



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 11:37 PM UTC

PDB ID : 1FUQ / pdb_00001fuq
Title : FUMARASE WITH BOUND 3-TRIMETHYLSILYLSUCCINIC ACID
Authors : Weaver, T.; Banaszak, L.
Deposited on : 1996-08-29
Resolution : 2.00 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

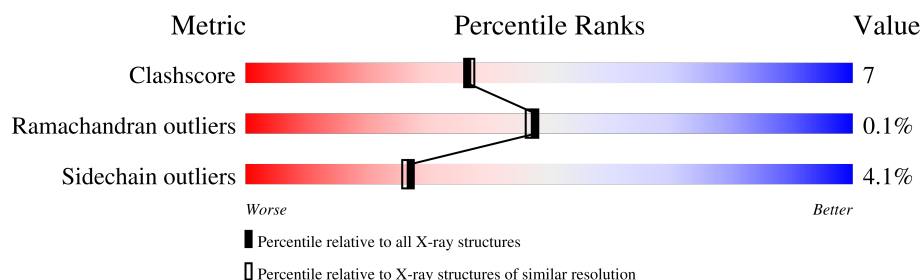
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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))
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	472	
1	B	472	

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	SIF	A	1000	X	-	-	-
2	SIF	B	1001	X	-	-	-
3	CIT	A	1001	-	X	-	-
3	CIT	B	1002	-	X	-	-

2 Entry composition [i](#)

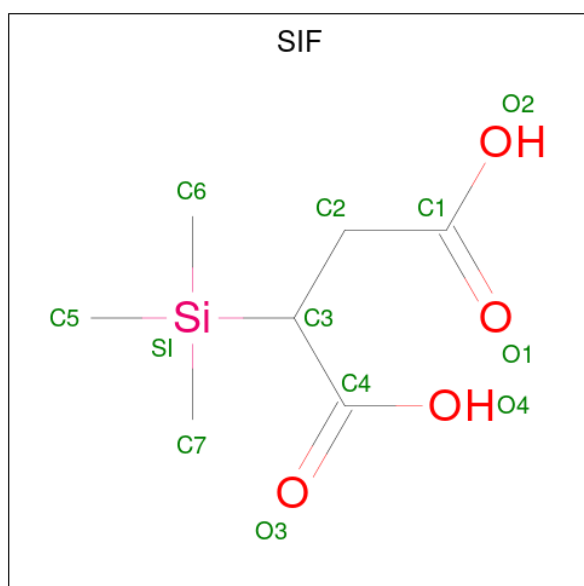
There are 4 unique types of molecules in this entry. The entry contains 7346 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 FUMARASE C.

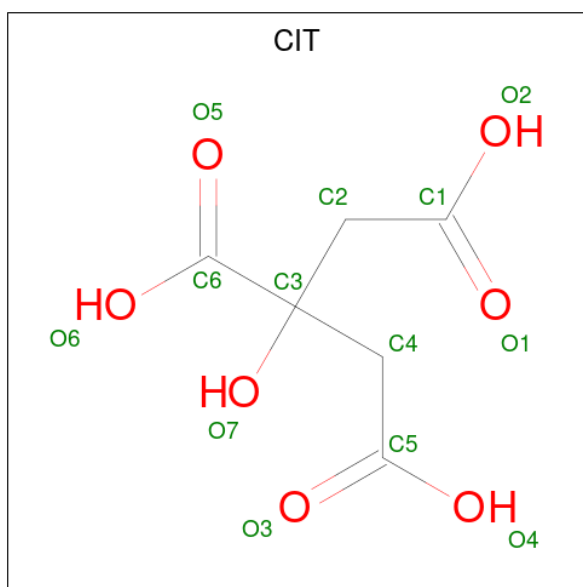
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	456	Total	C	N	O	S	0	0	0
			3456	2158	617	658	23			
1	B	455	Total	C	N	O	S	0	0	0
			3455	2157	617	657	24			

- Molecule 2 is 3-TRIMETHYLSILYLSUCCINIC ACID (CCD ID: SIF) (formula: $C_7H_{14}O_4Si$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	Si	0	0
			12	7	4	1		
2	B	1	Total	C	O	Si	0	0
			12	7	4	1		

- Molecule 3 is CITRIC ACID (CCD ID: CIT) (formula: $C_6H_8O_7$).



