



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 02:36 PM UTC

PDB ID : 8H1L / pdb_00008h1l
Title : Crystal structure of glucose-2-epimerase in complex with D-Glucitol from *Runella slithyformis* Runsl_4512
Authors : Wang, H.; Sun, X.M.; Saburi, W.; Yu, J.; Yao, M.
Deposited on : 2022-10-03
Resolution : 2.33 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) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

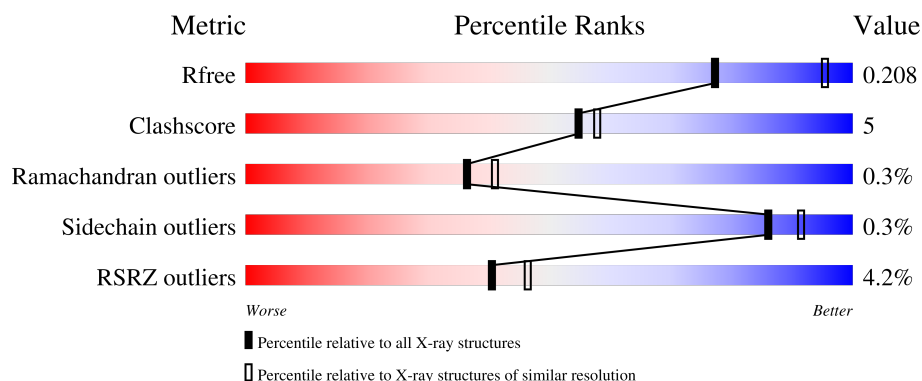
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.33 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}	180053	3031 (2.36-2.32)
Clashscore	190562	3127 (2.36-2.32)
Ramachandran outliers	187476	3095 (2.36-2.32)
Sidechain outliers	187428	3095 (2.36-2.32)
RSRZ outliers	180081	3033 (2.36-2.32)

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 $\leq 5\%$. 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	423	5% 88% 11%
1	B	423	2% 87% 13%
1	C	423	3% 89% 11%
1	D	423	6% 88% 11%

2 Entry composition [i](#)

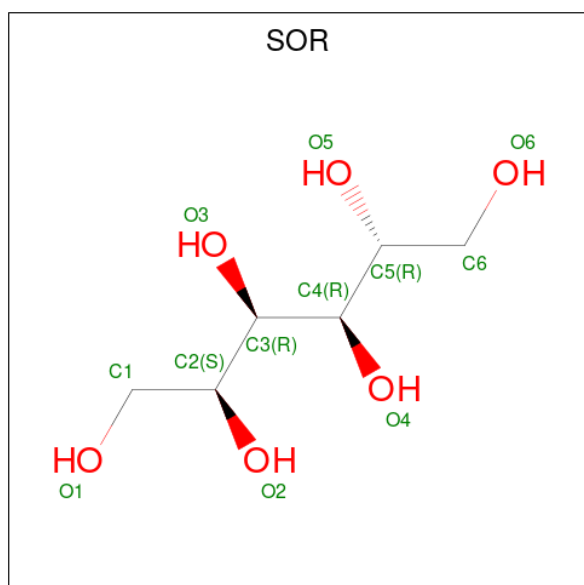
There are 3 unique types of molecules in this entry. The entry contains 14618 atoms, of which 28 are hydrogens and 0 are deuteriums.

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 N-acetylglucosamine 2-epimerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	418	Total	C	N	O	S	0	0	0
			3432	2200	578	637	17			
1	B	423	Total	C	N	O	S	0	0	0
			3464	2220	584	643	17			
1	C	422	Total	C	N	O	S	0	0	0
			3456	2215	583	642	16			
1	D	419	Total	C	N	O	S	0	0	0
			3436	2203	579	638	16			

- Molecule 2 is sorbitol (CCD ID: SOR) (formula: C₆H₁₄O₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	1	Total	C	H	O	0	0
			26	6	14	6		
2	C	1	Total	C	H	O	0	0
			26	6	14	6		

