



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:30 PM GMT

PDB ID : 4P42
Title : Extended-Synaptotagmin 2, SMP - C2A - C2B Domains
Authors : Schauder, C.M.; Wu, X.; Reinisch, K.M.
Deposited on : 2014-03-10
Resolution : 2.44 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 : 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

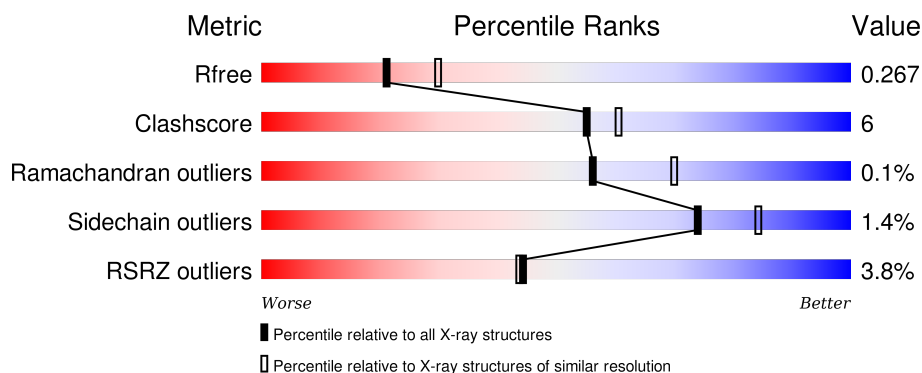
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.44 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 $\leq 5\%$. 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	474	<div> <div>2%</div> <div>82%</div> <div>14%</div> <div>.</div> </div>
1	B	474	<div> <div>5%</div> <div>73%</div> <div>18%</div> <div>9%</div> </div>

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	EGC	A	701	-	-	-	X
2	EGC	B	701	-	-	-	X
3	PEE	A	702	X	-	-	X
3	PEE	B	702	X	-	-	X

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 7493 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.

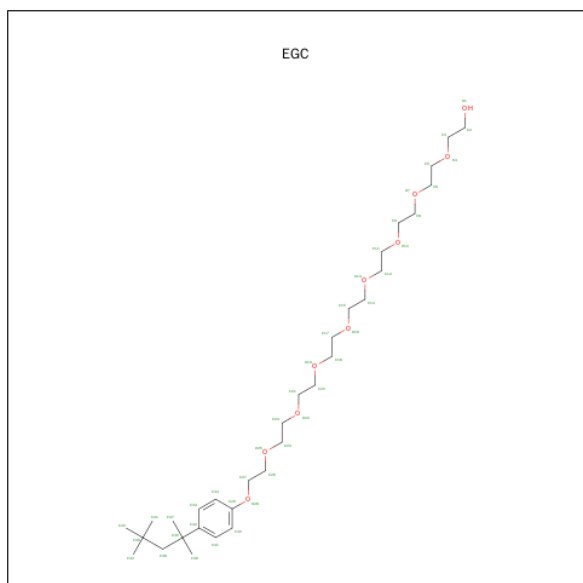
- Molecule 1 is a protein called Extended synaptotagmin-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	455	Total	C	N	O	S	0	0	0
			3666	2353	621	680	12			
1	B	431	Total	C	N	O	S	0	0	0
			3477	2239	591	635	12			

There are 4 discrepancies between the modelled and reference sequences:

