



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 11:19 AM UTC

PDB ID : 7N3Y / pdb_00007n3y
Title : Crystal Structure of *Saccharomyces cerevisiae* Apn2 Catalytic Domain
E59Q/D222N Mutant in Complex with DNA
Authors : Wojtaszek, J.L.; Krahn, J.; Wallace, B.D.; Williams, R.S.
Deposited on : 2021-06-02
Resolution : 2.73 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:

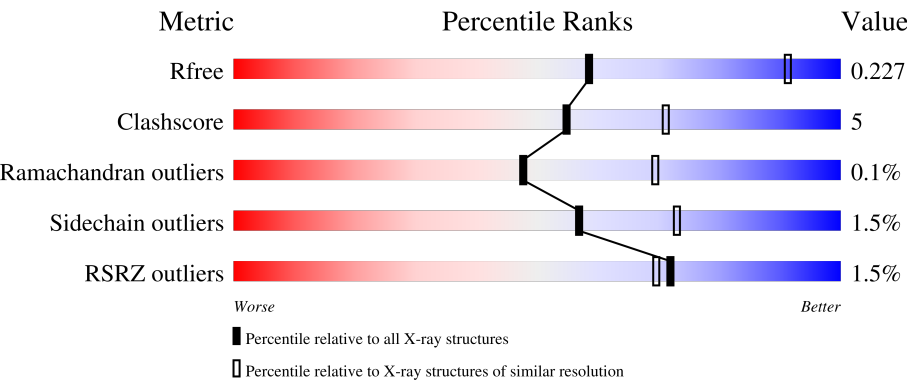
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.73 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	1819 (2.76-2.72)
Clashscore	190562	1866 (2.76-2.72)
Ramachandran outliers	187476	1830 (2.76-2.72)
Sidechain outliers	187428	1831 (2.76-2.72)
RSRZ outliers	180081	1819 (2.76-2.72)

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	413	84%7%8%
1	B	413	80%9%10%
1	C	413	2% 79%11%9%
1	D	413	2% 74%11%13%
2	E	13	38%62%

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Mol	Chain	Length	Quality of chain
2	F	13	 46% 54%
2	G	13	 8% 69% 31%
3	H	13	 62% 38%

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 12821 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 DNA-(apurinic or apyrimidinic site) endonuclease 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	378	Total	C	N	O	S	0	1	0
			2984	1901	523	545	15			
1	B	371	Total	C	N	O	S	0	2	0
			2919	1866	500	538	15			
1	C	374	Total	C	N	O	S	0	1	0
			2918	1856	509	537	16			
1	D	359	Total	C	N	O	S	0	1	0
			2806	1792	480	519	15			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	59	GLN	GLU	engineered mutation	UNP P38207
A	222	ASN	ASP	engineered mutation	UNP P38207
A	408	GLU	-	expression tag	UNP P38207
A	409	ASN	-	expression tag	UNP P38207
A	410	LEU	-	expression tag	UNP P38207
A	411	TYR	-	expression tag	UNP P38207
A	412	PHE	-	expression tag	UNP P38207
A	413	GLN	-	expression tag	UNP P38207
B	59	GLN	GLU	engineered mutation	UNP P38207
B	222	ASN	ASP	engineered mutation	UNP P38207
B	408	GLU	-	expression tag	UNP P38207
B	409	ASN	-	expression tag	UNP P38207
B	410	LEU	-	expression tag	UNP P38207
B	411	TYR	-	expression tag	UNP P38207
B	412	PHE	-	expression tag	UNP P38207
B	413	GLN	-	expression tag	UNP P38207
C	59	GLN	GLU	engineered mutation	UNP P38207
C	222	ASN	ASP	engineered mutation	UNP P38207
C	408	GLU	-	expression tag	UNP P38207
C	409	ASN	-	expression tag	UNP P38207
C	410	LEU	-	expression tag	UNP P38207

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Chain	Residue	Modelled	Actual	Comment	Reference
C	411	TYR	-	expression tag	UNP P38207
C	412	PHE	-	expression tag	UNP P38207
C	413	GLN	-	expression tag	UNP P38207
D	59	GLN	GLU	engineered mutation	UNP P38207
D	222	ASN	ASP	engineered mutation	UNP P38207
D	408	GLU	-	expression tag	UNP P38207
D	409	ASN	-	expression tag	UNP P38207
D	410	LEU	-	expression tag	UNP P38207
D	411	TYR	-	expression tag	UNP P38207
D	412	PHE	-	expression tag	UNP P38207
D	413	GLN	-	expression tag	UNP P38207

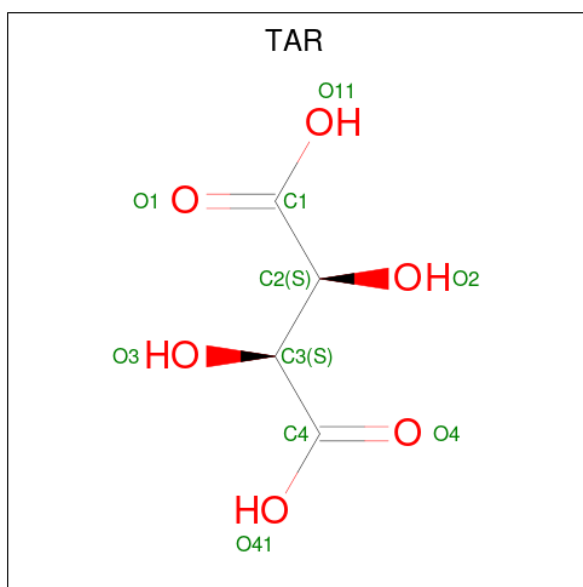
- Molecule 2 is a DNA chain called DNA (5'-D(*TP*CP*CP*GP*AP*AP*AP*TP*(PST)P*(PST)P*(SC)P*(GS)P*(GS))-3').