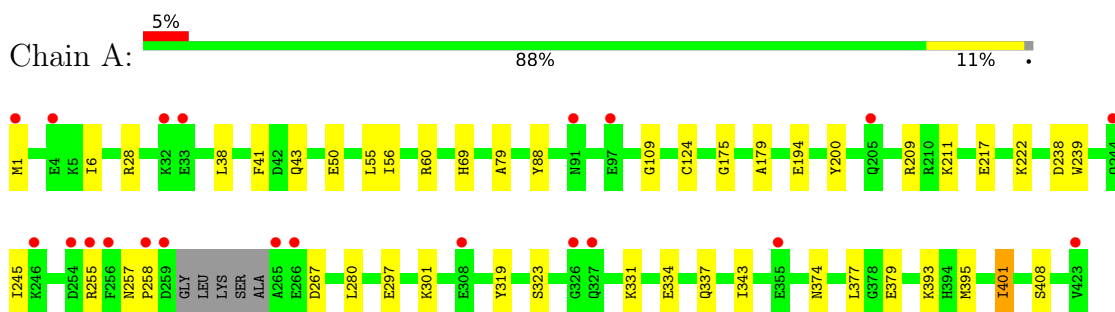
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	200	Total 200	O 200	0	0
3	B	228	Total 228	O 228	0	0
3	C	196	Total 196	O 196	0	0
3	D	154	Total 154	O 154	0	0

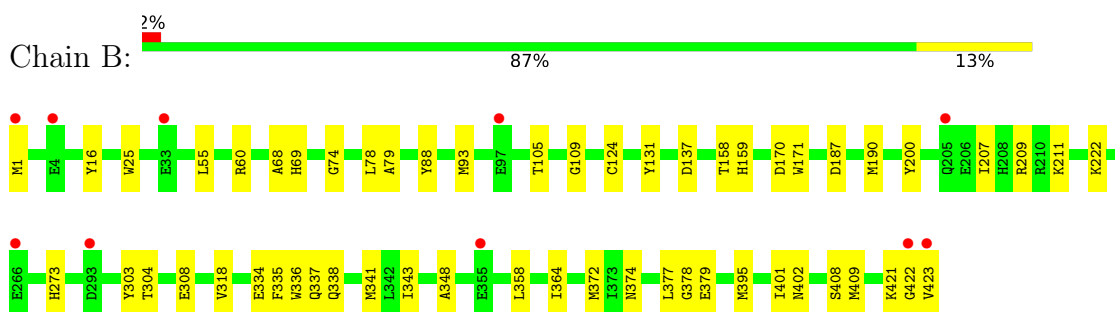
3 Residue-property plots [i](#)

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.

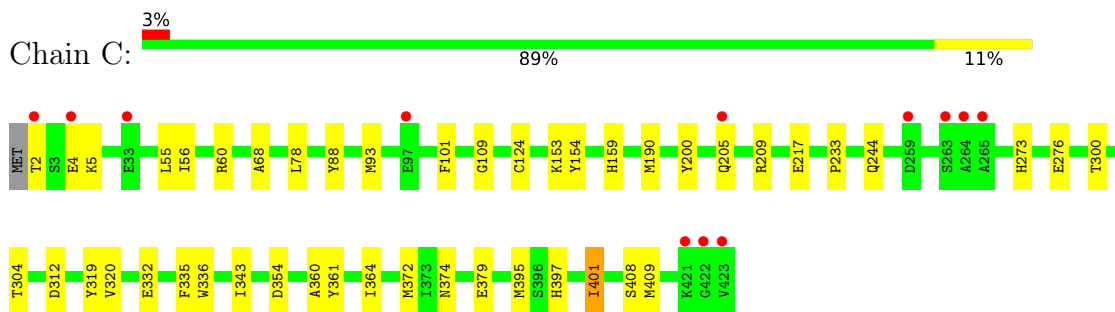
- Molecule 1: N-acetylglucosamine 2-epimerase



