



Full wwPDB X-ray Structure Validation Report ⓘ

Jul 26, 2023 – 03:36 AM EDT

PDB ID : 1A0C
Title : XYLOSE ISOMERASE FROM THERMOANAEROBACTERIUM THERMOSULFURIGENES
Authors : Gally, O.; Chopra, R.; Conti, E.; Brick, P.; Blow, D.
Deposited on : 1997-11-28
Resolution : 2.50 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 : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.34
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) : 2.34

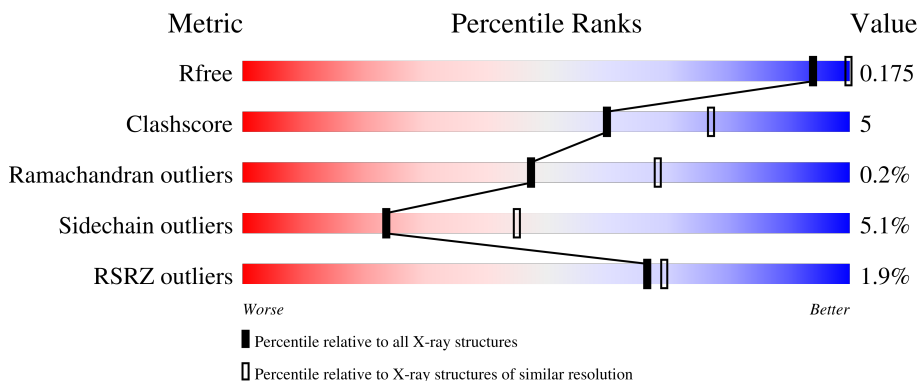
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


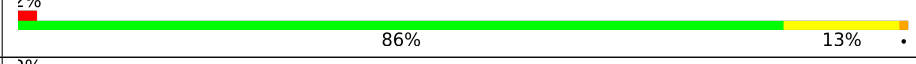


The reported resolution of this entry is 2.50 Å.

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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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	438	 87% 12% .
1	B	438	 86% 13% .
1	C	438	 86% 13% .
1	D	438	 86% 13% .

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 15116 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 XYLOSE ISOMERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	437	3498	2255	579	651	13	0	0	0
1	B	437	3498	2255	579	651	13	0	0	0
1	C	437	3498	2255	579	651	13	0	0	0
1	D	437	3498	2255	579	651	13	0	0	0

- Molecule 2 is COBALT (II) ION (three-letter code: CO) (formula: Co).

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

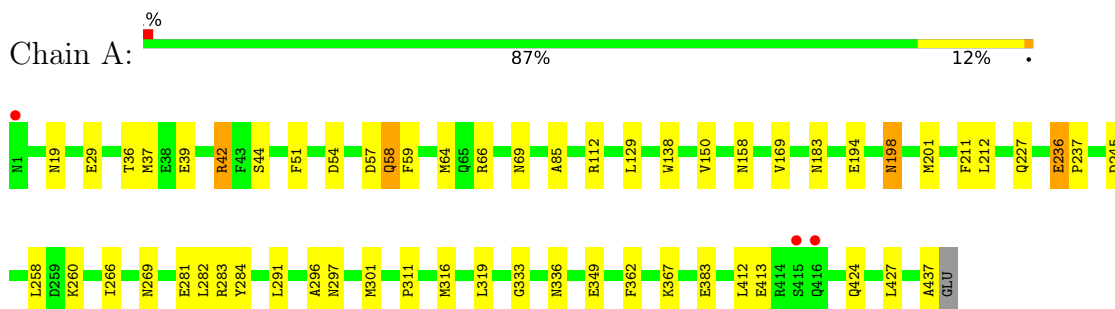
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	281	Total	O	0	0
			281	281		
3	B	282	Total	O	0	0
			282	282		
3	C	276	Total	O	0	0
			276	276		
3	D	277	Total	O	0	0
			277	277		