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	E	13	Total	C	N	O	P	S	0	0	0
			263	127	47	72	12	5			
2	F	13	Total	C	N	O	P	S	0	0	0
			263	127	47	72	12	5			
2	G	13	Total	C	N	O	P	S	0	0	0
			263	127	47	72	12	5			

- Molecule 3 is a DNA chain called DNA (5'-D(*CP*CP*GP*AP*AP*AP*TP*TP*(PST)P*(SC)P*(GS)P*(GS)P*(AS))-3').

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	H	13	Total	C	N	O	P	S	0	0	0
			247	117	45	68	12	5			

- Molecule 4 is D(-)-TARTARIC ACID (CCD ID: TAR) (formula: C₄H₆O₆).

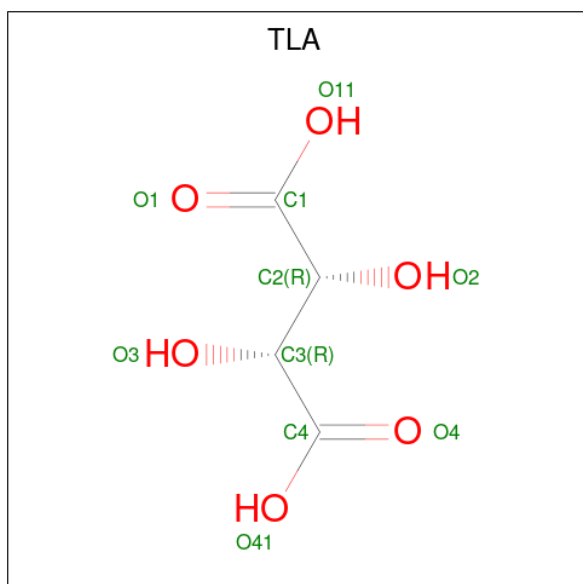


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			10	4	6		
4	C	1	Total	C	O	0	0
			10	4	6		

- Molecule 5 is CALCIUM ION (CCD ID: CA) (formula: Ca).

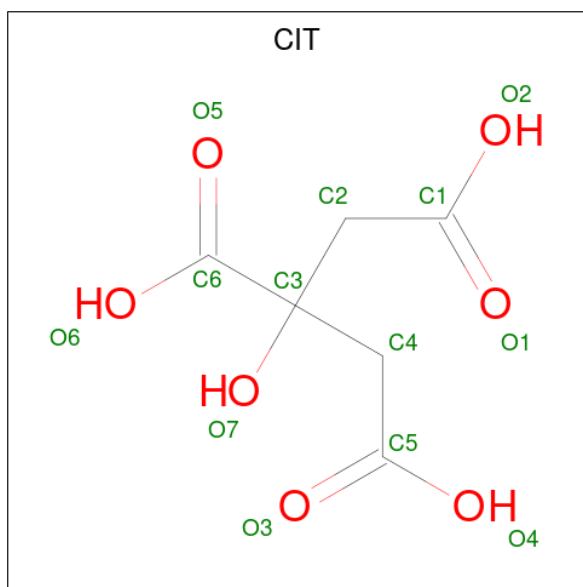
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Ca	0	0
			1	1		

- Molecule 6 is L(+)-TARTARIC ACID (CCD ID: TLA) (formula: C₄H₆O₆).



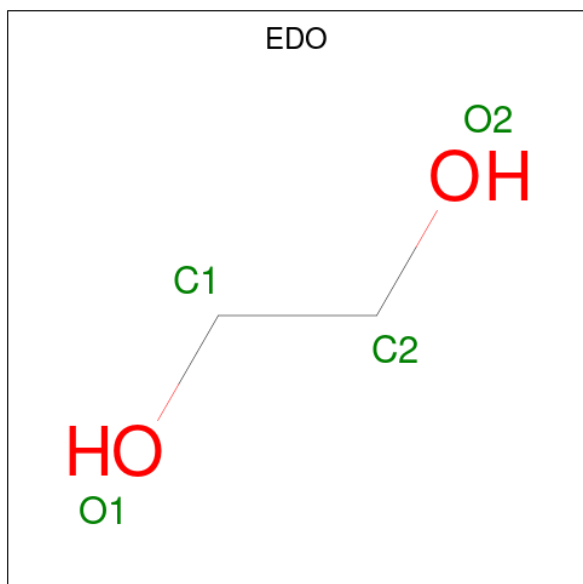
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			10	4	6		
6	D	1	Total	C	O	0	0
			10	4	6		

- Molecule 7 is CITRIC ACID (CCD ID: CIT) (formula: $C_6H_8O_7$).



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

- Molecule 8 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 9 is water.