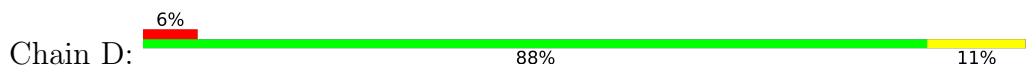
- Molecule 1: N-acetylglucosamine 2-epimerase

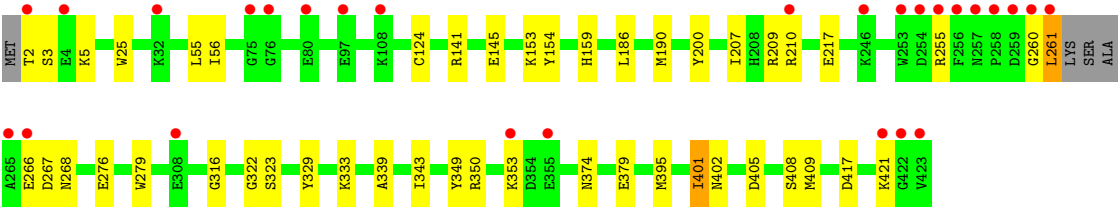


- Molecule 1: N-acetylglucosamine 2-epimerase



- Molecule 1: N-acetylglucosamine 2-epimerase





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	146.24Å 172.73Å 150.46Å 90.00° 116.96° 90.00°	Depositor
Resolution (Å)	48.53 – 2.33 48.53 – 2.33	Depositor EDS
% Data completeness (in resolution range)	99.2 (48.53-2.33) 99.2 (48.53-2.33)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.09 (at 2.34Å)	Xtriage
Refinement program	PHENIX 1.17_3644	Depositor
R, R_{free}	0.179 , 0.208 0.181 , 0.208	Depositor DCC
R_{free} test set	7027 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	34.1	Xtriage
Anisotropy	0.385	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 31.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.000 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	14618	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.08% 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, 0.333 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: SOR

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	0.35	0/3532	0.54	0/4782
1	B	0.36	0/3565	0.53	0/4827
1	C	0.34	0/3557	0.51	0/4817
1	D	0.34	0/3536	0.53	0/4788
All	All	0.35	0/14190	0.53	0/19214

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	3432	0	3249	30	0
1	B	3464	0	3287	33	0
1	C	3456	0	3275	33	0
1	D	3436	0	3251	36	0
2	B	12	14	14	2	0
2	C	12	14	14	4	0
3	A	200	0	0	2	0
3	B	228	0	0	1	0
3	C	196	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	154	0	0	2	0
All	All	14590	28	13090	128	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 5.