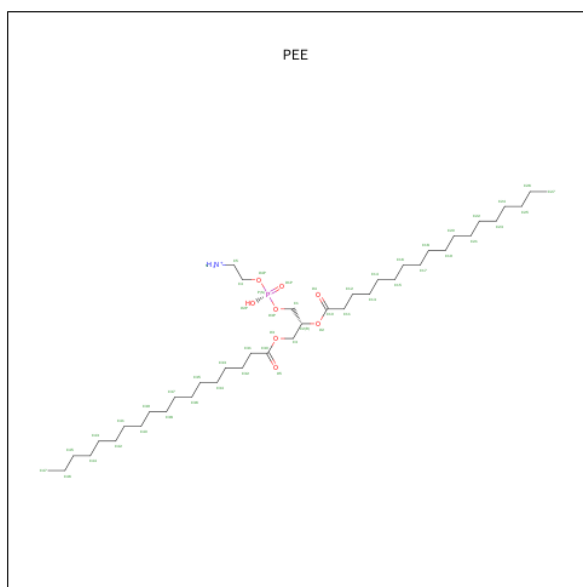
Chain	Residue	Modelled	Actual	Comment	Reference
A	161	GLY	-	expression tag	UNP A0FGR8
A	162	SER	-	expression tag	UNP A0FGR8
B	161	GLY	-	expression tag	UNP A0FGR8
B	162	SER	-	expression tag	UNP A0FGR8

- Molecule 2 is 2-(2-{2-[2-(2-{2-[2-(2-{2-[4-(1,1,3,3-TETRAMETHYL-BUTYL)-PHENOXY]-ETHOXY}-ETHOXY)-ETHOXY]-ETHOXY}-ETHOXY)-ETHOXY]-ETHOXY}-ETHOXY)-ETHANOL (three-letter code: EGC) (formula: C₃₂H₅₈O₁₀).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			29	24	5		
2	B	1	Total	C	O	0	0
			25	21	4		

- Molecule 3 is PHOSPHATIDYLETHANOLAMINE (three-letter code: PEE) (formula: $C_{41}H_{83}NO_8P$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			42	37	5		
3	B	1	Total	C	O	0	0
			42	37	5		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	110	Total	O	0	0
			110	110		
4	B	102	Total	O	0	0
			102	102		

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 ($\text{RSRZ} > 2$). 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.

- Chain A:
-
- Sequence logo for Chain A showing amino acid conservation across 1000 iterations. The y-axis lists amino acids in three columns. The x-axis shows iteration ranges from 0 to 1000. A green bar at the top indicates the percentage of iterations where a position is conserved (82%), with a yellow bar for 14% and a grey bar for 2%.