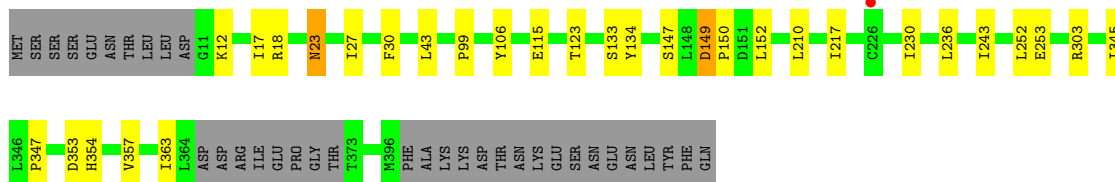
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	56	Total	O	0	0
			56	56		
9	B	39	Total	O	0	0
			39	39		
9	E	3	Total	O	0	0
			3	3		
9	F	2	Total	O	0	0
			2	2		

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 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.

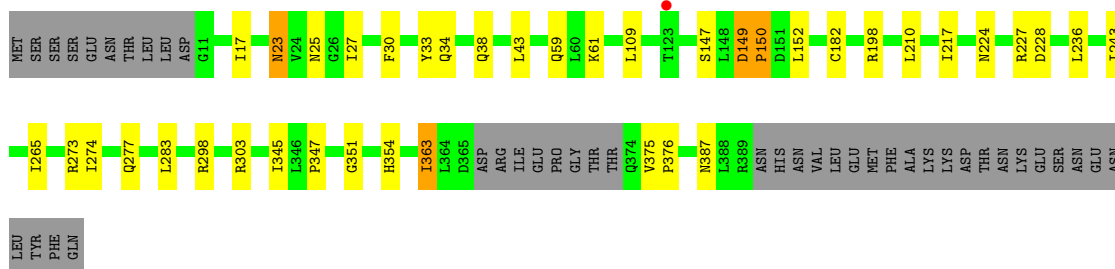
- Molecule 1: DNA-(apurinic or apyrimidinic site) endonuclease 2

Chain A: 



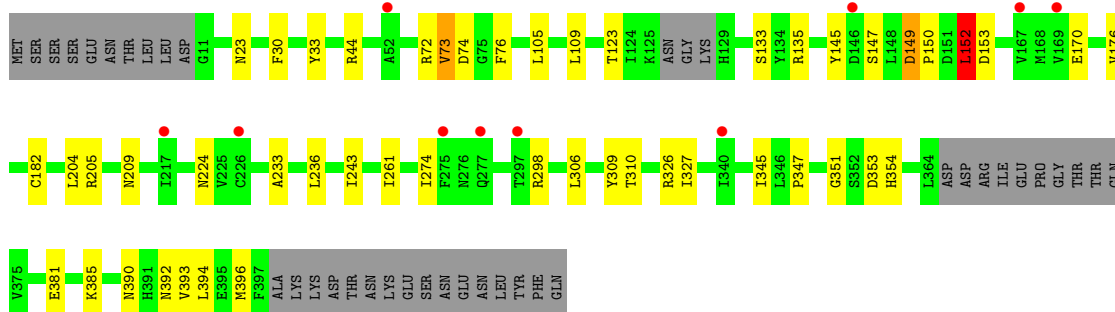
- Molecule 1: DNA-(apurinic or apyrimidinic site) endonuclease 2

Chain B: 

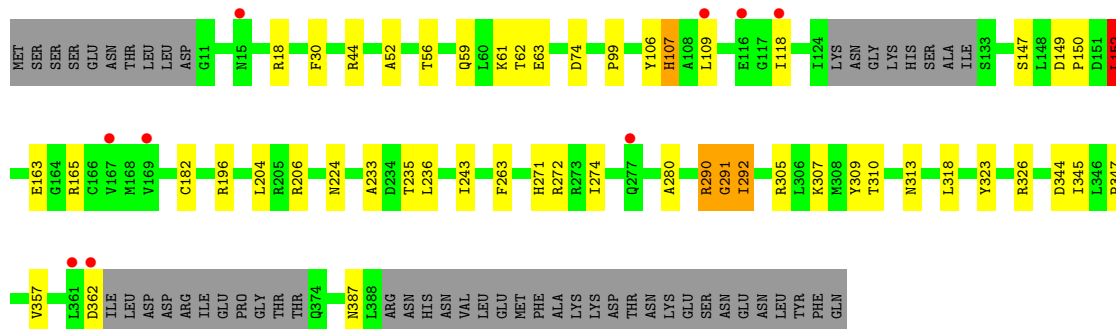
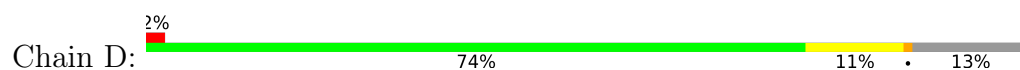


- Molecule 1: DNA-(apurinic or apyrimidinic site) endonuclease 2

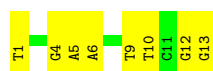
Chain C: 



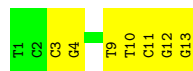
- Molecule 1: DNA-(apurinic or apyrimidinic site) endonuclease 2



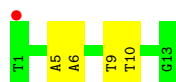
- Molecule 2: DNA (5'-D(*TP*CP*CP*GP*AP*AP*AP*TP*(PST)P*(PST)P*(SC)P*(GS)P*(GS))-3')



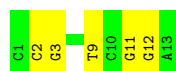
- Molecule 2: DNA (5'-D(*TP*CP*CP*GP*AP*AP*AP*TP*(PST)P*(PST)P*(SC)P*(GS)P*(GS))-3')



