



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 06:18 PM GMT

PDB ID : 3PG9
Title : Thermotoga maritima DAH7P synthase in complex with inhibitor
Authors : Cross, P.J.; Dobson, R.C.J.; Patchett, M.L.; Parker, E.J.
Deposited on : 2010-10-31
Resolution : 2.35 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

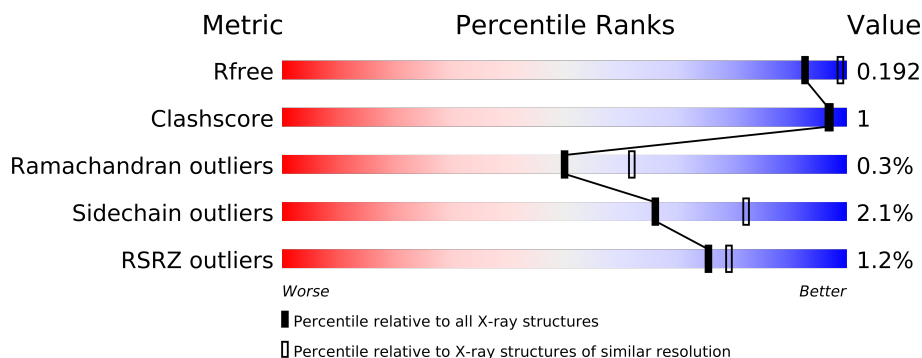
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.35 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}	66092	3327 (2.40-2.32)
Clashscore	79885	1064 (2.38-2.34)
Ramachandran outliers	78287	1048 (2.38-2.34)
Sidechain outliers	78261	1049 (2.38-2.34)
RSRZ outliers	66119	3330 (2.40-2.32)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	338	
1	B	338	
1	C	338	
1	D	338	
1	E	338	
1	F	338	
1	G	338	
1	H	338	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
4	NO3	A	342	X	X

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Mol	Type	Chain	Res	Geometry	Electron density
4	NO3	C	341	X	X
4	NO3	D	340	X	X
4	NO3	F	339	X	-
5	CL	B	342	-	X

2 Entry composition

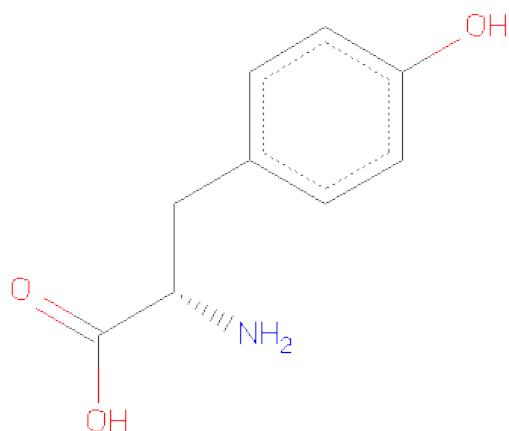
There are 6 unique types of molecules in this entry. The entry contains 21148 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Phospho-2-dehydro-3-deoxyheptonatealdolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	338	Total	C	N	O	S	0	0	0
			2540	1627	424	479	10			
1	B	338	Total	C	N	O	S	0	0	0
			2568	1641	431	486	10			
1	C	338	Total	C	N	O	S	0	1	0
			2538	1623	429	476	10			
1	D	338	Total	C	N	O	S	0	0	0
			2526	1613	421	482	10			
1	E	338	Total	C	N	O	S	0	0	0
			2579	1643	436	490	10			
1	F	338	Total	C	N	O	S	0	0	0
			2581	1643	439	489	10			
1	G	338	Total	C	N	O	S	0	1	0
			2587	1652	434	491	10			
1	H	338	Total	C	N	O	S	0	0	0
			2537	1622	431	474	10			

- Molecule 2 is TYROSINE (three-letter code: TYR) (formula: C₉H₁₁NO₃).