All (128) 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:379:GLU:HB2	1:A:395:MET:HE3	1.48	0.96
1:B:379:GLU:HB2	1:B:395:MET:HE3	1.49	0.95
1:C:379:GLU:HB2	1:C:395:MET:HE3	1.51	0.91
1:D:379:GLU:HB2	1:D:395:MET:HE3	1.55	0.89
1:D:207:ILE:HD13	1:D:210:ARG:NH2	1.91	0.85
1:D:379:GLU:CB	1:D:395:MET:HE3	2.08	0.84
1:B:379:GLU:CB	1:B:395:MET:HE3	2.10	0.81
1:C:379:GLU:CB	1:C:395:MET:HE3	2.12	0.78
1:A:379:GLU:CB	1:A:395:MET:HE3	2.17	0.74
1:D:210:ARG:NH1	3:D:501:HOH:O	2.21	0.73
1:B:207:ILE:HD11	1:B:211:LYS:HE3	1.73	0.71
1:B:222:LYS:NZ	3:B:601:HOH:O	2.22	0.71
1:C:200:TYR:CE1	1:C:209:ARG:HB2	2.26	0.70
1:D:207:ILE:CD1	1:D:210:ARG:NH2	2.54	0.69
1:D:207:ILE:HD13	1:D:210:ARG:HH21	1.63	0.63
1:D:200:TYR:CE1	1:D:209:ARG:HB2	2.35	0.61
1:D:374:ASN:HB3	1:D:395:MET:HE1	1.80	0.61
1:B:60:ARG:HH12	2:B:501:SOR:H61	1.66	0.60
1:D:268:ASN:HA	1:D:322:GLY:O	2.01	0.60
1:C:343:ILE:HD11	1:C:408:SER:HA	1.84	0.60
1:C:374:ASN:HB3	1:C:395:MET:HE1	1.83	0.60
1:B:304:THR:O	1:B:308:GLU:HG3	2.03	0.59
1:D:267:ASP:OD2	1:D:323:SER:HB2	2.04	0.56
1:D:186:LEU:HD12	1:D:186:LEU:O	2.06	0.56
1:D:409:MET:HA	1:D:409:MET:HE2	1.88	0.56
1:B:421:LYS:C	1:B:423:VAL:H	2.13	0.56
1:A:88:TYR:OH	1:A:109:GLY:HA2	2.07	0.55
1:A:377:LEU:HB2	1:A:395:MET:HE2	1.88	0.55
1:B:200:TYR:CE1	1:B:209:ARG:HB2	2.41	0.55
1:A:38:LEU:HB3	3:A:678:HOH:O	2.07	0.54
1:D:339:ALA:HB1	1:D:408:SER:HB2	1.90	0.53
1:B:190:MET:HE1	1:B:273:HIS:ND1	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:341:MET:HB3	1:B:364:ILE:HD13	1.89	0.53
1:C:401:ILE:HD12	1:C:401:ILE:N	2.24	0.52
1:A:343:ILE:HD11	1:A:408:SER:HA	1.91	0.52
1:A:334:GLU:HB3	1:A:337:GLN:OE1	2.09	0.52
1:C:409:MET:HE2	1:C:409:MET:HA	1.92	0.52
1:B:88:TYR:OH	1:B:109:GLY:HA2	2.10	0.51
1:D:316:GLY:O	1:D:333:LYS:HE2	2.10	0.51
1:C:273:HIS:CD2	2:C:501:SOR:O1	2.64	0.51
1:C:273:HIS:CD2	2:C:501:SOR:HO1	2.27	0.51
1:C:320:VAL:HG23	1:C:332:GLU:O	2.11	0.51
1:D:417:ASP:O	1:D:421:LYS:HG2	2.11	0.51
1:A:211:LYS:HE2	1:B:158:THR:HG23	1.93	0.50
1:C:273:HIS:NE2	2:C:501:SOR:O1	2.38	0.50
1:C:205:GLN:NE2	3:C:601:HOH:O	2.45	0.50
1:D:401:ILE:HD12	1:D:401:ILE:N	2.27	0.49
1:D:405:ASP:O	1:D:409:MET:HG2	2.12	0.49
1:D:153:LYS:HE2	1:D:154:TYR:CZ	2.48	0.49
1:C:300:THR:O	1:C:304:THR:HG22	2.13	0.49
1:D:255:ARG:NH1	3:D:503:HOH:O	2.46	0.49
1:C:88:TYR:OH	1:C:109:GLY:HA2	2.13	0.48
1:B:343:ILE:HD11	1:B:408:SER:HA	1.95	0.48
1:A:194:GLU:HB2	1:A:280:LEU:HD13	1.96	0.47
1:B:377:LEU:HB2	1:B:395:MET:HE2	1.96	0.47
1:C:190:MET:HE1	1:C:276:GLU:CD	2.38	0.47
1:B:335:PHE:HA	1:B:372:MET:SD	2.55	0.47
1:C:93:MET:O	1:C:101:PHE:HA	2.15	0.47
1:C:217:GLU:HB3	1:D:159:HIS:CE1	2.50	0.46
1:B:55:LEU:HD11	1:B:124:CYS:SG	2.55	0.46
1:D:141:ARG:O	1:D:145:GLU:HG3	2.15	0.46
1:A:374:ASN:HB3	1:A:395:MET:HE1	1.97	0.46
1:C:60:ARG:HH12	2:C:501:SOR:H61	1.81	0.46
1:D:5:LYS:HA	1:D:5:LYS:HD3	1.85	0.46
1:C:55:LEU:HD11	1:C:124:CYS:SG	2.55	0.46
1:C:159:HIS:CE1	1:D:217:GLU:HB3	2.51	0.45
1:D:343:ILE:HD11	1:D:408:SER:HA	1.98	0.45