- Molecule 2: DNA (5'-D(*TP*CP*CP*GP*AP*AP*AP*TP*(PST)P*(PST)P*(SC)P*(GS)P*(GS))-3')



- Molecule 3: DNA (5'-D(*CP*CP*GP*AP*AP*AP*TP*TP*(PST)P*(SC)P*(GS)P*(GS)P*(A S))-3')



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	69.41Å 101.47Å 144.97Å 90.00° 90.14° 90.00°	Depositor
Resolution (Å)	36.97 – 2.73 36.97 – 2.73	Depositor EDS
% Data completeness (in resolution range)	95.6 (36.97-2.73) 95.7 (36.97-2.73)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.06 (at 2.72Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.200 , 0.228 0.200 , 0.227	Depositor DCC
R_{free} test set	1897 reflections (3.40%)	wwPDB-VP
Wilson B-factor (Å ²)	67.9	Xtriage
Anisotropy	0.279	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 63.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.044 for h,-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	12821	wwPDB-VP
Average B, all atoms (Å ²)	101.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.54% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SC, PST, CIT, TAR, CA, GS, EDO, AS, TLA

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	0.21	0/3042	0.36	3/4118 (0.1%)
1	B	0.29	1/2979 (0.0%)	0.38	1/4035 (0.0%)
1	C	0.27	2/2974 (0.1%)	0.39	4/4028 (0.1%)
1	D	0.28	2/2862 (0.1%)	0.47	5/3881 (0.1%)
2	E	0.23	0/179	0.40	0/274
2	F	0.17	0/179	0.39	0/274
2	G	0.23	0/179	0.41	0/274
3	H	0.18	0/179	0.36	0/274
All	All	0.26	5/12573 (0.0%)	0.40	13/17158 (0.1%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	147	SER	C-N	-8.46	1.21	1.33
1	B	147	SER	C-N	-7.89	1.21	1.33
1	C	152	LEU	C-N	7.73	1.45	1.33
1	C	147	SER	C-N	-7.72	1.22	1.33
1	D	152	LEU	C-N	-7.70	1.21	1.33

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	290	ARG	N-CA-C	9.56	121.78	111.36
1	D	147	SER	N-CA-C	8.11	122.22	111.28
1	D	387	ASN	N-CA-C	7.82	120.06	110.91
1	D	291	GLY	N-CA-C	7.62	122.36	110.71
1	B	387	ASN	N-CA-C	7.46	121.36	111.28
1	A	147	SER	N-CA-C	6.95	119.71	111.02
1	C	149	ASP	CA-C-N	6.31	125.54	118.97
1	C	149	ASP	C-N-CA	6.31	125.54	118.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	147	SER	O-C-N	-6.03	115.97	123.33
1	C	147	SER	N-CA-C	5.66	117.53	110.91
1	A	149	ASP	CA-C-N	5.38	125.02	119.05
1	A	149	ASP	C-N-CA	5.38	125.02	119.05
1	D	292	ILE	N-CA-C	5.21	119.70	112.35