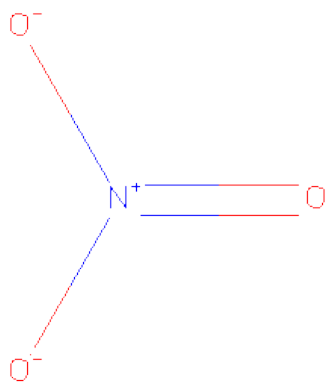
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			13	9	1	3		
2	A	1	Total	C	N	O	0	0
			13	9	1	3		
2	B	1	Total	C	N	O	0	0
			13	9	1	3		
2	B	1	Total	C	N	O	0	0
			13	9	1	3		
2	C	1	Total	C	N	O	0	0
			13	9	1	3		
2	C	1	Total	C	N	O	0	0
			13	9	1	3		
2	D	1	Total	C	N	O	0	0
			13	9	1	3		
2	H	1	Total	C	N	O	0	0
			13	9	1	3		

- Molecule 3 is AZIDE ION (three-letter code: AZI) (formula: N₃).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	N	0	0
			3	3		
3	B	1	Total	N	0	0
			3	3		

- Molecule 4 is NITRATE ION (three-letter code: NO3) (formula: NO₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	N	O	0	0
			4	1	3		
4	C	1	Total	N	O	0	0
			4	1	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	D	1	Total	N	O	0	0
			4	1	3		
4	F	1	Total	N	O	0	0
			4	1	3		

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Cl	0	0
			1	1		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	78	Total	O	0	0
			78	78		
6	B	81	Total	O	0	0
			81	81		
6	C	77	Total	O	0	0
			77	77		
6	D	61	Total	O	0	0
			61	61		
6	E	64	Total	O	0	0
			64	64		
6	F	65	Total	O	0	0
			65	65		
6	G	87	Total	O	0	0
			87	87		
6	H	52	Total	O	0	0
			52	52		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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: Phospho-2-dehydro-3-deoxyheptonatealdolase

Chain A: 



- Molecule 1: Phospho-2-dehydro-3-deoxyheptonatealdolase

Chain B: 



- Molecule 1: Phospho-2-dehydro-3-deoxyheptonatealdolase

Chain C: 



- Molecule 1: Phospho-2-dehydro-3-deoxyheptonatealdolase

Chain D: 



- Molecule 1: Phospho-2-dehydro-3-deoxyheptonatealdolase

Chain E: 



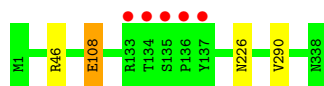
- Molecule 1: Phospho-2-dehydro-3-deoxyheptonatealdolase

Chain F: 



- Molecule 1: Phospho-2-dehydro-3-deoxyheptonatealdolase

Chain G: 



- Molecule 1: Phospho-2-dehydro-3-deoxyheptonatealdolase

Chain H: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	81.61Å 121.00Å 133.38Å 90.00° 92.12° 90.00°	Depositor
Resolution (Å)	52.57 – 2.35 52.57 – 2.35	Depositor EDS
% Data completeness (in resolution range)	97.2 (52.57-2.35) 97.2 (52.57-2.35)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.02 (at 2.34Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.1.357)	Depositor
R, R_{free}	0.171 , 0.222 0.189 , 0.192	Depositor DCC
R_{free} test set	5202 reflections (4.97%)	DCC
Wilson B-factor (Å ²)	34.2	Xtriage
Anisotropy	0.259	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 31.4	EDS
Estimated twinning fraction	0.026 for h,-k,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 104686 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	21148	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.84% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: AZI, CL, NO3

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	0.23	0/2582	0.40	0/3495
1	B	0.23	0/2611	0.40	0/3532
1	C	0.23	0/2583	0.39	0/3496
1	D	0.22	0/2567	0.39	0/3481
1	E	0.22	0/2621	0.40	0/3543
1	F	0.22	0/2623	0.39	0/3543
1	G	0.23	0/2630	0.40	0/3557
1	H	0.22	0/2579	0.39	0/3492
All	All	0.23	0/20796	0.39	0/28139

