390 C391 E392 L393 F394 E395 Y400 G401 F402 Q403 N404 I407 V408 R409 Y410 T411 R412 T419 P420 T421 L422 V423 S426 R427 S428 L429 G433 T434 K435 C436 C437 A438 K439 P440
R444 M445 I455 H463 E464 K465 T466 P467 E470 T473 L480 V481 R484 P485 T491 L492 K499 P500 F501 D502 G503 E504 T507 A510 D511 I512 T518 E519 K520 Q525 T526 V529 E530 L531 H534 A538 T539 D540 E541 Q542 L543 K544 T545 V546 M547
E548 N549 F550 V554 D562 K563 E564 G565 L569 L574 L582 A583

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	78.75Å 80.93Å 110.53Å 90.01° 75.90° 72.22°	Depositor
Resolution (Å)	40.00 – 2.50 39.47 – 2.50	Depositor EDS
% Data completeness (in resolution range)	98.2 (40.00-2.50) 98.2 (39.47-2.50)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.06 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.197 , 0.246 0.198 , 0.246	Depositor DCC
R_{free} test set	1707 reflections (2.00%)	wwPDB-VP
Wilson B-factor (Å^2)	57.8	Xtriage
Anisotropy	0.046	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 61.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.45$, $< L^2 > = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	19131	wwPDB-VP
Average B, all atoms (Å^2)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.27% 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 (i)

5.1 Standard geometry (i)

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

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	0.92	0/4724	1.03	0/6376
1	B	0.93	0/4723	1.04	0/6374
1	C	0.90	0/4724	1.00	0/6376
1	D	0.96	0/4733	1.04	0/6387
All	All	0.93	0/18904	1.03	0/25513

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 (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	4628	0	4537	210	0
1	B	4627	0	4537	200	1
1	C	4628	0	4537	191	1
1	D	4634	0	4550	177	2
2	A	10	0	14	1	0
2	B	10	0	14	1	0
2	C	10	0	14	0	0
3	A	16	0	14	12	0
3	B	16	0	14	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	24	0	21	6	0
3	D	32	0	28	15	0
4	C	7	0	10	1	0
4	D	7	0	10	2	0
5	A	108	0	0	6	0
5	B	124	0	0	5	0
5	C	124	0	0	9	0
5	D	126	0	0	10	0
All	All	19131	0	18300	773	2

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 21.

The worst 5 of 773 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:498:PRO:O	1:B:500:PRO:HD3	1.31	1.26
1:A:116:LYS:HE3	1:B:116:LYS:HE3	1.28	1.08
1:C:86:ASP:O	1:C:89:ASP:HB2	1.60	1.02
1:B:539:THR:HB	1:B:542:GLN:HB2	1.44	0.99
1:C:499:LYS:HG3	1:C:500:PRO:HD2	1.45	0.98

All (2) 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)
1:B:41:LYS:NZ	1:D:313:GLU:OE2[1_545]	2.05	0.15
1:C:312:LYS:NZ	1:D:361:ALA:O[1_546]	2.15	0.05

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	579/583 (99%)	518 (90%)	58 (10%)	3 (0%)	29	48
1	B	579/583 (99%)	523 (90%)	54 (9%)	2 (0%)	41	61
1	C	579/583 (99%)	515 (89%)	62 (11%)	2 (0%)	41	61
1	D	580/583 (100%)	517 (89%)	60 (10%)	3 (0%)	29	48
All	All	2317/2332 (99%)	2073 (90%)	234 (10%)	10 (0%)	34	54

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	499	LYS
1	A	269	THR
1	B	441	GLU
1	D	79	THR
1	A	360	CYS

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	515/517 (100%)	477 (93%)	38 (7%)	13	27
1	B	515/517 (100%)	487 (95%)	28 (5%)	22	42
1	C	515/517 (100%)	482 (94%)	33 (6%)	17	33
1	D	516/517 (100%)	483 (94%)	33 (6%)	17	33
All	All	2061/2068 (100%)	1929 (94%)	132 (6%)	17	33

5 of 132 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	293	ASP
1	D	314	VAL
1	D	564	GLU
1	B	213	TRP
1	B	202	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	300	ASN
1	C	397	HIS
1	D	463	HIS
1	D	20	GLN
1	D	145	HIS

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)

16 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	$\#\|Z\| > 2$
3	PRO	D	602	-	8,8,8	0.93	0	10,10,10	1.92	2 (20%)
3	PRO	A	602	-	8,8,8	1.06	1 (12%)	10,10,10	1.95	2 (20%)
4	PEG	C	602	-	6,6,6	0.47	0	5,5,5	0.52	0
2	PGE	A	601	-	9,9,9	0.60	0	8,8,8	0.29	0
3	PRO	C	603	-	8,8,8	0.89	0	10,10,10	1.17	1 (10%)
3	PRO	C	605	-	8,8,8	0.72	0	10,10,10	1.46	2 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
4	PEG	D	601	-	6,6,6	0.45	0	5,5,5	0.34	0
3	PRO	A	603	-	8,8,8	0.66	0	10,10,10	1.45	2 (20%)
3	PRO	C	604	-	8,8,8	1.02	1 (12%)	10,10,10	1.56	1 (10%)
3	PRO	D	603	-	8,8,8	0.93	0	10,10,10	1.69	2 (20%)
3	PRO	B	603	-	8,8,8	0.84	0	10,10,10	1.54	3 (30%)
3	PRO	D	604	-	8,8,8	0.88	0	10,10,10	1.28	1 (10%)
3	PRO	B	602	-	8,8,8	0.89	0	10,10,10	1.28	1 (10%)
2	PGE	C	601	-	9,9,9	0.59	0	8,8,8	0.68	0
3	PRO	D	605	-	8,8,8	0.83	0	10,10,10	1.29	1 (10%)
2	PGE	B	601	-	9,9,9	0.56	0	8,8,8	0.78	0