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	2984	0	2965	16	0
1	B	2919	0	2889	26	0
1	C	2918	0	2846	35	0
1	D	2806	0	2738	31	0
2	E	263	0	151	6	0
2	F	263	0	151	3	0
2	G	263	0	151	1	0
3	H	247	0	138	2	0
4	A	10	0	4	1	0
4	C	10	0	4	0	0
5	A	1	0	0	0	0
6	B	10	0	4	0	0
6	D	10	0	4	0	0
7	B	13	0	5	0	0
8	B	4	0	6	3	0
9	A	56	0	0	0	0
9	B	39	0	0	1	0
9	E	3	0	0	0	0
9	F	2	0	0	0	0
All	All	12821	0	12056	118	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 (118) 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:280:ALA:HB2	1:D:291:GLY:O	1.70	0.92
1:C:72:ARG:NH1	1:C:390:ASN:HA	1.98	0.79
1:C:152:LEU:HD23	1:C:152:LEU:O	1.82	0.78
1:B:198:ARG:HD2	8:B:503:EDO:O1	1.94	0.68
1:C:381:GLU:O	1:C:385:LYS:CB	2.42	0.68
1:C:152:LEU:HD23	1:C:152:LEU:C	2.20	0.67
1:B:210:LEU:HB2	1:B:217:ILE:HD11	1.79	0.65
1:A:236:LEU:HD13	1:A:243:ILE:HD11	1.83	0.60
1:A:253:GLU:OE2	1:A:303:ARG:NH2	2.32	0.60
1:B:149:ASP:HB3	1:B:152:LEU:HB2	1.84	0.59
1:A:149:ASP:HB3	1:A:152:LEU:HB2	1.85	0.59
1:C:44:ARG:NH1	1:C:74:ASP:O	2.35	0.59
1:A:345:ILE:HG13	1:A:347:PRO:HD3	1.85	0.58
1:C:327:ILE:HD11	1:C:354:HIS:HE1	1.68	0.58
1:D:280:ALA:CB	1:D:291:GLY:O	2.47	0.58
1:C:182:CYS:O	1:C:224:ASN:ND2	2.35	0.58
1:D:152:LEU:O	1:D:152:LEU:HD23	2.02	0.58
1:B:198:ARG:NH1	8:B:503:EDO:O1	2.37	0.58
1:C:345:ILE:HG13	1:C:347:PRO:HD3	1.88	0.56
1:D:305:ARG:NH1	1:D:344:ASP:OD1	2.38	0.56
1:B:59:GLN:HE21	1:B:61:LYS:HE3	1.71	0.55
1:B:149:ASP:OD1	1:B:150:PRO:HD2	2.05	0.55
1:C:243:ILE:HD12	1:C:306:LEU:HD13	1.89	0.54
1:D:44:ARG:NH1	1:D:74:ASP:O	2.41	0.53
1:B:274:ILE:O	1:B:277[B]:GLN:HG3	2.09	0.53
1:A:345:ILE:HG22	1:A:357:VAL:HG22	1.92	0.52
1:B:277[A]:GLN:OE1	2:E:12:GS:S2P	2.67	0.51
1:D:62:THR:OG1	1:D:63:GLU:N	2.43	0.51
1:B:27:ILE:HD11	1:B:43:LEU:HD21	1.91	0.51
1:D:345:ILE:HG22	1:D:357:VAL:HG22	1.93	0.51
1:C:149:ASP:HB3	1:C:152:LEU:HB2	1.91	0.51
1:A:123:THR:HA	1:A:133:SER:HA	1.94	0.50
1:C:394:LEU:C	1:C:396:MET:H	2.19	0.50
1:A:27:ILE:HD11	1:A:43:LEU:HD21	1.95	0.49
1:C:205:ARG:NH1	1:C:209:ASN:OD1	2.46	0.49
1:B:17:ILE:HD12	1:B:363:ILE:HG12	1.94	0.49
4:A:501:TAR:O4	4:A:501:TAR:O2	2.15	0.49
1:B:265:ILE:HA	1:B:273:ARG:HD3	1.95	0.48
2:F:3:DC:H2"	2:F:4:DG:C8	2.48	0.48
1:C:236:LEU:HD13	1:C:243:ILE:HD11	1.96	0.47
1:C:204:LEU:HD12	1:C:274:ILE:HG22	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:307:LYS:HA	1:D:309:TYR:CZ	2.49	0.47
1:A:17:ILE:HD12	1:A:363:ILE:HD13	1.97	0.46
1:C:394:LEU:C	1:C:396:MET:N	2.72	0.46
1:B:25:ASN:HA	1:B:59:GLN:HG2	1.98	0.46
1:B:375:VAL:CG1	1:B:376:PRO:HD2	2.45	0.46
1:A:99:PRO:HG2	1:A:106:TYR:HA	1.98	0.46
1:D:204:LEU:HD12	1:D:274:ILE:HG22	1.97	0.46
1:A:210:LEU:HB2	1:A:217:ILE:HD11	1.97	0.46
1:B:236:LEU:HD13	1:B:243:ILE:HD11	1.97	0.46
1:D:310:THR:HG23	1:D:326:ARG:HG3	1.98	0.45
1:C:327:ILE:HD11	1:C:354:HIS:CE1	2.49	0.45
1:D:149:ASP:HB3	1:D:152:LEU:HB3	1.97	0.45
2:E:5:DA:H2''	2:E:6:DA:C8	2.52	0.45
1:D:196:ARG:NH2	1:D:224:ASN:O	2.50	0.45
1:B:59:GLN:NE2	1:B:61:LYS:HE3	2.32	0.45