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2540	0	0	2	0
1	B	2568	0	0	3	0
1	C	2538	0	0	3	0
1	D	2526	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	2579	0	0	2	0
1	F	2581	0	0	5	0
1	G	2587	0	0	2	0
1	H	2537	0	0	4	0
2	A	26	0	16	0	0
2	B	26	0	16	0	0
2	C	26	0	16	0	0
2	D	13	0	8	0	0
2	H	13	0	8	0	0
3	A	3	0	0	0	0
3	B	3	0	0	0	0
4	A	4	0	0	0	0
4	C	4	0	0	0	0
4	D	4	0	0	0	0
4	F	4	0	0	0	0
5	B	1	0	0	0	0
6	A	78	0	0	0	0
6	B	81	0	0	0	0
6	C	77	0	0	0	0
6	D	61	0	0	0	0
6	E	64	0	0	0	0
6	F	65	0	0	0	0
6	G	87	0	0	0	0
6	H	52	0	0	1	0
All	All	21148	0	64	20	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 1.

All (20) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:92:ASN:ND2	1:B:93:GLY:N	2.54	0.56
1:B:92:ASN:CG	1:B:93:GLY:N	2.60	0.55
1:C:35:GLU:OE2	1:E:46:ARG:NH2	2.43	0.51
1:F:266:ILE:N	1:F:293:HIS:CD2	2.80	0.49
1:D:135:SER:O	1:D:137:TYR:N	2.46	0.49
1:A:237:ARG:O	1:A:237:ARG:CG	2.61	0.48
1:H:115:HIS:CD2	1:H:157:TYR:CE1	3.03	0.46
1:C:243:GLU:OE2	1:D:214:ILE:N	2.49	0.46
1:G:108:GLU:CD	1:G:108:GLU:N	2.69	0.45
1:A:189:GLN:O	1:A:190:ASN:CB	2.64	0.45
1:H:52:LYS:NZ	1:H:52:LYS:N	2.64	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:H:1:MET:N	6:H:416:HOH:O	2.50	0.45
1:F:92:ASN:OD1	1:F:293:HIS:CE1	2.70	0.44
1:E:186:ARG:N	1:E:186:ARG:CD	2.81	0.44
1:C:266:ILE:N	1:C:293:HIS:CD2	2.85	0.44
1:H:266:ILE:N	1:H:293:HIS:CD2	2.86	0.43
1:B:35:GLU:OE2	1:G:46:ARG:NH2	2.51	0.43
1:F:237:ARG:CG	1:F:237:ARG:O	2.68	0.42
1:F:269:ASP:OD2	1:F:272:HIS:ND1	2.54	0.41
1:F:74:ARG:NH1	1:F:80:ASP:OD1	2.54	0.41

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	336/338 (99%)	324 (96%)	10 (3%)	2 (1%)	33	39
1	B	336/338 (99%)	329 (98%)	6 (2%)	1 (0%)	50	62
1	C	337/338 (100%)	329 (98%)	7 (2%)	1 (0%)	50	62
1	D	336/338 (99%)	325 (97%)	9 (3%)	2 (1%)	33	39
1	E	336/338 (99%)	328 (98%)	8 (2%)	0	100	100
1	F	336/338 (99%)	328 (98%)	8 (2%)	0	100	100
1	G	337/338 (100%)	328 (97%)	9 (3%)	0	100	100
1	H	336/338 (99%)	328 (98%)	7 (2%)	1 (0%)	50	62
All	All	2690/2704 (100%)	2619 (97%)	64 (2%)	7 (0%)	50	62

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	136	PRO
1	D	137	TYR
1	A	190	ASN

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Mol	Chain	Res	Type
1	C	135	SER
1	H	51	ASP
1	A	135	SER
1	B	133	ARG

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	259/286 (91%)	254 (98%)	5 (2%)	69	84
1	B	268/286 (94%)	261 (97%)	7 (3%)	59	75
1	C	258/286 (90%)	254 (98%)	4 (2%)	75	87
1	D	254/286 (89%)	248 (98%)	6 (2%)	61	78
1	E	271/286 (95%)	265 (98%)	6 (2%)	64	81
1	F	273/286 (96%)	266 (97%)	7 (3%)	59	75
1	G	269/286 (94%)	266 (99%)	3 (1%)	84	93
1	H	260/286 (91%)	254 (98%)	6 (2%)	63	79
All	All	2112/2288 (92%)	2068 (98%)	44 (2%)	66	82

