



Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 05:55 am BST

PDB ID : 4R83
Title : Crystal structure of Sialyltransferase from Photobacterium damsela
Authors : Fisher, A.J.; Chen, X.; Li, Y.; Huynh, N.
Deposited on : 2014-08-29
Resolution : 1.93 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.11
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) : 2.11

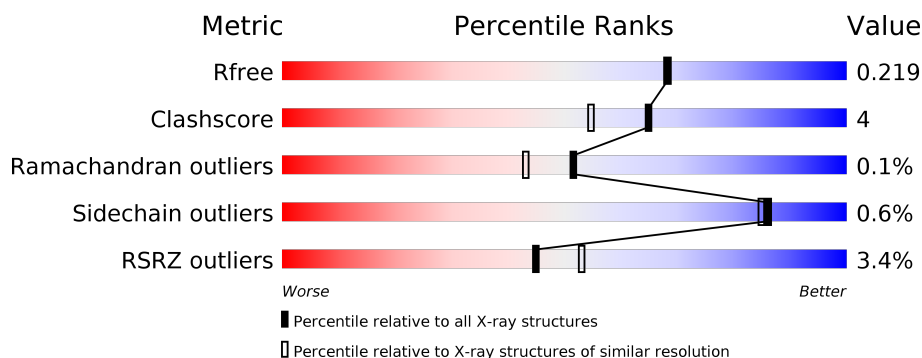
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.93 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	4310 (1.96-1.92)
Clashscore	141614	1023 (1.94-1.94)
Ramachandran outliers	138981	1007 (1.94-1.94)
Sidechain outliers	138945	1007 (1.94-1.94)
RSRZ outliers	127900	4250 (1.96-1.92)

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 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	503	<div> <div>2%</div> <div> <div></div> <div>86%</div> <div>8%</div> <div>6%</div> </div> </div>
1	B	503	<div> <div>3%</div> <div> <div></div> <div>87%</div> <div>7%</div> <div>6%</div> </div> </div>
1	C	503	<div> <div>2%</div> <div> <div></div> <div>88%</div> <div>6%</div> <div>6%</div> </div> </div>
1	D	503	<div> <div>6%</div> <div> <div></div> <div>83%</div> <div>11%</div> <div>6%</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 16660 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 Sialyltransferase 0160.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	474	Total	C	N	O	S	0	8	0
			3835	2453	609	762	11			
1	B	473	Total	C	N	O	S	0	3	0
			3805	2433	606	756	10			
1	C	474	Total	C	N	O	S	0	4	0
			3816	2442	606	757	11			
1	D	474	Total	C	N	O	S	0	3	0
			3805	2434	605	756	10			

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	MET	-	EXPRESSION TAG	UNP O66375
A	-4	GLY	-	EXPRESSION TAG	UNP O66375
A	-3	SER	-	EXPRESSION TAG	UNP O66375
A	-2	SER	-	EXPRESSION TAG	UNP O66375
A	-1	HIS	-	EXPRESSION TAG	UNP O66375
A	0	HIS	-	EXPRESSION TAG	UNP O66375
A	1	HIS	-	EXPRESSION TAG	UNP O66375
A	2	HIS	-	EXPRESSION TAG	UNP O66375
A	3	HIS	-	EXPRESSION TAG	UNP O66375
A	4	HIS	-	EXPRESSION TAG	UNP O66375
A	5	SER	-	EXPRESSION TAG	UNP O66375
A	6	SER	-	EXPRESSION TAG	UNP O66375
A	7	GLY	-	EXPRESSION TAG	UNP O66375
A	8	LEU	-	EXPRESSION TAG	UNP O66375
A	9	VAL	-	EXPRESSION TAG	UNP O66375
A	10	PRO	-	EXPRESSION TAG	UNP O66375
A	11	ARG	-	EXPRESSION TAG	UNP O66375
A	12	GLY	-	EXPRESSION TAG	UNP O66375
A	13	SER	-	EXPRESSION TAG	UNP O66375
A	14	HIS	-	EXPRESSION TAG	UNP O66375
A	15	MET	-	EXPRESSION TAG	UNP O66375