- Chain B:
-
- Sequence logo for Chain B. The y-axis represents information content in bits (0.00 to 0.15). The x-axis lists amino acids. A green bar at the top indicates the total information content, with 73% (green), 18% (yellow), and 9% (grey).
- | Position | Amino Acid | Information Content (bits) |
|----------|------------|----------------------------|
| 1 | L406 | 0.02 |
| 2 | R518 | 0.01 |
| 3 | K525 | 0.02 |
| 4 | I526 | 0.01 |
| 5 | H540 | 0.02 |
| 6 | K541 | 0.02 |
| 7 | I564 | 0.01 |
| 8 | E575 | 0.01 |
| 9 | V576 | 0.01 |
| 10 | R577 | 0.01 |
| 11 | L592 | 0.02 |
| 12 | D600 | 0.01 |
| 13 | M601 | 0.01 |
| 14 | T602 | 0.01 |
| 15 | R606 | 0.01 |
| 16 | L627 | 0.01 |
| 17 | H628 | 0.01 |
| 18 | L629 | 0.01 |
| 19 | E630 | 0.01 |
| 20 | LYS | 0.01 |
| 21 | ARG | 0.01 |
| 22 | GLU | 0.01 |
| 23 | ARG | 0.01 |
| 24 | L345 | 0.01 |
| 25 | N316 | 0.02 |
| 26 | L324 | 0.01 |
| 27 | I327 | 0.01 |
| 28 | S328 | 0.01 |
| 29 | L331 | 0.01 |
| 30 | N335 | 0.01 |
| 31 | R336 | 0.02 |
| 32 | I337 | 0.01 |
| 33 | T338 | 0.01 |
| 34 | V339 | 0.01 |
| 35 | S343 | 0.02 |
| 36 | GLU | 0.01 |
| 37 | VAL | 0.01 |
| 38 | GLN | 0.01 |
| 39 | ASN | 0.01 |
| 40 | VAL | 0.01 |
| 41 | ALA | 0.01 |
| 42 | ASP | 0.01 |
| 43 | K233 | 0.01 |
| 44 | I236 | 0.01 |
| 45 | I237 | 0.02 |
| 46 | L240 | 0.01 |
| 47 | C248 | 0.01 |
| 48 | S265 | 0.01 |
| 49 | I266 | 0.01 |
| 50 | Q267 | 0.01 |
| 51 | R273 | 0.01 |
| 52 | L276 | 0.01 |
| 53 | L279 | 0.02 |
| 54 | I280 | 0.01 |
| 55 | G281 | 0.02 |
| 56 | D282 | 0.01 |
| 57 | M283 | 0.01 |
| 58 | P284 | 0.01 |
| 59 | L289 | 0.01 |
| 60 | S290 | 0.01 |
| 61 | I291 | 0.01 |
| 62 | R295 | 0.02 |
| 63 | K296 | 0.02 |
| 64 | L299 | 0.01 |
| 65 | E300 | 0.01 |
| 66 | I301 | 0.01 |
| 67 | N302 | 0.01 |
| 68 | V312 | 0.01 |
| 69 | L369 | 0.02 |
| 70 | GLN | 0.01 |
| 71 | GLY | 0.01 |
| 72 | LYS | 0.01 |
| 73 | ASP | 0.01 |
| 74 | THR | 0.01 |
| 75 | TYR | 0.01 |
| 76 | LEU | 0.01 |
| 77 | GLY | 0.01 |
| 78 | LEU | 0.01 |
| 79 | VAL | 0.01 |
| 80 | LYS | 0.01 |
| 81 | GLY | 0.01 |
| 82 | LYS | 0.01 |
| 83 | SER | 0.01 |
| 84 | ASP | 0.01 |
| 85 | P386 | 0.02 |
| 86 | Y387 | 0.01 |
| 87 | V401 | 0.01 |
| 88 | I402 | 0.02 |
| 89 | K403 | 0.02 |
| 90 | V512 | 0.01 |

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	74.33Å 88.38Å 167.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.14 – 2.44 47.14 – 2.44	Depositor EDS
% Data completeness (in resolution range)	99.9 (47.14-2.44) 96.0 (47.14-2.44)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.49 (at 2.45Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1452)	Depositor
R, R_{free}	0.210 , 0.256 0.226 , 0.267	Depositor DCC
R_{free} test set	1999 reflections (5.23%)	DCC
Wilson B-factor (Å ²)	42.5	Xtriage
Anisotropy	0.249	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 30.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 41775 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7493	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.29% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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

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

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	0.22	0/3739	0.44	0/5068
1	B	0.23	0/3546	0.44	0/4801
All	All	0.23	0/7285	0.44	0/9869

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

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	3666	0	3731	42	0
1	B	3477	0	3554	53	0
2	A	29	0	39	1	0
2	B	25	0	33	1	0
3	A	42	0	68	4	0
3	B	42	0	68	4	0
4	A	110	0	0	3	0
4	B	102	0	0	1	0
All	All	7493	0	7493	93	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 6.