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	45	ASP
1	A	120	LEU
1	A	126	ARG
1	A	150	LEU
1	A	237	ARG
1	B	56	LEU
1	B	57	ASP
1	B	126	ARG
1	B	147	LEU
1	B	171	LEU
1	B	189	GLN
1	B	336	LYS
1	C	126	ARG

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Mol	Chain	Res	Type
1	C	139	PHE
1	C	193	LEU
1	C	194	LEU
1	D	147	LEU
1	D	150	LEU
1	D	162	VAL
1	D	207	LYS
1	D	219	LEU
1	D	318	LEU
1	E	92	ASN
1	E	147	LEU
1	E	150	LEU
1	E	186	ARG
1	E	219	LEU
1	E	237	ARG
1	F	150	LEU
1	F	171	LEU
1	F	194	LEU
1	F	219	LEU
1	F	237	ARG
1	F	244	LYS
1	F	290	VAL
1	G	108	GLU
1	G	226	ASN
1	G	290	VAL
1	H	51	ASP
1	H	52	LYS
1	H	147	LEU
1	H	219	LEU
1	H	237	ARG
1	H	312	GLN

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

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 15 ligands modelled in this entry, 1 is monoatomic - leaving 14 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$
2	TYR	A	339	-	13,13,13	0.59	0	17,17,17	0.82	1 (5%)
2	TYR	A	340	-	13,13,13	0.62	0	17,17,17	0.83	1 (5%)
3	AZI	A	341	-	2,2,2	1.41	0	0,1,1	0.00	-
4	NO3	A	342	-	3,3,3	3.12	3 (100%)	3,3,3	0.18	0
2	TYR	B	339	-	13,13,13	0.60	0	17,17,17	0.92	1 (5%)
2	TYR	B	340	-	13,13,13	0.59	0	17,17,17	0.86	1 (5%)
3	AZI	B	341	-	2,2,2	1.40	0	0,1,1	0.00	-
2	TYR	C	339	-	13,13,13	0.60	0	17,17,17	0.88	1 (5%)
2	TYR	C	340	-	13,13,13	0.60	0	17,17,17	0.79	1 (5%)
4	NO3	C	341	-	3,3,3	3.11	3 (100%)	3,3,3	0.08	0
2	TYR	D	339	-	13,13,13	0.58	0	17,17,17	0.89	1 (5%)
4	NO3	D	340	-	3,3,3	3.12	3 (100%)	3,3,3	0.10	0
4	NO3	F	339	-	3,3,3	3.14	3 (100%)	3,3,3	0.13	0
2	TYR	H	339	-	13,13,13	0.61	0	17,17,17	0.92	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
2	TYR	A	339	-	-	0/8/8/8	0/1/1/1
2	TYR	A	340	-	-	0/8/8/8	0/1/1/1
3	AZI	A	341	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NO3	A	342	-	-	0/0/0/0	0/0/0/0
2	TYR	B	339	-	-	0/8/8/8	0/1/1/1
2	TYR	B	340	-	-	0/8/8/8	0/1/1/1
3	AZI	B	341	-	-	0/0/0/0	0/0/0/0
2	TYR	C	339	-	-	0/8/8/8	0/1/1/1
2	TYR	C	340	-	-	0/8/8/8	0/1/1/1
4	NO3	C	341	-	-	0/0/0/0	0/0/0/0
2	TYR	D	339	-	-	0/8/8/8	0/1/1/1
4	NO3	D	340	-	-	0/0/0/0	0/0/0/0
4	NO3	F	339	-	-	0/0/0/0	0/0/0/0
2	TYR	H	339	-	-	0/8/8/8	0/1/1/1

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	340	NO3	O1-N	3.76	1.40	1.24
4	F	339	NO3	O1-N	3.71	1.40	1.24
4	C	341	NO3	O1-N	3.70	1.39	1.24
4	A	342	NO3	O1-N	3.59	1.39	1.24
4	A	342	NO3	O3-N	2.91	1.40	1.25
4	F	339	NO3	O2-N	2.82	1.40	1.25
4	A	342	NO3	O2-N	2.80	1.40	1.25
4	C	341	NO3	O2-N	2.80	1.40	1.25
4	F	339	NO3	O3-N	2.79	1.40	1.25
4	D	340	NO3	O3-N	2.78	1.40	1.25
4	C	341	NO3	O3-N	2.73	1.39	1.25
4	D	340	NO3	O2-N	2.72	1.39	1.25