1:D:107:HIS:CD2	1:D:107:HIS:O	2.70	0.45
1:A:12:LYS:HB3	1:A:18:ARG:NH2	2.32	0.45
1:A:115:GLU:HG3	1:A:134:TYR:CG	2.52	0.45
1:B:228:ASP:CG	1:B:303:ARG:HH22	2.24	0.45
1:C:261:ILE:HG21	2:E:1:DT:H5''	1.98	0.45
1:C:153:ASP:OD1	1:C:153:ASP:N	2.49	0.45
1:D:233:ALA:HB2	1:D:309:TYR:CZ	2.51	0.45
1:B:227:ARG:NE	1:B:228:ASP:OD2	2.51	0.44
1:D:182:CYS:O	1:D:224:ASN:ND2	2.50	0.44
1:D:345:ILE:HG13	1:D:347:PRO:HD3	1.99	0.44
1:A:353:ASP:OD1	1:A:353:ASP:N	2.50	0.44
1:D:118:ILE:O	1:D:206:ARG:NH1	2.50	0.44
1:D:99:PRO:HG2	1:D:106:TYR:HA	2.00	0.44
2:E:4:DG:H2''	2:E:5:DA:C8	2.53	0.44
1:C:23:ASN:HB3	1:C:354:HIS:CG	2.52	0.44
9:B:624:HOH:O	2:E:13:GS:H8	2.18	0.44
1:C:298:ARG:HA	1:C:298:ARG:HD3	1.77	0.44
1:D:236:LEU:HD13	1:D:243:ILE:HD11	1.99	0.44
2:F:12:GS:H2'	2:F:13:GS:H8	1.99	0.44
1:B:198:ARG:CD	8:B:503:EDO:O1	2.64	0.43
1:B:345:ILE:HG13	1:B:347:PRO:HD3	2.00	0.43
1:D:235:THR:HG21	1:D:263:PHE:HE1	1.83	0.43
1:C:73:VAL:HB	1:C:76:PHE:HB2	1.99	0.43
1:C:109:LEU:HD23	1:C:109:LEU:N	2.33	0.43
1:B:149:ASP:CG	1:B:150:PRO:HD2	2.43	0.43
1:C:33:TYR:CG	1:C:351:GLY:HA2	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:163:GLU:OE1	1:D:165:ARG:NE	2.43	0.43
3:H:11:GS:H2'	3:H:12:GS:H8	2.01	0.43
1:C:310:THR:HG23	1:C:326:ARG:HG3	2.01	0.43
1:A:230:ILE:HG22	1:A:252:LEU:HD22	2.01	0.42
1:B:182:CYS:O	1:B:224:ASN:ND2	2.43	0.42
1:D:233:ALA:HB2	1:D:309:TYR:CE2	2.53	0.42
1:C:152:LEU:C	1:C:152:LEU:CD2	2.85	0.42
3:H:2:DC:H2''	3:H:3:DG:C8	2.54	0.42
1:C:105:LEU:O	1:C:109:LEU:HG	2.18	0.42
2:G:5:DA:H2''	2:G:6:DA:C8	2.53	0.42
1:A:149:ASP:CG	1:A:150:PRO:HD2	2.44	0.42
1:C:233:ALA:HB2	1:C:309:TYR:CZ	2.55	0.42
1:C:353:ASP:OD1	1:C:353:ASP:N	2.52	0.42
1:B:34:GLN:OE1	1:B:38:GLN:NE2	2.52	0.42
1:D:18:ARG:HB3	1:D:52:ALA:HA	2.02	0.42
1:D:59:GLN:OE1	1:D:61:LYS:HE3	2.20	0.42
1:D:149:ASP:HA	1:D:150:PRO:HD2	1.78	0.42
1:A:23:ASN:HB3	1:A:354:HIS:CG	2.55	0.42
1:C:135:ARG:NH1	1:C:145:TYR:HB3	2.35	0.42
1:C:149:ASP:HA	1:C:150:PRO:HD3	1.82	0.41
1:B:33:TYR:CD1	1:B:351:GLY:HA2	2.55	0.41
1:B:17:ILE:HD13	1:B:109:LEU:HD21	2.01	0.41
1:B:298:ARG:HD3	1:B:298:ARG:HA	1.71	0.41
1:D:99:PRO:HG3	1:D:109:LEU:HD12	2.02	0.41
1:D:271:HIS:CD2	1:D:272:ARG:HG3	2.55	0.41
1:C:381:GLU:O	1:C:385:LYS:N	2.45	0.41
1:D:107:HIS:CD2	1:D:107:HIS:C	2.99	0.41
1:C:123:THR:HA	1:C:133:SER:HA	2.02	0.41
1:C:170:GLU:HG3	1:C:176:VAL:HG22	2.03	0.41
1:D:280:ALA:HB2	1:D:291:GLY:C	2.40	0.41
1:B:23:ASN:HB3	1:B:354:HIS:CG	2.56	0.41
1:D:313:ASN:HB3	1:D:318:LEU:HD12	2.04	0.40
1:D:318:LEU:HD13	1:D:323:TYR:HD1	1.86	0.40
1:C:33:TYR:CD1	1:C:351:GLY:HA2	2.56	0.40
1:C:149:ASP:HB3	1:C:152:LEU:CB	2.51	0.40
2:E:4:DG:H1	2:F:11:SC:HN41	1.68	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	375/413 (91%)	359 (96%)	16 (4%)	0	100	100
1	B	369/413 (89%)	354 (96%)	14 (4%)	1 (0%)	36	54
1	C	369/413 (89%)	352 (95%)	17 (5%)	0	100	100
1	D	354/413 (86%)	335 (95%)	19 (5%)	0	100	100
All	All	1467/1652 (89%)	1400 (95%)	66 (4%)	1 (0%)	48	69