All (93) 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:510:LEU:HB2	1:A:564:ILE:HD11	1.59	0.82
1:B:510:LEU:HB2	1:B:564:ILE:HD11	1.65	0.79
1:A:335:ASN:HB3	2:A:701:EGC:H241	1.69	0.75
1:B:452:GLU:O	1:B:455:ARG:NH1	2.20	0.74
1:A:327:ILE:HG23	3:A:702:PEE:H62	1.70	0.72
1:B:366:ALA:HB3	1:B:408:PRO:HD2	1.72	0.71
1:B:455:ARG:HG3	1:B:630:GLU:HG2	1.72	0.71
1:A:336:ARG:NH1	4:A:801:HOH:O	2.24	0.71
1:A:546:LYS:NZ	1:B:186:GLU:OE2	2.24	0.70
1:B:369:LEU:HB2	1:B:406:LEU:HD22	1.73	0.70
1:B:402:ILE:HD12	1:B:408:PRO:HB2	1.74	0.69
1:B:444:LEU:HD12	1:B:471:LEU:HD23	1.79	0.65
1:B:362:HIS:HB2	1:B:474:ARG:HB3	1.79	0.63
1:B:364:ILE:HG22	1:B:365:GLU:HG3	1.82	0.62
1:A:326:ILE:HD13	3:A:702:PEE:H13	1.82	0.61
1:B:283:MET:HG3	1:B:284:PRO:HA	1.83	0.61
1:A:385:ASP:HB2	1:A:433:GLU:HB3	1.82	0.60
1:A:227:TYR:HB3	1:A:237:ILE:HB	1.86	0.57
1:A:564:ILE:HD13	1:A:592:LEU:HD13	1.85	0.57
1:A:531:ASN:HB2	1:A:579:GLU:HG3	1.86	0.57
1:B:478:LEU:HD23	1:B:627:LEU:HB3	1.85	0.57
1:A:267:GLN:HB2	1:A:300:GLU:HB2	1.87	0.57
1:A:362:HIS:HB2	1:A:474:ARG:HB3	1.87	0.57
1:B:425:GLU:HG2	1:B:447:ASP:HA	1.86	0.56
1:B:365:GLU:HG2	1:B:409:LYS:HG3	1.88	0.56
1:B:236:ILE:HB	1:B:276:LEU:HB2	1.89	0.55
1:A:283:MET:HG3	1:A:284:PRO:HA	1.89	0.55
1:A:265:SER:OG	1:A:302:ASN:ND2	2.32	0.54
1:A:433:GLU:O	1:A:435:PRO:HD3	2.08	0.54
1:B:564:ILE:HD13	1:B:592:LEU:HD13	1.91	0.53
1:B:335:ASN:HB3	2:B:701:EGC:H241	1.90	0.53
1:B:454:GLU:O	1:B:456:LEU:N	2.43	0.52
1:A:356:LYS:HD2	1:A:420:GLU:OE2	2.10	0.52
1:A:331:LEU:HD21	3:A:702:PEE:H68	1.91	0.52
1:B:265:SER:OG	1:B:302:ASN:ND2	2.40	0.51
1:B:267:GLN:HB2	1:B:300:GLU:HB3	1.91	0.51
1:B:432:ASP:HB3	1:B:439:ASP:HB3	1.91	0.51
1:B:444:LEU:HD11	1:B:461:PHE:HB2	1.93	0.51
1:B:227:TYR:HB3	1:B:237:ILE:HB	1.92	0.50
1:A:381:LYS:NZ	1:A:434:ASP:O	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:481:MET:SD	1:A:486:ASN:ND2	2.84	0.50
1:A:625:ARG:NH1	4:A:842:HOH:O	2.33	0.50
1:B:518:ARG:NH2	4:B:802:HOH:O	2.44	0.49
1:B:352:PHE:CE1	1:B:513:TYR:HB2	2.47	0.49
1:A:287:GLY:HA2	1:A:342:VAL:HG22	1.94	0.48
1:B:204:LEU:HD21	1:B:315:LEU:HD11	1.95	0.48
1:A:474:ARG:NH1	1:A:476:GLU:OE2	2.47	0.48
1:B:312:VAL:HB	1:B:315:LEU:HD12	1.96	0.48