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	339	TYR	OXT-C-O	-2.81	117.71	124.07
2	H	339	TYR	OXT-C-O	-2.72	117.93	124.07
2	D	339	TYR	OXT-C-O	-2.65	118.08	124.07
2	A	340	TYR	OXT-C-O	-2.63	118.13	124.07
2	C	339	TYR	OXT-C-O	-2.60	118.19	124.07
2	B	340	TYR	OXT-C-O	-2.60	118.19	124.07
2	A	339	TYR	OXT-C-O	-2.58	118.24	124.07
2	C	340	TYR	OXT-C-O	-2.51	118.39	124.07

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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	338/338 (100%)	-0.32	7 (2%) 60 63	16, 35, 73, 166	0
1	B	338/338 (100%)	-0.36	0 100 100	17, 35, 57, 93	0
1	C	338/338 (100%)	-0.19	5 (1%) 70 74	18, 35, 73, 148	0
1	D	338/338 (100%)	-0.28	3 (0%) 81 84	21, 42, 64, 120	0
1	E	338/338 (100%)	-0.26	4 (1%) 75 79	17, 39, 62, 139	0
1	F	338/338 (100%)	-0.27	8 (2%) 56 59	18, 39, 67, 127	0
1	G	338/338 (100%)	-0.17	5 (1%) 70 74	17, 37, 61, 115	0
1	H	338/338 (100%)	-0.04	1 (0%) 91 94	20, 45, 68, 110	0
All	All	2704/2704 (100%)	-0.24	33 (1%) 75 79	16, 38, 66, 166	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	136	PRO	8.5
1	D	137	TYR	7.9
1	C	136	PRO	6.9
1	E	137	TYR	6.4
1	F	245	ALA	6.4
1	C	137	TYR	5.3
1	F	136	PRO	5.1
1	A	139	PHE	4.7
1	G	137	TYR	4.2
1	F	137	TYR	4.1
1	A	133	ARG	3.5
1	A	137	TYR	3.4
1	E	136	PRO	3.4
1	E	135	SER	3.3
1	G	136	PRO	3.1
1	G	134	THR	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	138	SER	3.0
1	E	134	THR	2.9
1	F	139	PHE	2.8
1	C	140	GLN	2.8
1	G	133	ARG	2.7
1	C	138	SER	2.7
1	A	135	SER	2.5
1	C	130	TYR	2.5
1	F	135	SER	2.4
1	F	138	SER	2.4
1	H	245	ALA	2.3
1	F	246	THR	2.3
1	D	136	PRO	2.2
1	F	134	THR	2.1
1	G	135	SER	2.1
1	D	134	THR	2.1
1	A	76	PHE	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
4	NO3	C	341	4/4	0.25	5.58	36,36,38,41	0
4	NO3	D	340	4/4	0.24	4.80	37,38,39,42	0
5	CL	B	342	1/1	0.24	3.78	66,66,66,66	0
4	NO3	A	342	4/4	0.20	2.15	29,31,34,35	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	AZI	B	341	3/3	0.16	1.77	78,78,79,79	0
4	NO3	F	339	4/4	0.19	1.74	28,29,31,32	0
3	AZI	A	341	3/3	0.12	0.47	71,71,72,72	0
2	TYR	C	339	13/13	0.10	0.03	17,20,26,27	0
2	TYR	A	339	13/13	0.09	-0.38	18,20,23,23	0
2	TYR	A	340	13/13	0.10	-0.42	24,27,32,36	0
2	TYR	H	339	13/13	0.10	-0.59	25,29,31,32	0
2	TYR	B	340	13/13	0.10	-0.73	22,29,35,36	0
2	TYR	B	339	13/13	0.08	-0.91	18,25,31,34	0
2	TYR	C	340	13/13	0.07	-1.52	21,23,26,26	0
2	TYR	D	339	13/13	0.08	-1.68	27,30,35,40	0

6.5 Other polymers ⓘ

There are no such residues in this entry.