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	150	PRO

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	324/373 (87%)	322 (99%)	2 (1%)	78	87
1	B	316/373 (85%)	311 (98%)	5 (2%)	55	72
1	C	311/373 (83%)	306 (98%)	5 (2%)	55	72
1	D	301/373 (81%)	294 (98%)	7 (2%)	44	65
All	All	1252/1492 (84%)	1233 (98%)	19 (2%)	57	73

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	23	ASN
1	A	30	PHE
1	B	23	ASN
1	B	30	PHE
1	B	149	ASP
1	B	283	LEU
1	B	363	ILE
1	C	30	PHE
1	C	73	VAL
1	C	152	LEU
1	C	392	ASN
1	C	393	VAL
1	D	30	PHE
1	D	56	THR
1	D	107	HIS
1	D	152	LEU
1	D	290	ARG
1	D	292	ILE
1	D	362	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	23	ASN
1	A	58	GLN
1	A	222	ASN
1	C	23	ASN
1	C	59	GLN
1	D	23	ASN
1	D	59	GLN
1	D	107	HIS
1	D	140	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

20 non-standard protein/DNA/RNA residues 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	SC	G	11	2,3	17,20,21	0.30	0	23,28,31	0.42	0
3	AS	H	13	3	0,3,24	-	-	0,3,36	-	-
2	GS	G	12	2,3	21,24,25	0.38	0	30,35,38	0.41	0
2	PST	E	9	2	18,21,22	0.28	0	25,30,33	0.74	1 (4%)
2	PST	E	10	2	18,21,22	0.26	0	25,30,33	0.70	1 (4%)
3	SC	H	10	2,3	17,20,21	0.31	0	23,28,31	0.49	0
2	PST	G	10	2,3	18,21,22	0.27	0	25,30,33	0.68	1 (4%)
3	PST	H	9	2,3	18,21,22	0.28	0	25,30,33	0.74	1 (4%)
3	GS	H	12	2,3	21,24,25	0.37	0	30,35,38	0.40	0
2	GS	F	13	2	21,24,25	0.36	0	30,35,38	0.29	0
2	SC	F	11	2	17,20,21	0.31	0	23,28,31	0.47	0
2	GS	E	12	2	21,24,25	0.39	0	30,35,38	0.38	0
2	PST	G	9	2,3	18,21,22	0.28	0	25,30,33	0.69	1 (4%)
2	GS	G	13	2,3	21,24,25	0.38	0	30,35,38	0.35	0
2	PST	F	9	2	18,21,22	0.30	0	25,30,33	0.77	1 (4%)
2	GS	F	12	2	21,24,25	0.40	0	30,35,38	0.42	0
3	GS	H	11	2,3	21,24,25	0.38	0	30,35,38	0.42	0
2	SC	E	11	2	17,20,21	0.32	0	23,28,31	0.51	0
2	PST	F	10	2	18,21,22	0.27	0	25,30,33	0.73	1 (4%)
2	GS	E	13	2	21,24,25	0.39	0	30,35,38	0.36	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
2	SC	G	11	2,3	-	0/7/21/22	0/2/2/2
2	GS	G	12	2,3	-	0/7/21/22	0/3/3/3
2	PST	E	9	2	-	0/7/21/22	0/2/2/2
2	PST	E	10	2	-	0/7/21/22	0/2/2/2
3	SC	H	10	2,3	-	0/7/21/22	0/2/2/2
2	PST	G	10	2,3	-	0/7/21/22	0/2/2/2
3	PST	H	9	2,3	-	0/7/21/22	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GS	H	12	2,3	-	0/7/21/22	0/3/3/3
2	GS	F	13	2	-	0/7/21/22	0/3/3/3
2	SC	F	11	2	-	0/7/21/22	0/2/2/2
2	GS	E	12	2	-	0/7/21/22	0/3/3/3
2	PST	G	9	2,3	-	0/7/21/22	0/2/2/2
2	GS	G	13	2,3	-	0/7/21/22	0/3/3/3
2	PST	F	9	2	-	3/7/21/22	0/2/2/2
2	GS	F	12	2	-	0/7/21/22	0/3/3/3
3	GS	H	11	2,3	-	0/7/21/22	0/3/3/3
2	SC	E	11	2	-	0/7/21/22	0/2/2/2
2	PST	F	10	2	-	0/7/21/22	0/2/2/2
2	GS	E	13	2	-	0/7/21/22	0/3/3/3

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	9	PST	O4-C4-C5	-2.54	122.01	124.92
2	F	9	PST	O4-C4-C5	-2.41	122.16	124.92
3	H	9	PST	O4-C4-C5	-2.40	122.17	124.92
2	F	10	PST	O4-C4-C5	-2.36	122.22	124.92
2	G	10	PST	O4-C4-C5	-2.29	122.30	124.92
2	E	10	PST	O4-C4-C5	-2.24	122.36	124.92
2	G	9	PST	O4-C4-C5	-2.20	122.40	124.92

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	F	9	PST	O4'-C4'-C5'-O5'
2	F	9	PST	C3'-C4'-C5'-O5'
2	F	9	PST	C4'-C5'-O5'-P

There are no ring outliers.

7 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	H	12	GS	1	0
2	F	13	GS	1	0
2	F	11	SC	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	12	GS	1	0
2	F	12	GS	1	0
3	H	11	GS	1	0
2	E	13	GS	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 1 is monoatomic - leaving 6 for Mogul analysis.

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	$\# Z > 2$
6	TLA	D	501	-	9,9,9	1.22	0	12,12,12	0.99	0
4	TAR	C	501	-	9,9,9	1.27	0	12,12,12	0.93	0
4	TAR	A	501	-	9,9,9	1.77	3 (33%)	12,12,12	1.23	2 (16%)
8	EDO	B	503	-	3,3,3	0.30	0	2,2,2	0.42	0
6	TLA	B	501	-	9,9,9	1.16	0	12,12,12	0.99	0
7	CIT	B	502	-	12,12,12	1.06	0	17,17,17	1.49	1 (5%)

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
6	TLA	D	501	-	-	10/12/12/12	-
4	TAR	C	501	-	-	4/12/12/12	-
4	TAR	A	501	-	-	4/12/12/12	-
8	EDO	B	503	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	TLA	B	501	-	-	6/12/12/12	-
7	CIT	B	502	-	-	6/16/16/16	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	501	TAR	C3-C4	-3.06	1.48	1.52
4	A	501	TAR	C2-C1	-2.67	1.48	1.52
4	A	501	TAR	O11-C1	-2.49	1.22	1.30

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	B	502	CIT	O6-C6-C3	3.78	120.40	113.14
4	A	501	TAR	O4-C4-C3	-2.09	116.04	121.62
4	A	501	TAR	O11-C1-C2	2.01	118.89	113.31

There are no chirality outliers.