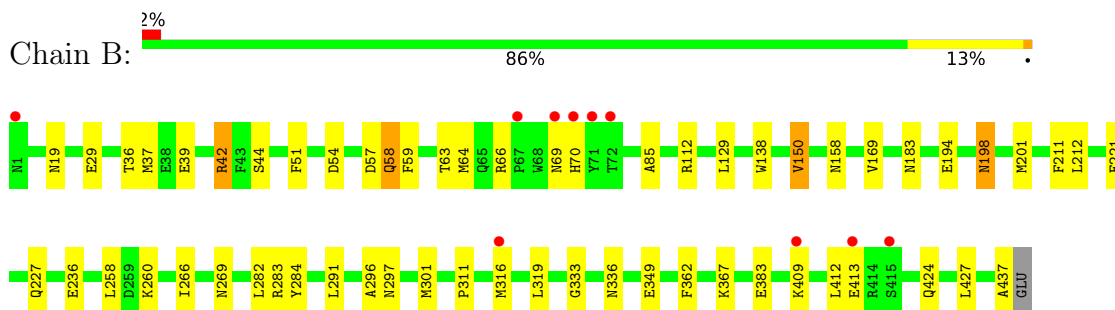
3 Residue-property plots [i](#)

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.

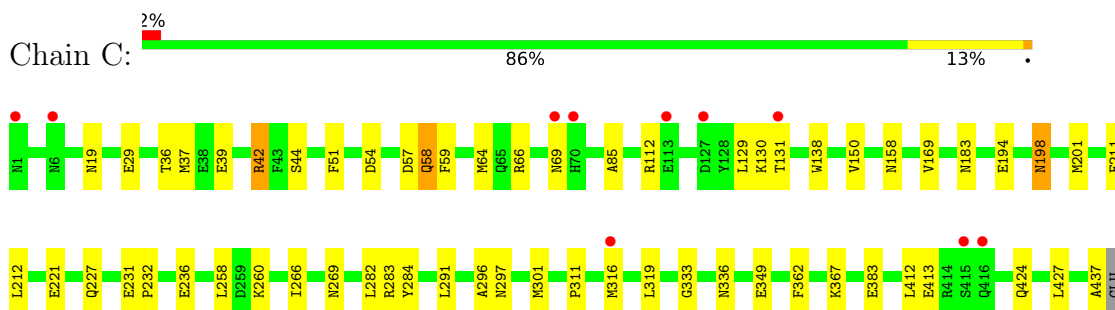
- Molecule 1: XYLOSE ISOMERASE



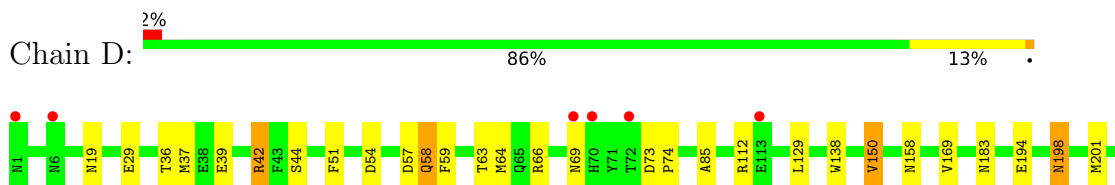
- Molecule 1: XYLOSE ISOMERASE

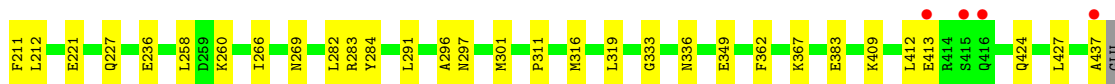


- Molecule 1: XYLOSE ISOMERASE



- Molecule 1: XYLOSE ISOMERASE





4 Data and refinement statistics i

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	85.66Å 153.73Å 158.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.50 9.97 – 2.50	Depositor EDS
% Data completeness (in resolution range)	84.9 (10.00-2.50) 84.9 (9.97-2.50)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.10 (at 2.50Å)	Xtrriage
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.168 , 0.177 0.168 , 0.175	Depositor DCC
R_{free} test set	3081 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	19.8	Xtrriage
Anisotropy	0.251	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 58.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.006 for -h,l,k	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	15116	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.32% 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:
CO

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.47	0/3589	0.62	0/4851
1	B	0.47	0/3589	0.62	0/4851
1	C	0.47	0/3589	0.62	0/4851
1	D	0.47	0/3589	0.62	0/4851
All	All	0.47	0/14356	0.62	0/19404

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	3498	0	3323	36	0
1	B	3498	0	3323	38	4
1	C	3498	0	3323	34	6
1	D	3498	0	3323	37	2
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	A	281	0	0	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	282	0	0	7	4
3	C	276	0	0	5	0
3	D	277	0	0	7	0
All	All	15116	0	13292	126	8