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-5	MET	-	EXPRESSION TAG	UNP O66375
B	-4	GLY	-	EXPRESSION TAG	UNP O66375
B	-3	SER	-	EXPRESSION TAG	UNP O66375
B	-2	SER	-	EXPRESSION TAG	UNP O66375
B	-1	HIS	-	EXPRESSION TAG	UNP O66375
B	0	HIS	-	EXPRESSION TAG	UNP O66375
B	1	HIS	-	EXPRESSION TAG	UNP O66375
B	2	HIS	-	EXPRESSION TAG	UNP O66375
B	3	HIS	-	EXPRESSION TAG	UNP O66375
B	4	HIS	-	EXPRESSION TAG	UNP O66375
B	5	SER	-	EXPRESSION TAG	UNP O66375
B	6	SER	-	EXPRESSION TAG	UNP O66375
B	7	GLY	-	EXPRESSION TAG	UNP O66375
B	8	LEU	-	EXPRESSION TAG	UNP O66375
B	9	VAL	-	EXPRESSION TAG	UNP O66375
B	10	PRO	-	EXPRESSION TAG	UNP O66375
B	11	ARG	-	EXPRESSION TAG	UNP O66375
B	12	GLY	-	EXPRESSION TAG	UNP O66375
B	13	SER	-	EXPRESSION TAG	UNP O66375
B	14	HIS	-	EXPRESSION TAG	UNP O66375
B	15	MET	-	EXPRESSION TAG	UNP O66375
C	-5	MET	-	EXPRESSION TAG	UNP O66375
C	-4	GLY	-	EXPRESSION TAG	UNP O66375
C	-3	SER	-	EXPRESSION TAG	UNP O66375
C	-2	SER	-	EXPRESSION TAG	UNP O66375
C	-1	HIS	-	EXPRESSION TAG	UNP O66375
C	0	HIS	-	EXPRESSION TAG	UNP O66375
C	1	HIS	-	EXPRESSION TAG	UNP O66375
C	2	HIS	-	EXPRESSION TAG	UNP O66375
C	3	HIS	-	EXPRESSION TAG	UNP O66375
C	4	HIS	-	EXPRESSION TAG	UNP O66375
C	5	SER	-	EXPRESSION TAG	UNP O66375
C	6	SER	-	EXPRESSION TAG	UNP O66375
C	7	GLY	-	EXPRESSION TAG	UNP O66375
C	8	LEU	-	EXPRESSION TAG	UNP O66375
C	9	VAL	-	EXPRESSION TAG	UNP O66375
C	10	PRO	-	EXPRESSION TAG	UNP O66375
C	11	ARG	-	EXPRESSION TAG	UNP O66375
C	12	GLY	-	EXPRESSION TAG	UNP O66375
C	13	SER	-	EXPRESSION TAG	UNP O66375
C	14	HIS	-	EXPRESSION TAG	UNP O66375
C	15	MET	-	EXPRESSION TAG	UNP O66375

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-5	MET	-	EXPRESSION TAG	UNP O66375
D	-4	GLY	-	EXPRESSION TAG	UNP O66375
D	-3	SER	-	EXPRESSION TAG	UNP O66375
D	-2	SER	-	EXPRESSION TAG	UNP O66375
D	-1	HIS	-	EXPRESSION TAG	UNP O66375
D	0	HIS	-	EXPRESSION TAG	UNP O66375
D	1	HIS	-	EXPRESSION TAG	UNP O66375
D	2	HIS	-	EXPRESSION TAG	UNP O66375
D	3	HIS	-	EXPRESSION TAG	UNP O66375
D	4	HIS	-	EXPRESSION TAG	UNP O66375
D	5	SER	-	EXPRESSION TAG	UNP O66375
D	6	SER	-	EXPRESSION TAG	UNP O66375
D	7	GLY	-	EXPRESSION TAG	UNP O66375
D	8	LEU	-	EXPRESSION TAG	UNP O66375
D	9	VAL	-	EXPRESSION TAG	UNP O66375
D	10	PRO	-	EXPRESSION TAG	UNP O66375
D	11	ARG	-	EXPRESSION TAG	UNP O66375
D	12	GLY	-	EXPRESSION TAG	UNP O66375
D	13	SER	-	EXPRESSION TAG	UNP O66375
D	14	HIS	-	EXPRESSION TAG	UNP O66375
D	15	MET	-	EXPRESSION TAG	UNP O66375

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total Ca 1 1	0	0
2	A	1	Total Ca 1 1	0	0
2	D	1	Total Ca 1 1	0	0
2	C	1	Total Ca 1 1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	345	Total O 345 345	0	0
3	B	321	Total O 321 321	0	0
3	C	433	Total O 433 433	0	0