1:B:369:LEU:HD22	1:B:441:LEU:HB3	1.96	0.47
1:B:221:ILE:HD13	1:B:240:LEU:HD23	1.96	0.47
1:A:318:LEU:HD22	1:A:322:ILE:HG21	1.95	0.47
1:A:457:LEU:HD22	1:B:526:ILE:HD12	1.96	0.47
1:A:454:GLU:HG3	1:B:526:ILE:HD11	1.97	0.47
1:B:365:GLU:O	1:B:471:LEU:HD12	2.14	0.47
1:B:352:PHE:N	1:B:353:PRO:HD3	2.30	0.47
1:B:434:ASP:HB3	1:B:435:PRO:HD3	1.97	0.47
1:A:226:VAL:HG23	1:B:169:TRP:HB2	1.97	0.47
1:B:474:ARG:NH1	1:B:476:GLU:OE2	2.48	0.46
1:B:540:HIS:ND1	1:B:541:LYS:HG3	2.31	0.46
1:A:273:ARG:NH2	4:A:803:HOH:O	2.43	0.46
1:B:600:ASP:O	1:B:602:THR:HG23	2.15	0.46
1:A:282:ASP:OD1	1:A:283:MET:N	2.48	0.46
1:B:331:LEU:HD21	3:B:702:PEE:H66	1.96	0.45
1:B:299:LEU:HD21	1:B:328:SER:HB2	1.96	0.45
1:A:312:VAL:HG12	1:A:314:GLY:H	1.82	0.45
1:B:289:LEU:HB2	1:B:339:VAL:HB	1.98	0.45
1:B:213:ASP:O	1:B:248:CYS:HB2	2.17	0.45
1:A:217:GLN:HA	1:A:218:PRO:HD3	1.73	0.45
3:B:702:PEE:H34	3:B:702:PEE:H57	1.98	0.44
1:A:203:HIS:HB2	1:A:314:GLY:HA3	1.98	0.44
1:A:187:LYS:NZ	1:B:282:ASP:OD1	2.36	0.44
1:B:387:TYR:HB3	1:B:401:VAL:HG22	1.99	0.44
1:B:327:ILE:HG23	3:B:702:PEE:H56	2.00	0.44
1:B:432:ASP:HB2	1:B:441:LEU:HD11	1.99	0.44
1:B:291:ILE:HB	1:B:337:ILE:HB	2.00	0.44
1:A:252:LEU:HD12	1:A:309:LEU:HD11	1.99	0.43
1:B:494:ILE:HG23	1:B:505:LEU:HB2	1.99	0.43
1:B:360:ARG:HD2	1:B:476:GLU:OE1	2.19	0.43
1:A:384:SER:O	1:A:386:PRO:HD3	2.18	0.43
3:A:702:PEE:H58	3:A:702:PEE:H53	1.92	0.42
1:A:535:GLN:OE1	1:A:542:ALA:HB1	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:437:LYS:HA	1:A:437:LYS:HD2	1.82	0.42
1:A:219:LEU:HD12	1:A:244:PHE:CD1	2.55	0.42
1:B:170:LEU:HD23	1:B:170:LEU:HA	1.94	0.41
3:B:702:PEE:H72	3:B:702:PEE:H67	1.55	0.41
1:A:224:VAL:HG22	1:A:240:LEU:HD22	2.02	0.41
1:B:575:GLU:HG3	1:B:577:ARG:HG3	2.02	0.41
1:A:265:SER:HG	1:A:302:ASN:HD22	1.59	0.41
1:A:530:PRO:O	1:A:532:PRO:HD3	2.21	0.41
1:B:440:PHE:HZ	1:B:443:SER:HB3	1.87	0.40
1:A:547:ILE:HG21	1:A:579:GLU:HG2	2.03	0.40
1:B:299:LEU:HG	1:B:324:LEU:HD22	2.04	0.40
1:A:466:VAL:HA	1:A:467:PRO:HD3	1.95	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	449/474 (95%)	431 (96%)	18 (4%)	0	100	100
1	B	419/474 (88%)	401 (96%)	17 (4%)	1 (0%)	52	64
All	All	868/948 (92%)	832 (96%)	35 (4%)	1 (0%)	56	70