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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	196	Total	O	0	0
			196	196		
4	B	189	Total	O	0	0
			189	189		

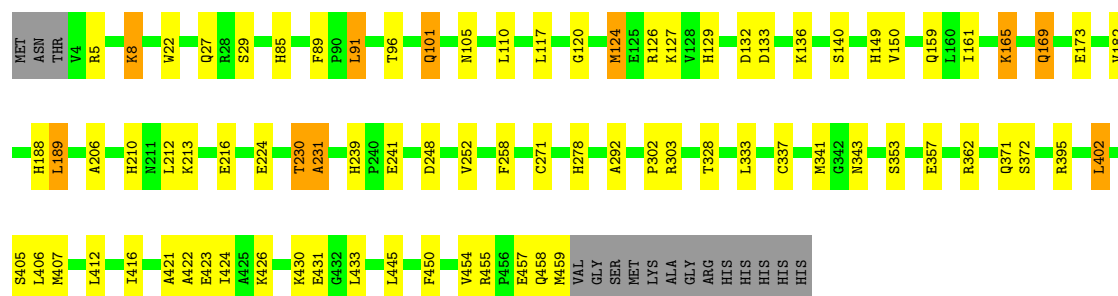
3 Residue-property plots

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. 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. 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.

Note EDS was not executed.

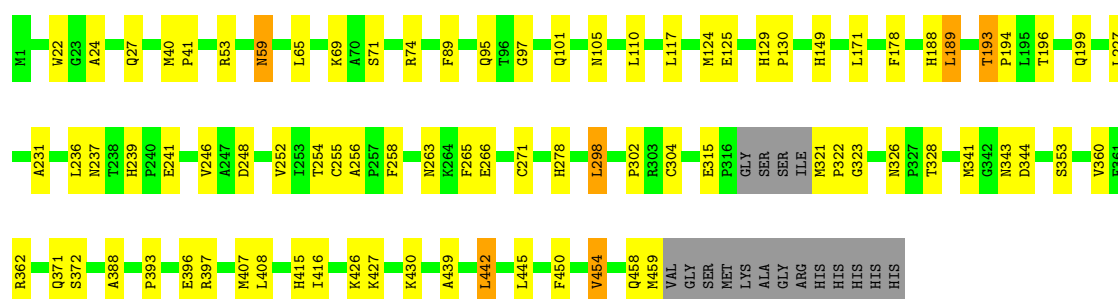
• Molecule 1: FUMARASE C

Chain A: 



• Molecule 1: FUMARASE C

Chain B: 



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	104.00Å 219.90Å 86.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.00	Depositor
% Data completeness (in resolution range)	(Not available) (8.00-2.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.187 , 0.233	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7346	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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

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	0.47	0/3514	0.95	9/4760 (0.2%)
1	B	0.47	0/3512	0.96	13/4756 (0.3%)
All	All	0.47	0/7026	0.95	22/9516 (0.2%)

There are no bond length outliers.

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	231	ALA	N-CA-C	9.26	120.98	111.07
1	A	353	SER	N-CA-C	7.21	120.93	112.72
1	B	362	ARG	N-CA-C	6.90	122.13	112.75
1	A	328	THR	N-CA-C	6.23	118.07	111.28
1	B	231	ALA	N-CA-C	6.01	118.35	111.02
1	B	193	THR	CA-C-N	5.96	125.93	120.03
1	B	193	THR	C-N-CA	5.96	125.93	120.03
1	A	362	ARG	N-CA-C	5.82	120.67	112.75
1	B	454	VAL	N-CA-C	5.72	112.33	106.21
1	B	271	CYS	N-CA-C	-5.68	103.72	111.56
1	B	388	ALA	N-CA-C	5.68	117.93	111.11
1	A	395	ARG	N-CA-C	5.65	118.17	111.33
1	A	357	GLU	N-CA-C	5.64	120.01	113.18
1	B	124	MET	N-CA-C	5.54	119.13	112.38
1	B	353	SER	N-CA-C	5.46	118.74	112.57
1	A	271	CYS	N-CA-C	-5.32	104.21	111.56
1	B	24	ALA	N-CA-C	5.17	116.60	111.07
1	A	91	LEU	N-CA-C	5.17	117.93	110.28
1	B	328	THR	N-CA-C	5.13	116.87	111.28
1	B	407	MET	N-CA-C	5.12	118.79	112.54
1	B	416	ILE	N-CA-C	5.08	118.03	113.10
1	A	126	ARG	N-CA-C	5.03	117.18	110.35

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	3456	0	3473	55	0
1	B	3455	0	3473	47	0
2	A	12	0	2	1	0
2	B	12	0	2	0	0
3	A	13	0	3	1	0
3	B	13	0	3	0	0
4	A	196	0	0	4	0
4	B	189	0	0	7	0
All	All	7346	0	6956	100	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 7.