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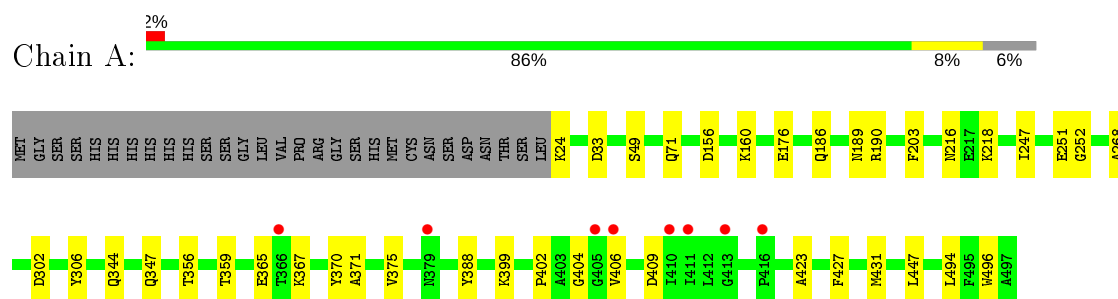
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	D	296	Total	O	0	0
			296	296		

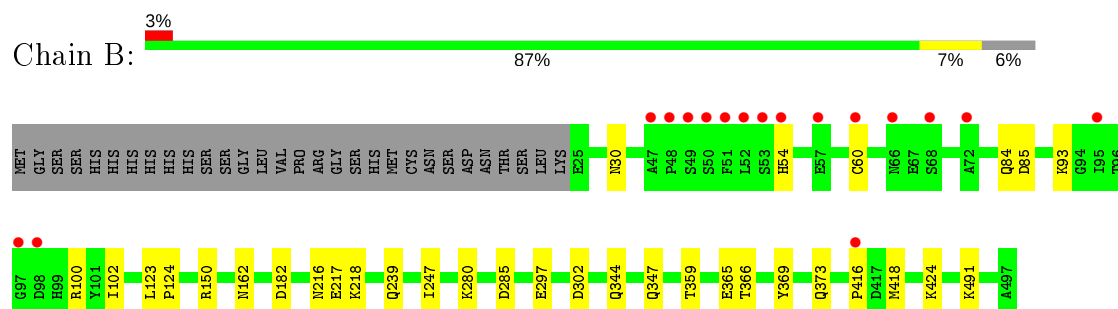
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