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 (126) 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:B:58:GLN:H	1:B:58:GLN:CD	1.94	0.71
1:C:58:GLN:CD	1:C:58:GLN:H	1.94	0.71
1:A:58:GLN:H	1:A:58:GLN:CD	1.93	0.71
1:D:58:GLN:H	1:D:58:GLN:CD	1.94	0.71
1:B:138:TRP:HB3	1:B:183:ASN:HB2	1.74	0.69
1:B:58:GLN:HG2	1:B:59:PHE:CE1	2.27	0.69
1:C:58:GLN:HG2	1:C:59:PHE:CE1	2.27	0.69
1:D:58:GLN:HG2	1:D:59:PHE:CE1	2.27	0.69
1:A:58:GLN:HG2	1:A:59:PHE:CE1	2.27	0.69
1:C:138:TRP:HB3	1:C:183:ASN:HB2	1.74	0.68
1:A:138:TRP:HB3	1:A:183:ASN:HB2	1.75	0.68
1:D:138:TRP:HB3	1:D:183:ASN:HB2	1.75	0.67
1:A:112:ARG:HG2	1:B:412:LEU:HD22	1.79	0.63
1:A:412:LEU:HD22	1:B:112:ARG:HG2	1.79	0.63
1:C:437:ALA:HA	3:C:653:HOH:O	2.02	0.60
1:B:437:ALA:HA	3:B:654:HOH:O	2.01	0.60
1:A:437:ALA:HA	3:A:622:HOH:O	2.01	0.60
1:C:112:ARG:HG2	1:D:412:LEU:HD22	1.83	0.59
1:C:36:THR:OG1	1:C:39:GLU:HG2	2.03	0.59
1:C:412:LEU:HD22	1:D:112:ARG:HG2	1.84	0.59
1:D:36:THR:OG1	1:D:39:GLU:HG2	2.03	0.58
1:A:57:ASP:HB2	1:A:58:GLN:OE1	2.03	0.58
1:B:57:ASP:HB2	1:B:58:GLN:OE1	2.03	0.58
1:D:437:ALA:HA	3:D:685:HOH:O	2.02	0.58
1:C:57:ASP:HB2	1:C:58:GLN:OE1	2.03	0.58
1:A:36:THR:OG1	1:A:39:GLU:HG2	2.03	0.58
1:B:36:THR:OG1	1:B:39:GLU:HG2	2.03	0.57
1:A:194:GLU:HG2	1:B:424:GLN:HE22	1.69	0.57
1:D:57:ASP:HB2	1:D:58:GLN:OE1	2.03	0.57
1:B:58:GLN:HG2	1:B:59:PHE:CD1	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:194:GLU:HG2	1:D:424:GLN:HE22	1.71	0.56
1:C:58:GLN:HG2	1:C:59:PHE:CD1	2.41	0.56
1:A:58:GLN:HG2	1:A:59:PHE:CD1	2.41	0.55
1:A:58:GLN:NE2	3:A:618:HOH:O	2.40	0.55
1:A:112:ARG:HG3	3:B:523:HOH:O	2.07	0.55
1:D:58:GLN:HG2	1:D:59:PHE:CD1	2.41	0.55
1:C:66:ARG:H	1:C:69:ASN:ND2	2.06	0.54
1:A:58:GLN:HE21	1:C:58:GLN:HE21	1.54	0.54
1:D:66:ARG:H	1:D:69:ASN:ND2	2.06	0.54
1:B:58:GLN:NE2	3:B:650:HOH:O	2.40	0.54
1:B:112:ARG:HG3	3:B:722:HOH:O	2.07	0.54
1:C:58:GLN:NE2	3:C:649:HOH:O	2.40	0.54
1:C:424:GLN:HE22	1:D:194:GLU:HG2	1.72	0.54
1:D:112:ARG:HG3	3:D:752:HOH:O	2.07	0.54
1:C:112:ARG:HG3	3:D:554:HOH:O	2.07	0.54
1:D:58:GLN:NE2	3:D:681:HOH:O	2.40	0.54
1:A:66:ARG:H	1:A:69:ASN:ND2	2.06	0.53
1:B:66:ARG:H	1:B:69:ASN:ND2	2.06	0.53
1:D:297:ASN:HA	1:D:311:PRO:HD3	1.91	0.53