All (100) 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:230:THR:HG23	1:A:231:ALA:H	1.46	0.80
1:A:407:MET:SD	1:B:321:MET:HG2	2.22	0.80
1:A:343:ASN:HD21	1:A:371:GLN:HE21	1.34	0.75
1:A:455:ARG:HH11	1:A:458:GLN:HE22	1.35	0.74
1:B:343:ASN:HD21	1:B:371:GLN:HE21	1.39	0.71
1:B:263:ASN:HD22	1:B:266:GLU:H	1.40	0.70
1:A:210:HIS:O	1:A:213:LYS:HG2	1.96	0.66
1:A:431:GLU:HB3	1:A:433:LEU:HD13	1.79	0.65
1:A:230:THR:HG22	4:A:1019:HOH:O	1.98	0.63
1:B:450:PHE:O	1:B:454:VAL:HG12	1.98	0.62
1:A:22:TRP:HE1	1:A:27:GLN:NE2	1.98	0.60
1:B:125:GLU:HG2	4:B:1114:HOH:O	2.02	0.60
1:B:439:ALA:HB1	1:B:445:LEU:HD21	1.84	0.59
1:A:230:THR:CG2	1:A:231:ALA:H	2.14	0.58
1:B:196:THR:H	1:B:199:GLN:NE2	2.01	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:415:HIS:HE1	4:B:1093:HOH:O	1.85	0.57
1:A:89:PHE:HA	1:A:105:ASN:HD21	1.70	0.57
1:B:239:HIS:HD2	1:B:241:GLU:H	1.51	0.57
1:A:188:HIS:O	1:A:189:LEU:HB2	2.04	0.57
1:B:188:HIS:O	1:B:189:LEU:HB2	2.04	0.56
1:B:89:PHE:HA	1:B:105:ASN:HD21	1.69	0.56
1:A:85:HIS:HD2	4:A:1070:HOH:O	1.87	0.56
1:A:96:THR:HG21	4:A:1165:HOH:O	2.06	0.55
1:A:8:LYS:HB2	1:A:8:LYS:NZ	2.22	0.55
1:A:210:HIS:HA	1:A:213:LYS:HE3	1.88	0.55
1:A:445:LEU:HD13	1:A:450:PHE:HB2	1.89	0.54
1:B:450:PHE:CE1	1:B:454:VAL:HG11	2.43	0.54
1:A:230:THR:CG2	1:A:231:ALA:N	2.71	0.52
1:A:239:HIS:CD2	1:A:241:GLU:H	2.27	0.52
1:A:149:HIS:HD2	1:A:224:GLU:O	1.93	0.51
1:B:454:VAL:O	1:B:454:VAL:HG13	2.10	0.51
1:B:427:LYS:HE2	1:B:442:LEU:HD13	1.92	0.51
1:A:302:PRO:HG2	1:A:303:ARG:HG2	1.93	0.51
1:B:95:GLN:HB2	1:B:101:GLN:NE2	2.26	0.51
1:A:421:ALA:O	1:A:424:ILE:HG12	2.11	0.50
1:A:161:ILE:HG22	1:A:165:LYS:HE2	1.93	0.50
1:A:22:TRP:HE1	1:A:27:GLN:HE21	1.58	0.50
1:B:22:TRP:HE1	1:B:27:GLN:NE2	2.09	0.50
1:B:408:LEU:HD12	4:B:1101:HOH:O	2.12	0.50
1:B:326:ASN:HB2	4:B:1155:HOH:O	2.11	0.49
1:B:22:TRP:HE1	1:B:27:GLN:HE21	1.60	0.49
1:A:124:MET:SD	1:A:124:MET:N	2.79	0.49
1:A:29:SER:OG	1:A:101:GLN:HG3	2.13	0.48
1:A:120:GLY:HA2	1:A:127:LYS:HE2	1.94	0.48
1:A:455:ARG:NH1	1:A:458:GLN:HE22	2.09	0.48
1:A:206:ALA:O	1:A:210:HIS:HD2	1.97	0.48
1:A:278:HIS:HE1	1:A:372:SER:OG	1.96	0.48
1:A:239:HIS:CD2	1:A:241:GLU:HB2	2.49	0.47
1:B:236:LEU:HD23	1:B:237:ASN:N	2.29	0.47
1:A:120:GLY:CA	1:A:127:LYS:HE2	2.44	0.47