All (31) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	501	TAR	O3-C3-C4-O41
6	B	501	TLA	O11-C1-C2-C3
7	B	502	CIT	C2-C3-C6-O5
7	B	502	CIT	C2-C3-C6-O6
7	B	502	CIT	O7-C3-C6-O5
7	B	502	CIT	O7-C3-C6-O6
6	D	501	TLA	C1-C2-C3-O3
6	D	501	TLA	O2-C2-C3-C4
4	A	501	TAR	O3-C3-C4-O4
4	A	501	TAR	O3-C3-C4-O41
4	C	501	TAR	O3-C3-C4-O4
6	D	501	TLA	O3-C3-C4-O4
6	D	501	TLA	O3-C3-C4-O41
4	C	501	TAR	C2-C3-C4-O4
4	C	501	TAR	C2-C3-C4-O41
6	B	501	TLA	O1-C1-C2-C3
6	D	501	TLA	O1-C1-C2-C3
6	D	501	TLA	O11-C1-C2-C3
6	D	501	TLA	O2-C2-C3-O3
6	B	501	TLA	O1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
6	B	501	TLA	O11-C1-C2-O2
6	B	501	TLA	O3-C3-C4-O4
6	B	501	TLA	O3-C3-C4-O41
6	D	501	TLA	O1-C1-C2-O2
6	D	501	TLA	O11-C1-C2-O2
6	D	501	TLA	C1-C2-C3-C4
4	A	501	TAR	C2-C3-C4-O4
7	B	502	CIT	O2-C1-C2-C3
4	A	501	TAR	C2-C3-C4-O41
8	B	503	EDO	O1-C1-C2-O2
7	B	502	CIT	O1-C1-C2-C3

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	501	TAR	1	0
8	B	503	EDO	3	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	378/413 (91%)	-0.34	1 (0%) 90 91	34, 57, 102, 150	1 (0%)
1	B	371/413 (89%)	-0.24	1 (0%) 90 91	24, 59, 114, 172	2 (0%)
1	C	374/413 (90%)	0.44	10 (2%) 56 53	57, 129, 173, 193	1 (0%)
1	D	359/413 (86%)	0.44	9 (2%) 58 55	54, 147, 198, 218	1 (0%)
2	E	8/13 (61%)	0.14	0 100 100	102, 120, 151, 158	0
2	F	8/13 (61%)	-0.37	0 100 100	46, 55, 75, 76	0
2	G	8/13 (61%)	0.29	1 (12%) 8 8	137, 141, 157, 163	0
3	H	8/13 (61%)	-0.58	0 100 100	98, 109, 126, 127	0
All	All	1514/1704 (88%)	0.07	22 (1%) 72 69	24, 103, 175, 218	5 (0%)

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	167	VAL	4.4
1	C	52	ALA	3.0
1	D	277	GLN	2.8
1	D	15	ASN	2.7
1	C	226[A]	CYS	2.6
1	D	116	GLU	2.6
1	C	275	PHE	2.6
1	C	297	THR	2.5
1	D	362	ASP	2.5
1	C	217	ILE	2.4
1	D	361	LEU	2.4
2	G	1	DT	2.4
1	C	340	ILE	2.4
1	A	226[A]	CYS	2.3
1	D	109	LEU	2.3
1	B	123	THR	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	277	GLN	2.2
1	D	118	ILE	2.2
1	C	169	VAL	2.1
1	D	169	VAL	2.1
1	C	146	ASP	2.0
1	C	167	VAL	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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	AS	H	13	4/22	0.62	0.10	183,190,193,198	0
2	GS	F	13	22/23	0.69	0.11	125,141,159,163	0
2	PST	F	10	20/21	0.73	0.14	80,109,136,145	0
3	GS	H	12	22/23	0.75	0.11	122,136,150,163	0
2	GS	F	12	22/23	0.77	0.09	107,121,140,142	0
3	GS	H	11	22/23	0.77	0.12	117,136,148,159	0
2	PST	F	9	20/21	0.79	0.13	71,95,116,128	0
2	SC	F	11	19/20	0.80	0.11	89,117,142,148	0
3	SC	H	10	19/20	0.82	0.14	124,141,151,160	0
2	PST	G	10	20/21	0.84	0.12	96,126,156,193	0
2	PST	G	9	20/21	0.84	0.12	130,142,175,197	0
3	PST	H	9	20/21	0.86	0.11	113,136,158,167	0
2	PST	E	9	20/21	0.88	0.09	60,83,136,139	0
2	SC	G	11	19/20	0.89	0.10	98,115,151,152	0
2	SC	E	11	19/20	0.90	0.09	49,63,107,108	0
2	GS	E	12	22/23	0.91	0.09	42,48,85,88	0
2	PST	E	10	20/21	0.91	0.10	52,68,106,121	0
2	GS	G	13	22/23	0.93	0.09	83,93,105,121	0
2	GS	G	12	22/23	0.94	0.08	86,101,132,135	0
2	GS	E	13	22/23	0.97	0.05	36,42,50,59	0

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(Å ²)	Q<0.9
7	CIT	B	502	13/13	0.74	0.15	106,119,132,136	0
8	EDO	B	503	4/4	0.80	0.13	75,80,83,92	0
4	TAR	C	501	10/10	0.83	0.10	129,139,148,156	0
6	TLA	D	501	10/10	0.84	0.10	140,147,154,159	0
6	TLA	B	501	10/10	0.90	0.11	47,79,95,95	0
4	TAR	A	501	10/10	0.90	0.10	88,104,115,118	0
5	CA	A	502	1/1	0.93	0.13	108,108,108,108	0

6.5 Other polymers [i](#)

There are no such residues in this entry.