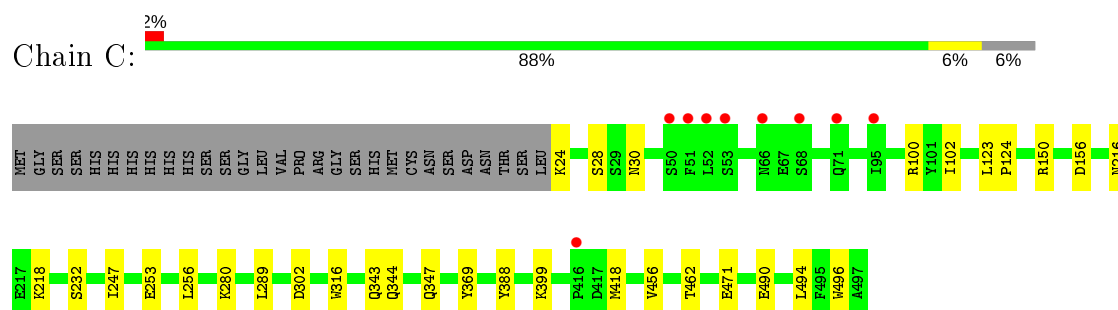
- Molecule 1: Sialyltransferase 0160



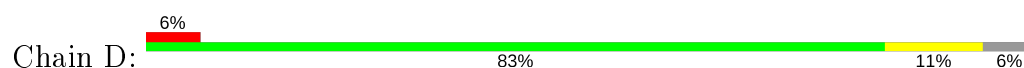
- Molecule 1: Sialyltransferase 0160

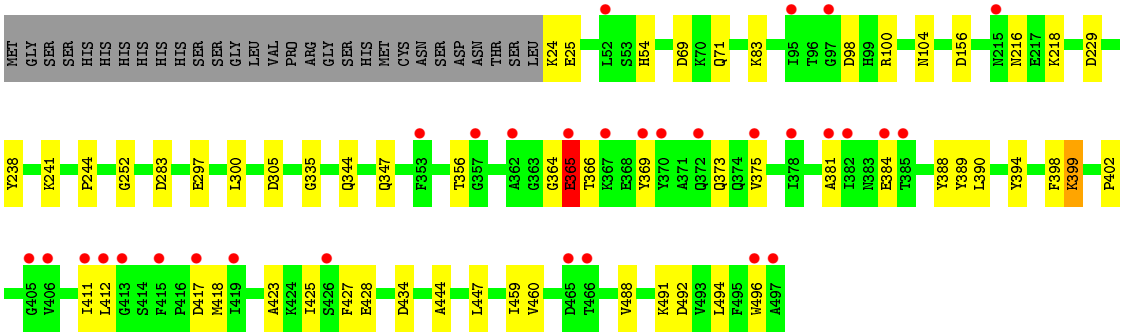


- Molecule 1: Sialyltransferase 0160



- Molecule 1: Sialyltransferase 0160





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	64.67Å 81.34Å 111.84Å 98.60° 92.76° 100.85°	Depositor
Resolution (Å)	34.84 – 1.93 38.08 – 1.93	Depositor EDS
% Data completeness (in resolution range)	94.2 (34.84-1.93) 94.2 (38.08-1.93)	Depositor EDS
R_{merge}	0.03	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.32 (at 1.94Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, R_{free}	0.179 , 0.219 0.179 , 0.219	Depositor DCC
R_{free} test set	7871 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	30.6	Xtrriage
Anisotropy	0.347	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 51.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	16660	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 45.19 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.3703e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical 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: CA

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	0.39	0/3949	0.53	0/5382
1	B	0.37	0/3904	0.52	0/5323
1	C	0.40	0/3921	0.54	0/5344
1	D	0.37	0/3907	0.53	0/5326
All	All	0.38	0/15681	0.53	0/21375

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	D	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	365	GLU	Peptide

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	3835	0	3700	37	0
1	B	3805	0	3660	24	0
1	C	3816	0	3679	23	0
1	D	3805	0	3666	43	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	345	0	0	10	0
3	B	321	0	0	12	0
3	C	433	0	0	8	0
3	D	296	0	0	12	0
All	All	16660	0	14705	122	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 4.