1:B:263:ASN:HD21	1:B:265:PHE:HB2	1.80	0.47
1:B:239:HIS:CD2	1:B:241:GLU:H	2.30	0.46
1:B:254:THR:O	1:B:255:CYS:HB2	2.16	0.46
1:A:454:VAL:HG13	1:A:454:VAL:O	2.16	0.46
1:B:256:ALA:HB3	1:B:258:PHE:CE2	2.51	0.45
1:A:405:SER:HB3	1:B:304:CYS:SG	2.56	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:278:HIS:HE1	1:B:372:SER:OG	2.00	0.45
1:B:248:ASP:O	1:B:252:VAL:HG23	2.17	0.45
1:A:412:LEU:HD13	1:A:424:ILE:HD11	1.98	0.44
1:B:439:ALA:HB1	1:B:445:LEU:CD2	2.47	0.44
1:B:193:THR:HA	1:B:194:PRO:HD3	1.84	0.44
1:A:149:HIS:HE1	4:A:1033:HOH:O	2.00	0.44
1:A:239:HIS:HD2	1:A:241:GLU:HB2	1.82	0.44
1:A:450:PHE:O	1:A:454:VAL:HG12	2.17	0.44
1:B:53:ARG:HG3	1:B:74:ARG:HG3	2.00	0.44
1:A:140:SER:N	3:A:1001:CIT:O2	2.43	0.43
1:A:182:VAL:HG21	1:A:457:GLU:HA	2.01	0.43
1:A:423:GLU:HA	1:A:426:LYS:HD2	1.98	0.43
1:A:412:LEU:O	1:A:416:ILE:HG22	2.19	0.43
1:A:450:PHE:CE2	1:A:454:VAL:HG11	2.53	0.43
1:A:129:HIS:O	1:A:133:ASP:HB2	2.19	0.43
1:A:169:GLN:O	1:A:173:GLU:HG3	2.19	0.43
1:B:236:LEU:HD12	4:B:1061:HOH:O	2.19	0.43
1:A:182:VAL:HG12	1:A:402:LEU:HD11	2.01	0.42
1:B:415:HIS:HD2	4:B:1094:HOH:O	2.02	0.42
1:A:248:ASP:O	1:A:252:VAL:HG23	2.20	0.42
1:B:196:THR:OG1	1:B:199:GLN:HG3	2.20	0.42
1:B:426:LYS:O	1:B:430:LYS:HD3	2.19	0.42
1:A:422:ALA:O	1:A:426:LYS:HG3	2.20	0.42
1:B:302:PRO:HG3	1:B:323:GLY:HA3	2.02	0.42
1:B:97:GLY:HA3	1:B:360:VAL:O	2.20	0.42
1:B:178:PHE:CZ	1:B:393:PRO:HD3	2.55	0.42
1:B:53:ARG:CG	1:B:74:ARG:HG3	2.50	0.41
1:B:129:HIS:HA	1:B:130:PRO:HD3	1.86	0.41
1:A:91:LEU:HD13	1:A:101:GLN:HB3	2.03	0.41
1:A:132:ASP:O	1:A:136:LYS:HE3	2.21	0.41
1:B:196:THR:H	1:B:199:GLN:HE21	1.67	0.41
1:B:227:LEU:HD23	1:B:246:VAL:HG21	2.03	0.41
1:A:129:HIS:HB3	2:A:1000:SIF:C1	2.50	0.41
1:A:150:VAL:HA	1:A:258:PHE:CZ	2.56	0.41
1:A:337:CYS:O	1:A:341:MET:HG2	2.21	0.41
1:B:149:HIS:HE1	4:B:1023:HOH:O	2.03	0.41
1:B:298:LEU:HD12	1:B:298:LEU:HA	1.92	0.41
1:A:292:ALA:HB2	1:A:333:LEU:HD23	2.03	0.40
1:B:40:MET:HA	1:B:41:PRO:HD3	1.97	0.40
1:B:427:LYS:HE2	1:B:442:LEU:CD1	2.51	0.40
1:B:59:ASN:HD22	1:B:59:ASN:HA	1.70	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:278:HIS:HD2	1:B:344:ASP:OD1	2.05	0.40
1:A:5:ARG:HD2	1:A:124:MET:HE1	2.03	0.40
1:A:212:LEU:O	1:A:216:GLU:HG3	2.22	0.40