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
3	PRO	D	602	-	-	4/4/11/11	0/1/1/1
3	PRO	A	602	-	-	4/4/11/11	0/1/1/1
4	PEG	C	602	-	-	3/4/4/4	-
2	PGE	A	601	-	-	4/7/7/7	-
3	PRO	C	603	-	-	2/4/11/11	0/1/1/1
3	PRO	C	605	-	-	2/4/11/11	0/1/1/1
4	PEG	D	601	-	-	2/4/4/4	-
3	PRO	A	603	-	-	4/4/11/11	0/1/1/1
3	PRO	C	604	-	-	4/4/11/11	0/1/1/1
3	PRO	D	603	-	-	4/4/11/11	0/1/1/1
3	PRO	B	603	-	-	4/4/11/11	0/1/1/1
3	PRO	D	604	-	-	4/4/11/11	0/1/1/1
3	PRO	B	602	-	-	2/4/11/11	0/1/1/1
2	PGE	C	601	-	-	3/7/7/7	-
3	PRO	D	605	-	-	4/4/11/11	0/1/1/1
2	PGE	B	601	-	-	5/7/7/7	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	602	PRO	OXT-C	-2.68	1.21	1.30
3	C	604	PRO	OXT-C	-2.48	1.22	1.30

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	602	PRO	OXT-C-O	-4.80	113.20	124.09
3	D	602	PRO	OXT-C-O	-4.16	114.64	124.09
3	C	604	PRO	OXT-C-O	-3.43	116.31	124.09
3	D	603	PRO	OXT-C-O	-3.43	116.31	124.09
3	D	602	PRO	OXT-C-CA	3.20	124.05	113.40

There are no chirality outliers.

5 of 55 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	602	PRO	O-C-CA-N
3	A	602	PRO	OXT-C-CA-N
3	A	602	PRO	O-C-CA-CB
3	A	602	PRO	OXT-C-CA-CB
3	A	603	PRO	O-C-CA-N

There are no ring outliers.

14 monomers are involved in 44 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	602	PRO	9	0
3	A	602	PRO	9	0
4	C	602	PEG	1	0
2	A	601	PGE	1	0
3	C	603	PRO	3	0
4	D	601	PEG	2	0
3	A	603	PRO	3	0
3	C	604	PRO	3	0
3	D	603	PRO	2	0
3	B	603	PRO	1	0
3	D	604	PRO	1	0
3	B	602	PRO	5	0
3	D	605	PRO	3	0
2	B	601	PGE	1	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 (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	581/583 (99%)	-0.16	16 (2%)	53	56	33, 62, 96, 118	0
1	B	581/583 (99%)	-0.01	29 (4%)	28	30	33, 60, 104, 138	0
1	C	581/583 (99%)	0.02	31 (5%)	26	28	36, 62, 106, 154	0
1	D	581/583 (99%)	-0.19	16 (2%)	53	56	32, 60, 97, 133	0
All	All	2324/2332 (99%)	-0.09	92 (3%)	38	41	32, 61, 102, 154	0

The worst 5 of 92 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	70	PHE	5.3
1	C	501	PHE	5.1
1	C	500	PRO	4.8
1	B	89	ASP	4.7
1	D	81	ARG	4.4

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 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, 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	B-factors(Å^2)	Q<0.9
3	PRO	B	603	8/8	0.79	0.17	80,86,91,92	0
3	PRO	D	603	8/8	0.85	0.29	74,86,104,105	0
3	PRO	B	602	8/8	0.87	0.25	75,88,94,97	0
3	PRO	D	604	8/8	0.88	0.14	66,77,83,86	0
3	PRO	A	603	8/8	0.89	0.14	81,82,90,92	0
3	PRO	C	604	8/8	0.90	0.17	68,74,81,90	0
3	PRO	C	603	8/8	0.92	0.21	74,84,86,90	0
3	PRO	D	605	8/8	0.92	0.13	80,83,100,100	0
3	PRO	C	605	8/8	0.93	0.28	78,88,91,91	0
3	PRO	A	602	8/8	0.93	0.21	78,84,88,92	0
2	PGE	C	601	10/10	0.94	0.14	52,61,68,75	0
4	PEG	D	601	7/7	0.94	0.15	52,53,62,63	0
4	PEG	C	602	7/7	0.95	0.20	55,66,77,83	0
3	PRO	D	602	8/8	0.95	0.16	61,70,89,100	0
2	PGE	A	601	10/10	0.96	0.20	47,71,85,97	0
2	PGE	B	601	10/10	0.97	0.16	45,55,86,87	0

6.5 Other polymers (i)

There are no such residues in this entry.