1:A:238:ASP:O	1:A:239:TRP:HB2	2.17	0.45
1:B:334:GLU:HB3	1:B:337:GLN:OE1	2.16	0.45
1:C:4:GLU:H	1:C:4:GLU:CD	2.24	0.45
1:B:187:ASP:OD1	2:B:501:SOR:O2	2.33	0.45
1:D:276:GLU:HA	1:D:279:TRP:CD1	2.52	0.45
1:A:401:ILE:N	1:A:401:ILE:HD12	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:335:PHE:HA	1:C:372:MET:SD	2.57	0.45
1:B:318:VAL:HG12	1:B:338:GLN:OE1	2.17	0.45
1:D:55:LEU:HD11	1:D:124:CYS:SG	2.57	0.44
1:A:43:GLN:OE1	1:A:393:LYS:HE2	2.17	0.44
1:D:401:ILE:HG22	1:D:402:ASN:N	2.32	0.44
1:A:245:ILE:HD13	1:A:245:ILE:HG21	1.70	0.44
1:B:74:GLY:HA3	1:B:78:LEU:HG	1.98	0.44
1:C:361:TYR:CD2	1:C:361:TYR:C	2.95	0.44
1:B:374:ASN:HB3	1:B:395:MET:HE1	1.99	0.44
1:C:312:ASP:HB2	1:C:319:TYR:CE1	2.51	0.44
1:A:175:GLY:O	1:A:179:ALA:HB3	2.18	0.44
1:A:267:ASP:O	1:A:323:SER:HA	2.17	0.44
1:D:261:LEU:HD12	1:D:329:TYR:HA	1.99	0.43
1:B:93:MET:HE3	1:B:105:THR:HG23	1.99	0.43
1:A:222:LYS:HD2	1:A:239:TRP:CG	2.52	0.43
1:A:255:ARG:HG2	3:A:521:HOH:O	2.19	0.43
1:A:200:TYR:CE1	1:A:209:ARG:HB2	2.53	0.43
1:C:5:LYS:HA	1:C:5:LYS:HD3	1.77	0.43
1:C:233:PRO:HG2	1:C:244:GLN:OE1	2.19	0.43
1:D:266:GLU:OE1	1:D:266:GLU:HA	2.19	0.43
1:A:69:HIS:CE1	1:A:79:ALA:HB2	2.54	0.43
1:C:56:ILE:HD13	1:C:56:ILE:HA	1.87	0.43
1:D:349:TYR:O	1:D:353:LYS:HE3	2.19	0.42
1:D:260:GLY:HA2	1:D:329:TYR:O	2.20	0.42
1:D:350:ARG:O	1:D:353:LYS:HE3	2.19	0.42
1:B:16:TYR:OH	1:B:378:GLY:O	2.37	0.42
1:B:69:HIS:CE1	1:B:79:ALA:HB2	2.54	0.42
1:B:303:TYR:CG	1:B:348:ALA:HB2	2.54	0.42
1:B:409:MET:HA	1:B:409:MET:HE2	2.01	0.42
1:A:56:ILE:O	1:A:60:ARG:HB2	2.19	0.42
1:B:131:TYR:CE2	1:B:137:ASP:HB3	2.54	0.42
1:A:55:LEU:HD11	1:A:124:CYS:SG	2.60	0.42
1:B:68:ALA:HB3	1:B:78:LEU:HD13	2.02	0.42
1:A:28:ARG:HB3	1:A:41:PHE:CZ	2.54	0.41
1:C:335:PHE:CG	1:C:336:TRP:N	2.87	0.41
1:B:170:ASP:O	1:B:171:TRP:HB2	2.20	0.41
1:D:25:TRP:CG	1:D:402:ASN:HD22	2.38	0.41
1:C:68:ALA:HB3	1:C:78:LEU:HD13	2.02	0.41
1:C:360:ALA:O	1:C:364:ILE:HG12	2.20	0.41
1:B:25:TRP:CG	1:B:402:ASN:HD22	2.37	0.41
1:D:56:ILE:HD13	1:D:56:ILE:HA	1.92	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:319:TYR:CD1	1:A:331:LYS:HA	2.56	0.41
1:B:1:MET:HE3	1:B:358:LEU:HB3	2.01	0.41
1:C:200:TYR:CZ	1:C:209:ARG:HB2	2.54	0.41
1:A:297:GLU:HG2	1:A:301:LYS:HE3	2.02	0.41
1:D:186:LEU:HD12	1:D:190:MET:HB2	2.02	0.41
1:A:267:ASP:OD2	1:A:323:SER:HB2	2.20	0.41
1:A:1:MET:CE	1:A:6:ILE:HG12	2.51	0.41
1:D:379:GLU:HB3	1:D:395:MET:HE3	2.00	0.40
1:B:335:PHE:CG	1:B:336:TRP:N	2.89	0.40
1:A:50:GLU:OE1	1:A:50:GLU:N	2.46	0.40
1:A:217:GLU:HB3	1:B:159:HIS:CE1	2.56	0.40
1:A:257:ASN:HA	1:A:258:PRO:HD3	1.94	0.40
1:C:153:LYS:HE2	1:C:154:TYR:CZ	2.55	0.40
1:C:354:ASP:C	1:C:354:ASP:OD2	2.65	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	414/423 (98%)	407 (98%)	6 (1%)	1 (0%)	43	50
1	B	421/423 (100%)	408 (97%)	11 (3%)	2 (0%)	24	26
1	C	420/423 (99%)	406 (97%)	13 (3%)	1 (0%)	43	50
1	D	415/423 (98%)	406 (98%)	8 (2%)	1 (0%)	43	50
All	All	1670/1692 (99%)	1627 (97%)	38 (2%)	5 (0%)	36	41