All (122) 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:D:418:MET:SD	3:D:895:HOH:O	2.03	1.12
1:B:60:CYS:SG	3:B:867:HOH:O	2.17	1.00
1:D:156:ASP:OD1	3:D:871:HOH:O	1.82	0.97
1:D:305:ASP:OD1	3:D:781:HOH:O	1.83	0.96
1:A:186:GLN:OE1	3:A:805:HOH:O	1.91	0.89
1:A:409:ASP:OD1	3:A:874:HOH:O	1.92	0.86
1:D:394:TYR:OH	3:D:845:HOH:O	1.95	0.84
1:A:33:ASP:OD2	3:A:824:HOH:O	1.99	0.81
1:C:24:LYS:N	3:C:827:HOH:O	2.14	0.80
1:D:297:GLU:OE1	3:D:778:HOH:O	2.03	0.77
1:D:364:GLY:O	1:D:366:THR:N	2.19	0.72
1:C:369:TYR:OH	3:C:1002:HOH:O	2.08	0.71
1:B:424:LYS:NZ	3:B:912:HOH:O	2.25	0.70
1:B:297:GLU:OE1	3:B:692:HOH:O	2.12	0.68
1:B:285:ASP:OD2	3:B:858:HOH:O	2.11	0.67
1:D:434[A]:ASP:OD1	3:D:838:HOH:O	2.13	0.67
1:B:162:ASN:OD1	3:B:918:HOH:O	2.13	0.66
1:A:176:GLU:OE2	3:A:899:HOH:O	2.15	0.64
1:A:402:PRO:HA	1:A:423:ALA:HB1	1.80	0.64
1:C:232:SER:OG	3:C:1019:HOH:O	2.14	0.63
1:A:252:GLY:O	3:A:726:HOH:O	2.15	0.63
1:A:216:ASN:HD21	1:A:218:LYS:NZ	1.98	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:280:LYS:NZ	3:C:744:HOH:O	2.32	0.62
1:B:416:PRO:HB3	1:D:104:ASN:HB3	1.83	0.61
1:D:252:GLY:O	3:D:724:HOH:O	2.16	0.60
1:B:280:LYS:NZ	3:B:821:HOH:O	2.36	0.59
1:D:216:ASN:OD1	1:D:218:LYS:HG2	2.03	0.58
1:B:216:ASN:OD1	1:B:218:LYS:HG2	2.03	0.57
1:D:356:THR:HG21	1:D:447:LEU:HD11	1.86	0.57
1:A:71:GLN:NE2	3:A:892:HOH:O	2.35	0.56
1:B:344:GLN:HA	1:B:347:GLN:HG3	1.87	0.56
1:B:84:GLN:HB3	3:B:902:HOH:O	2.06	0.56
1:D:216:ASN:HD21	1:D:218:LYS:NZ	2.05	0.55
1:A:388:TYR:CZ	1:A:494:LEU:HD21	2.41	0.55
1:D:417:ASP:HB3	3:D:888:HOH:O	2.06	0.55
1:D:344:GLN:HA	1:D:347:GLN:HG3	1.87	0.54
1:C:388:TYR:CZ	1:C:494:LEU:HD21	2.43	0.54
1:C:456:VAL:O	3:C:618:HOH:O	2.18	0.53
1:D:428:GLU:OE2	3:D:831:HOH:O	2.18	0.53
1:D:375:VAL:HG23	1:D:411:ILE:HD13	1.90	0.53
1:B:182:ASP:HB2	3:B:879:HOH:O	2.08	0.53
1:C:100:ARG:NH2	1:C:102:ILE:HD11	2.24	0.53
1:D:369:TYR:O	1:D:373:GLN:HG2	2.08	0.53
1:A:251[B]:GLU:HG2	1:A:306:TYR:HE1	1.74	0.53
1:B:217:GLU:HB2	3:B:908:HOH:O	2.09	0.53
1:A:367:LYS:HD3	1:A:406:VAL:HG13	1.91	0.52
1:D:388:TYR:CZ	1:D:494:LEU:HD21	2.45	0.52
1:A:251[B]:GLU:HG2	1:A:306:TYR:CE1	2.45	0.52
1:D:398:PHE:HB2	1:D:418:MET:SD	2.50	0.51
1:A:365:GLU:HB2	1:A:370:TYR:CZ	2.46	0.51
1:D:365:GLU:O	1:D:369:TYR:HB3	2.12	0.50
1:D:412:LEU:HA	1:D:418:MET:CE	2.40	0.50
1:A:190:ARG:HD2	3:A:736:HOH:O	2.12	0.50
1:C:100:ARG:HH22	1:C:102:ILE:HD11	1.77	0.50
1:C:471:GLU:OE1	3:C:989:HOH:O	2.19	0.50
1:B:150:ARG:HD2	3:B:872:HOH:O	2.12	0.49
1:D:25:GLU:OE2	1:D:100:ARG:NH2	2.45	0.49
1:A:251[A]:GLU:HG2	1:A:306:TYR:HE1	1.76	0.49
1:A:49:SER:HB2	1:D:244:PRO:HA	1.94	0.48
1:C:344:GLN:HA	1:C:347:GLN:HG3	1.96	0.48
1:A:367:LYS:CD	1:A:406:VAL:HG13	2.44	0.48
1:A:406:VAL:HG12	3:A:925:HOH:O	2.13	0.48
1:B:239:GLN:OE1	3:B:786:HOH:O	2.20	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:344:GLN:HA	1:A:347:GLN:HG3	1.95	0.47