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	454/472 (96%)	439 (97%)	15 (3%)	0	100	100
1	B	451/472 (96%)	436 (97%)	14 (3%)	1 (0%)	43	42
All	All	905/944 (96%)	875 (97%)	29 (3%)	1 (0%)	48	46

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	322	PRO

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	368/381 (97%)	354 (96%)	14 (4%)	29	29
1	B	368/381 (97%)	352 (96%)	16 (4%)	26	25

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	736/762 (97%)	706 (96%)	30 (4%)	27	26

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	LYS
1	A	101	GLN
1	A	110	LEU
1	A	117	LEU
1	A	124	MET
1	A	159	GLN
1	A	165	LYS
1	A	169	GLN
1	A	189	LEU
1	A	230	THR
1	A	402	LEU
1	A	406	LEU
1	A	430	LYS
1	A	459	MET
1	B	59	ASN
1	B	65	LEU
1	B	69	LYS
1	B	71	SER
1	B	110	LEU
1	B	117	LEU
1	B	171	LEU
1	B	189	LEU
1	B	298	LEU
1	B	315	GLU
1	B	341	MET
1	B	396	GLU
1	B	397	ARG
1	B	442	LEU
1	B	458	GLN
1	B	459	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (41) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	25	GLN
1	A	27	GLN

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Mol	Chain	Res	Type
1	A	85	HIS
1	A	101	GLN
1	A	105	ASN
1	A	131	ASN
1	A	149	HIS
1	A	163	GLN
1	A	169	GLN
1	A	210	HIS
1	A	239	HIS
1	A	278	HIS
1	A	339	GLN
1	A	371	GLN
1	A	386	HIS
1	A	399	ASN
1	A	413	ASN
1	A	458	GLN
1	B	27	GLN
1	B	46	HIS
1	B	59	ASN
1	B	84	GLN
1	B	101	GLN
1	B	105	ASN
1	B	149	HIS
1	B	163	GLN
1	B	169	GLN
1	B	172	ASN
1	B	190	GLN
1	B	199	GLN
1	B	214	HIS
1	B	239	HIS
1	B	263	ASN
1	B	278	HIS
1	B	314	ASN
1	B	329	GLN
1	B	339	GLN
1	B	371	GLN
1	B	386	HIS
1	B	415	HIS
1	B	458	GLN

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 oligosaccharides 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	SIF	A	1000	-	9,11,11	9.77	6 (66%)	14,16,16	2.37	4 (28%)
2	SIF	B	1001	-	9,11,11	9.75	6 (66%)	14,16,16	2.37	4 (28%)
3	CIT	A	1001	-	12,12,12	4.27	4 (33%)	17,17,17	5.68	9 (52%)
3	CIT	B	1002	-	12,12,12	4.38	4 (33%)	17,17,17	5.69	9 (52%)

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	SIF	A	1000	-	1/1/4/4	6/13/14/14	-
2	SIF	B	1001	-	1/1/4/4	6/13/14/14	-
3	CIT	A	1001	-	-	9/16/16/16	-
3	CIT	B	1002	-	-	7/16/16/16	-

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1000	SIF	SI-C3	-17.39	1.54	1.90
2	B	1001	SIF	SI-C3	-17.34	1.54	1.90
2	A	1000	SIF	SI-C7	-13.52	1.54	1.87
2	B	1001	SIF	SI-C5	-13.51	1.54	1.87
2	B	1001	SIF	SI-C7	-13.50	1.54	1.87
2	A	1000	SIF	SI-C5	-13.49	1.54	1.87
2	A	1000	SIF	SI-C6	-13.46	1.54	1.87
2	B	1001	SIF	SI-C6	-13.42	1.54	1.87
3	B	1002	CIT	C2-C3	12.43	1.69	1.54
3	A	1001	CIT	C2-C3	11.95	1.68	1.54
3	B	1002	CIT	C4-C5	-7.09	1.29	1.50
3	A	1001	CIT	C4-C5	-7.04	1.29	1.50
3	A	1001	CIT	O7-C3	-2.97	1.37	1.43
3	B	1002	CIT	O7-C3	-2.89	1.37	1.43
3	A	1001	CIT	O4-C5	-2.38	1.22	1.30
3	B	1002	CIT	O4-C5	-2.38	1.23	1.30
2	B	1001	SIF	O1-C1	2.03	1.28	1.22
2	B	1001	SIF	O3-C4	2.02	1.28	1.22
2	A	1000	SIF	O1-C1	2.01	1.28	1.22
2	A	1000	SIF	O3-C4	2.00	1.28	1.22