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	401	ILE

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Mol	Chain	Res	Type
1	D	401	ILE
1	A	401	ILE
1	C	401	ILE
1	B	422	GLY

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	358/361 (99%)	358 (100%)	0	100	100
1	B	361/361 (100%)	361 (100%)	0	100	100
1	C	360/361 (100%)	358 (99%)	2 (1%)	78	86
1	D	358/361 (99%)	355 (99%)	3 (1%)	73	82
All	All	1437/1444 (100%)	1432 (100%)	5 (0%)	86	91

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	2	THR
1	C	397	HIS
1	D	2	THR
1	D	3	SER
1	D	261	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	11	GLN
1	A	34	ASN
1	A	96	ASN
1	A	273	HIS
1	B	96	ASN
1	B	168	ASN
1	B	268	ASN

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Mol	Chain	Res	Type
1	C	40	HIS
1	C	168	ASN
1	C	298	GLN
1	C	359	GLN
1	D	11	GLN
1	D	43	GLN
1	D	96	ASN
1	D	98	HIS
1	D	327	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 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	SOR	C	501	-	11,11,11	0.57	0	14,14,14	1.60	3 (21%)
2	SOR	B	501	-	11,11,11	0.59	0	14,14,14	0.95	1 (7%)

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	SOR	C	501	-	-	6/16/16/16	-
2	SOR	B	501	-	-	12/16/16/16	-

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	501	SOR	C2-C3-C4	-3.47	107.15	112.48
2	C	501	SOR	C5-C4-C3	2.85	116.85	112.48
2	C	501	SOR	O6-C6-C5	-2.47	105.98	111.16
2	B	501	SOR	O6-C6-C5	-2.10	106.75	111.16