1:C:216:ASN:OD1	1:C:218:LYS:HG2	2.15	0.47
1:B:247:ILE:HG13	1:B:302:ASP:HB2	1.96	0.47
1:A:356:THR:HG21	1:A:447:LEU:HD11	1.97	0.46
1:C:462:THR:HA	1:C:496:TRP:O	2.15	0.46
1:A:216:ASN:HD21	1:A:218:LYS:HZ3	1.64	0.46
1:D:418:MET:CE	3:D:895:HOH:O	2.55	0.46
1:B:85:ASP:OD1	3:B:658:HOH:O	2.21	0.46
1:A:216:ASN:HD21	1:A:218:LYS:HZ2	1.63	0.46
1:D:444:ALA:HB2	1:D:459:ILE:HB	1.97	0.45
1:D:460:VAL:HG13	1:D:496:TRP:HD1	1.80	0.45
1:D:381:ALA:HB1	1:D:390:LEU:HG	1.98	0.45
1:D:54:HIS:HE1	1:D:71:GLN:O	1.99	0.45
1:A:156:ASP:O	1:A:160:LYS:HG3	2.17	0.45
1:A:203:PHE:CZ	1:A:268:ALA:HB1	2.52	0.45
1:C:418:MET:HB3	1:C:418:MET:HE2	1.89	0.45
1:D:412:LEU:HA	1:D:418:MET:HE3	1.98	0.44
1:D:24:LYS:HB2	1:D:98:ASP:O	2.17	0.44
1:A:216:ASN:OD1	1:A:218:LYS:HG2	2.17	0.44
1:A:371:ALA:O	1:A:375:VAL:HG23	2.18	0.44
1:C:490:GLU:HG3	3:C:665:HOH:O	2.17	0.44
1:D:384:GLU:HG2	1:D:389:TYR:CZ	2.53	0.44
1:D:283:ASP:OD2	3:D:808:HOH:O	2.20	0.44
1:B:418:MET:HB3	1:B:418:MET:HE2	1.94	0.44
1:D:402:PRO:HA	1:D:423:ALA:HB1	1.99	0.43
1:A:399:LYS:HE3	1:A:399:LYS:HB3	1.81	0.43
1:C:123:LEU:HB3	1:C:124:PRO:HD3	2.00	0.43
1:A:409:ASP:HA	3:A:874:HOH:O	2.19	0.42
1:D:388:TYR:CE1	1:D:494:LEU:HD21	2.54	0.42
1:A:359:THR:HG22	1:A:404:GLY:HA2	2.01	0.42
1:A:388:TYR:CE1	1:A:494:LEU:HD21	2.55	0.42
1:B:100:ARG:NH2	1:B:102:ILE:HD11	2.34	0.42
1:C:253:GLU:HG2	1:C:256:LEU:HD12	2.01	0.42
1:C:150:ARG:HD2	3:C:865:HOH:O	2.19	0.42
1:B:366:THR:O	1:B:369:TYR:HB3	2.20	0.42
1:C:30:ASN:HB3	1:D:24:LYS:HG2	2.02	0.42
1:C:343:GLN:O	1:C:347:GLN:HG3	2.19	0.41
1:D:216:ASN:HD21	1:D:218:LYS:HZ1	1.66	0.41
1:D:399:LYS:HE3	1:D:425:ILE:O	2.19	0.41
1:D:398:PHE:CE1	1:D:411:ILE:HG21	2.55	0.41
1:A:24:LYS:HG3	1:B:30:ASN:HB3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:54:HIS:HA	1:B:93:LYS:O	2.20	0.41
1:C:247:ILE:HG13	1:C:302:ASP:HB2	2.02	0.41
1:D:335:GLY:O	1:D:425:ILE:HD11	2.20	0.41
1:A:189:ASN:O	1:A:218:LYS:HD2	2.20	0.41
1:D:488:VAL:HB	1:D:492:ASP:HB2	2.03	0.41
1:B:365:GLU:HG3	1:B:369:TYR:CE1	2.55	0.41
1:C:289:LEU:HD12	1:C:316:TRP:HZ2	1.86	0.41
1:B:369:TYR:O	1:B:373:GLN:HG2	2.20	0.41
1:A:247:ILE:HG13	1:A:302:ASP:HB2	2.03	0.41
1:D:69:ASP:OD2	3:D:735:HOH:O	2.22	0.41
1:A:402:PRO:HA	1:A:423:ALA:CB	2.49	0.41
1:C:28:SER:HA	1:D:25:GLU:O	2.21	0.41
1:D:238:TYR:O	1:D:241:LYS:HG2	2.21	0.40
1:A:431:MET:HB3	1:A:431:MET:HE2	1.89	0.40
1:B:123:LEU:HB3	1:B:124:PRO:HD3	2.02	0.40
1:C:399:LYS:HE3	1:C:399:LYS:HB3	1.87	0.40
1:A:71:GLN:HG2	3:A:928:HOH:O	2.22	0.40
1:A:365:GLU:HB2	1:A:370:TYR:CE2	2.57	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	480/503 (95%)	472 (98%)	8 (2%)	0	100	100
1	B	474/503 (94%)	464 (98%)	9 (2%)	1 (0%)	47	39
1	C	476/503 (95%)	466 (98%)	10 (2%)	0	100	100
1	D	475/503 (94%)	463 (98%)	11 (2%)	1 (0%)	47	39
All	All	1905/2012 (95%)	1865 (98%)	38 (2%)	2 (0%)	51	43