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1002	CIT	C3-C4-C5	12.48	148.04	113.92
3	A	1001	CIT	C3-C4-C5	12.43	147.90	113.92
3	A	1001	CIT	C4-C3-C6	-11.82	83.89	110.03
3	B	1002	CIT	C4-C3-C6	-11.82	83.89	110.03
3	B	1002	CIT	C3-C2-C1	11.48	145.30	113.92
3	A	1001	CIT	C3-C2-C1	11.37	145.00	113.92
3	B	1002	CIT	O7-C3-C2	6.94	125.20	109.38
3	A	1001	CIT	O7-C3-C2	6.91	125.13	109.38
2	B	1001	SIF	C2-C3-C4	6.71	128.05	113.19
2	A	1000	SIF	C2-C3-C4	6.69	128.00	113.19
3	A	1001	CIT	O7-C3-C4	4.76	120.23	109.38
3	B	1002	CIT	O7-C3-C4	4.71	120.12	109.38
3	B	1002	CIT	O6-C6-C3	4.39	121.57	113.14
3	A	1001	CIT	O6-C6-C3	4.39	121.55	113.14
2	A	1000	SIF	C3-C2-C1	3.66	122.17	112.81
2	B	1001	SIF	C3-C2-C1	3.65	122.13	112.81
3	A	1001	CIT	C2-C3-C6	-3.43	102.45	110.03
3	B	1002	CIT	C2-C3-C6	-3.29	102.77	110.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1000	SIF	O3-C4-C3	-2.84	117.59	124.71
2	B	1001	SIF	O3-C4-C3	-2.80	117.68	124.71
2	A	1000	SIF	O1-C1-C2	-2.51	115.12	122.84
2	B	1001	SIF	O1-C1-C2	-2.50	115.16	122.84
3	B	1002	CIT	O6-C6-O5	-2.26	116.64	123.86
3	A	1001	CIT	O6-C6-O5	-2.24	116.69	123.86
3	A	1001	CIT	O4-C5-O3	2.03	128.54	123.33
3	B	1002	CIT	O4-C5-O3	2.02	128.53	123.33

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	1000	SIF	C3
2	B	1001	SIF	C3

All (28) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1000	SIF	C1-C2-C3-C4
2	A	1000	SIF	C2-C3-SI-C5
2	A	1000	SIF	C2-C3-SI-C6
2	B	1001	SIF	C1-C2-C3-C4
2	B	1001	SIF	C2-C3-SI-C5
2	B	1001	SIF	C2-C3-SI-C6
3	A	1001	CIT	C1-C2-C3-O7
3	A	1001	CIT	O7-C3-C4-C5
3	A	1001	CIT	C6-C3-C4-C5
3	B	1002	CIT	O7-C3-C4-C5
3	B	1002	CIT	C6-C3-C4-C5
3	A	1001	CIT	C1-C2-C3-C6
3	A	1001	CIT	C2-C3-C6-O5
3	A	1001	CIT	C2-C3-C6-O6
3	B	1002	CIT	C2-C3-C4-C5
3	A	1001	CIT	C2-C3-C4-C5
3	B	1002	CIT	C2-C3-C6-O5
3	B	1002	CIT	C2-C3-C6-O6
2	A	1000	SIF	C2-C3-SI-C7
2	B	1001	SIF	C2-C3-SI-C7
3	B	1002	CIT	C1-C2-C3-O7
2	A	1000	SIF	C2-C3-C4-O3
2	B	1001	SIF	C2-C3-C4-O3
3	A	1001	CIT	C4-C3-C6-O5

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Mol	Chain	Res	Type	Atoms
2	A	1000	SIF	C2-C3-C4-O4
2	B	1001	SIF	C2-C3-C4-O4
3	A	1001	CIT	C4-C3-C6-O6
3	B	1002	CIT	C1-C2-C3-C6

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1000	SIF	1	0
3	A	1001	CIT	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

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.