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	501	SOR	O1-C1-C2-C3
2	B	501	SOR	O1-C1-C2-O2
2	B	501	SOR	C2-C3-C4-C5
2	B	501	SOR	C2-C3-C4-O4
2	B	501	SOR	O3-C3-C4-C5
2	C	501	SOR	C2-C3-C4-C5
2	C	501	SOR	C2-C3-C4-O4
2	C	501	SOR	O3-C3-C4-C5
2	B	501	SOR	O2-C2-C3-C4
2	B	501	SOR	C1-C2-C3-O3
2	B	501	SOR	C1-C2-C3-C4
2	B	501	SOR	O2-C2-C3-O3
2	C	501	SOR	O3-C3-C4-O4
2	C	501	SOR	O1-C1-C2-O2
2	B	501	SOR	O3-C3-C4-O4
2	C	501	SOR	O1-C1-C2-C3
2	B	501	SOR	O5-C5-C6-O6
2	B	501	SOR	C4-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	501	SOR	4	0
2	B	501	SOR	2	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	418/423 (98%)	-0.19	21 (5%) 34 40	20, 29, 49, 83	0
1	B	423/423 (100%)	-0.27	10 (2%) 59 65	21, 29, 46, 78	0
1	C	422/423 (99%)	-0.11	12 (2%) 55 61	22, 32, 51, 80	0
1	D	419/423 (99%)	0.03	27 (6%) 25 30	23, 34, 58, 108	0
All	All	1682/1692 (99%)	-0.14	70 (4%) 40 46	20, 31, 51, 108	0

All (70) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	423	VAL	8.6
1	D	256	PHE	7.1
1	C	423	VAL	7.0
1	D	423	VAL	6.4
1	A	265	ALA	6.2
1	D	261	LEU	6.2
1	D	254	ASP	6.2
1	D	4	GLU	6.0
1	A	254	ASP	5.7
1	D	265	ALA	5.4
1	A	259	ASP	5.3
1	C	2	THR	5.1
1	D	258	PRO	4.9
1	D	355	GLU	4.9
1	D	259	ASP	4.8
1	A	256	PHE	4.7
1	D	421	LYS	4.1
1	B	33	GLU	3.9
1	B	355	GLU	3.8
1	D	260	GLY	3.7
1	D	255	ARG	3.7

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Mol	Chain	Res	Type	RSRZ
1	D	80	GLU	3.6
1	D	75	GLY	3.6
1	D	2	THR	3.6
1	C	33	GLU	3.6
1	A	258	PRO	3.6
1	C	4	GLU	3.5
1	A	423	VAL	3.4
1	D	266	GLU	3.4
1	C	422	GLY	3.3
1	A	33	GLU	3.3
1	D	308	GLU	3.3
1	A	1	MET	3.2
1	D	422	GLY	3.2
1	B	422	GLY	3.2
1	D	246	LYS	3.1
1	D	257	ASN	3.0
1	D	97	GLU	3.0
1	B	293	ASP	3.0
1	B	1	MET	2.9
1	B	97	GLU	2.9
1	A	97	GLU	2.8
1	D	353	LYS	2.7
1	C	265	ALA	2.7
1	C	259	ASP	2.7
1	C	263	SER	2.7
1	C	264	ALA	2.6
1	D	108	LYS	2.6
1	C	421	LYS	2.5
1	A	246	LYS	2.5
1	D	253	TRP	2.5
1	B	266	GLU	2.4
1	C	97	GLU	2.4
1	D	210	ARG	2.4
1	A	266	GLU	2.4
1	B	4	GLU	2.4
1	A	205	GLN	2.3
1	A	355	GLU	2.2
1	A	326	GLY	2.2
1	D	76	GLY	2.2
1	A	244	GLN	2.2
1	A	4	GLU	2.2
1	A	91	ASN	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	327	GLN	2.1
1	B	205	GLN	2.1
1	C	205	GLN	2.1
1	A	32	LYS	2.1
1	A	308	GLU	2.1
1	A	255	ARG	2.1
1	D	32	LYS	2.0

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 oligosaccharides 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($\text{\AA}^2$)	Q<0.9
2	SOR	C	501	12/12	0.86	0.15	47,52,65,76	0
2	SOR	B	501	12/12	0.87	0.14	47,50,60,67	0

6.5 Other polymers [i](#)

There are no such residues in this entry.