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	455	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	418/433 (96%)	412 (99%)	6 (1%)	74	84
1	B	396/433 (92%)	391 (99%)	5 (1%)	76	85
All	All	814/866 (94%)	803 (99%)	11 (1%)	74	84

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

Mol	Chain	Res	Type
1	A	166	ARG
1	A	273	ARG
1	A	380	VAL
1	A	444	LEU
1	A	445	MET
1	A	624	LEU
1	B	273	ARG
1	B	427	GLU
1	B	433	GLU
1	B	606	ARG
1	B	629	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 ⓘ

4 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	EGC	A	701	-	29,29,42	0.96	1 (3%)	37,37,50	0.64	0
3	PEE	A	702	-	41,41,50	0.77	2 (4%)	43,43,55	0.94	2 (4%)
2	EGC	B	701	-	25,25,42	1.02	1 (4%)	33,33,50	0.63	0
3	PEE	B	702	-	41,41,50	0.76	2 (4%)	43,43,55	0.96	2 (4%)

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
2	EGC	A	701	-	-	0/27/27/40	0/1/1/1
3	PEE	A	702	-	1/1/3/4	0/43/43/54	0/0/0/0
2	EGC	B	701	-	-	0/23/23/40	0/1/1/1
3	PEE	B	702	-	1/1/3/4	0/43/43/54	0/0/0/0

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	702	PEE	O3-C30	2.77	1.41	1.33
3	A	702	PEE	O3-C30	2.90	1.42	1.33
3	B	702	PEE	O2-C10	3.01	1.43	1.34
2	A	701	EGC	O28-C29	3.04	1.44	1.37
3	A	702	PEE	O2-C10	3.06	1.43	1.34
2	B	701	EGC	O28-C29	3.08	1.45	1.37

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	702	PEE	O3-C30-C31	2.44	119.34	111.90
3	B	702	PEE	O3-C30-C31	2.54	119.63	111.90
3	A	702	PEE	O2-C10-C11	3.79	119.76	111.53
3	B	702	PEE	O2-C10-C11	4.06	120.36	111.53

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	B	702	PEE	C2
3	A	702	PEE	C2

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	701	EGC	1	0
3	A	702	PEE	4	0
2	B	701	EGC	1	0
3	B	702	PEE	4	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, 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	455/474 (95%)	0.07	10 (2%) 65 65	30, 46, 72, 115	0
1	B	431/474 (90%)	0.25	24 (5%) 28 26	29, 46, 95, 139	0
All	All	886/948 (93%)	0.16	34 (3%) 44 44	29, 46, 86, 139	0

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	352	PHE	6.9
1	B	351	ARG	5.0
1	B	281	GLY	5.0
1	B	406	LEU	4.7
1	B	540	HIS	4.5
1	B	295	ARG	4.0
1	A	230	ASN	3.9
1	B	541	LYS	3.9
1	B	496	ALA	3.9
1	A	528	SER	3.8
1	B	435	PRO	3.7
1	A	229	GLU	3.6
1	A	231	VAL	3.4
1	B	343	SER	3.3
1	B	403	LYS	3.0
1	B	316	ASN	3.0
1	B	468	LYS	2.9
1	B	369	LEU	2.9
1	B	525	LYS	2.8
1	B	438	ASP	2.8
1	A	315	LEU	2.7
1	A	378	GLY	2.7
1	B	408	PRO	2.6
1	B	402	ILE	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	296	LYS	2.4
1	B	366	ALA	2.4
1	A	345	VAL	2.4
1	B	504	GLY	2.4
1	A	527	SER	2.4
1	B	434	ASP	2.4
1	B	279	LEU	2.4
1	B	460	TRP	2.3
1	A	216	GLN	2.3
1	A	377	LYS	2.1

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](#)

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(\AA^2)	Q<0.9
3	PEE	B	702	42/51	0.86	0.27	4.26	41,55,78,81	0
2	EGC	A	701	29/42	0.87	0.23	2.51	26,43,68,73	0
3	PEE	A	702	42/51	0.78	0.30	2.44	37,57,80,81	0
2	EGC	B	701	25/42	0.92	0.17	2.08	28,39,48,50	0

6.5 Other polymers [i](#)

There are no such residues in this entry.