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	365	GLU
1	B	359	THR

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	432/450 (96%)	430 (100%)	2 (0%)	88	88
1	B	426/450 (95%)	425 (100%)	1 (0%)	93	94
1	C	428/450 (95%)	427 (100%)	1 (0%)	93	94
1	D	427/450 (95%)	420 (98%)	7 (2%)	62	52
All	All	1713/1800 (95%)	1702 (99%)	11 (1%)	86	85

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

Mol	Chain	Res	Type
1	A	427	PHE
1	A	496	TRP
1	B	491	LYS
1	C	156	ASP
1	D	83	LYS
1	D	229	ASP
1	D	300	LEU
1	D	365	GLU
1	D	399	LYS
1	D	427	PHE
1	D	491	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	216	ASN
1	D	54	HIS
1	D	216	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	474/503 (94%)	0.05	8 (1%) 70 75	21, 41, 73, 96	0
1	B	473/503 (94%)	0.06	17 (3%) 42 50	25, 42, 73, 102	0
1	C	474/503 (94%)	-0.08	9 (1%) 66 72	21, 36, 63, 82	0
1	D	474/503 (94%)	0.28	31 (6%) 18 25	21, 46, 99, 124	0
All	All	1895/2012 (94%)	0.08	65 (3%) 45 53	21, 41, 80, 124	0

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	375	VAL	11.6
1	B	52	LEU	8.6
1	D	496	TRP	6.7
1	B	416	PRO	4.6
1	D	406	VAL	4.6
1	B	49	SER	4.6
1	B	51	PHE	4.5
1	B	53	SER	4.1
1	D	415	PHE	4.1
1	B	95	ILE	4.0
1	B	50	SER	3.9
1	D	413	GLY	3.8
1	A	406	VAL	3.8
1	C	416	PRO	3.8
1	A	413	GLY	3.7
1	D	412	LEU	3.7
1	D	405	GLY	3.5
1	A	411	ILE	3.4
1	A	416	PRO	3.3
1	C	51	PHE	3.2
1	C	52	LEU	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	68	SER	3.0
1	B	97	GLY	3.0
1	D	353	PHE	2.9
1	D	411	ILE	2.9
1	D	215	ASN	2.9
1	B	57	GLU	2.8
1	D	417	ASP	2.8
1	D	381	ALA	2.8
1	B	66	ASN	2.8
1	D	419	ILE	2.7
1	B	98	ASP	2.7
1	D	357	GLY	2.6
1	D	382	ILE	2.6
1	A	410	ILE	2.6
1	D	95	ILE	2.6
1	D	465	ASP	2.5
1	D	378	ILE	2.5
1	D	365	GLU	2.5
1	D	52	LEU	2.5
1	B	72	ALA	2.4
1	C	53	SER	2.4
1	D	372	GLN	2.4
1	D	384	GLU	2.3
1	B	47	ALA	2.3
1	A	405	GLY	2.3
1	C	50	SER	2.3
1	D	370	TYR	2.2
1	D	497	ALA	2.2
1	C	95	ILE	2.2
1	B	54	HIS	2.2
1	A	366	THR	2.2
1	C	66	ASN	2.2
1	D	385	THR	2.2
1	D	97	GLY	2.2
1	D	369	TYR	2.2
1	D	466	THR	2.1
1	D	367	LYS	2.1
1	C	68	SER	2.1
1	C	71	GLN	2.1
1	D	362	ALA	2.0
1	B	48	PRO	2.0
1	A	379	ASN	2.0

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Mol	Chain	Res	Type	RSRZ
1	D	426	SER	2.0
1	B	60	CYS	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 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. 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(\AA^2)	Q<0.9
2	CA	D	501	1/1	0.65	0.07	81,81,81,81	0
2	CA	A	501	1/1	0.96	0.05	52,52,52,52	0
2	CA	C	501	1/1	0.99	0.07	32,32,32,32	0
2	CA	B	501	1/1	1.00	0.10	34,34,34,34	0

6.5 Other polymers [i](#)

There are no such residues in this entry.