1:A:201:MET:CE	1:B:284:TYR:HA	2.39	0.52
1:A:297:ASN:HA	1:A:311:PRO:HD3	1.91	0.52
1:B:297:ASN:HA	1:B:311:PRO:HD3	1.91	0.51
1:A:424:GLN:HE22	1:B:194:GLU:HG2	1.73	0.51
1:A:284:TYR:HA	1:B:201:MET:CE	2.41	0.51
1:C:297:ASN:HA	1:C:311:PRO:HD3	1.91	0.51
1:B:58:GLN:HE21	1:D:58:GLN:HE21	1.57	0.51
1:C:37:MET:HE1	1:C:367:LYS:HG3	1.93	0.49
1:C:201:MET:CE	1:D:284:TYR:HA	2.43	0.49
1:A:349:GLU:HG2	3:A:619:HOH:O	2.13	0.48
1:A:183:ASN:HD22	1:A:227:GLN:HB3	1.78	0.48
1:B:349:GLU:HG2	3:B:651:HOH:O	2.13	0.48
1:D:349:GLU:HG2	3:D:682:HOH:O	2.14	0.48
1:C:183:ASN:HD22	1:C:227:GLN:HB3	1.78	0.48
1:C:349:GLU:HG2	3:C:650:HOH:O	2.13	0.48
1:D:169:VAL:HG21	1:D:211:PHE:HZ	1.79	0.48
1:A:284:TYR:HA	1:B:201:MET:HE1	1.96	0.48
1:C:169:VAL:HG21	1:C:211:PHE:HZ	1.79	0.48
1:A:169:VAL:HG21	1:A:211:PHE:HZ	1.79	0.47
1:B:183:ASN:HD22	1:B:227:GLN:HB3	1.78	0.47
1:C:198:ASN:HD22	1:C:198:ASN:C	2.18	0.47
1:D:44:SER:HB3	1:D:336:ASN:HA	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:169:VAL:HG21	1:B:211:PHE:HZ	1.79	0.47
1:C:44:SER:HB3	1:C:336:ASN:HA	1.97	0.47
1:D:183:ASN:HD22	1:D:227:GLN:HB3	1.78	0.47
1:C:284:TYR:HA	1:D:201:MET:CE	2.45	0.47
1:A:198:ASN:C	1:A:198:ASN:HD22	2.18	0.47
1:A:44:SER:HB3	1:A:336:ASN:HA	1.97	0.46
1:B:63:THR:HG21	1:D:150:VAL:CG1	2.45	0.46
1:D:198:ASN:C	1:D:198:ASN:HD22	2.18	0.46
1:D:37:MET:HE1	1:D:367:LYS:HG3	1.97	0.46
1:B:44:SER:HB3	1:B:336:ASN:HA	1.97	0.46
1:B:198:ASN:HD22	1:B:198:ASN:C	2.18	0.45
1:B:301:MET:HG3	3:B:680:HOH:O	2.16	0.45
1:A:201:MET:HE1	1:B:284:TYR:HA	2.00	0.44
1:A:296:ALA:HB1	1:A:362:PHE:CE2	2.52	0.44
1:D:301:MET:HG3	3:D:710:HOH:O	2.17	0.44
1:B:296:ALA:HB1	1:B:362:PHE:CE2	2.52	0.44
1:C:301:MET:HG3	3:C:678:HOH:O	2.17	0.44
1:B:37:MET:HE1	1:B:367:LYS:HG3	2.00	0.44
1:D:296:ALA:HB1	1:D:362:PHE:CE2	2.52	0.44
1:A:301:MET:HG3	3:A:648:HOH:O	2.17	0.44
1:A:42:ARG:HD3	1:A:333:GLY:O	2.18	0.44
1:B:42:ARG:HD3	1:B:333:GLY:O	2.18	0.44
1:B:260:LYS:HG2	3:B:731:HOH:O	2.18	0.44
1:B:51:PHE:CZ	1:B:85:ALA:HA	2.53	0.43
1:A:37:MET:HE1	1:A:367:LYS:HG3	2.00	0.43
1:A:51:PHE:CZ	1:A:85:ALA:HA	2.53	0.43
1:B:150:VAL:CG1	1:D:63:THR:HG21	2.48	0.43
1:C:296:ALA:HB1	1:C:362:PHE:CE2	2.52	0.43
1:A:260:LYS:HG2	3:A:698:HOH:O	2.18	0.43
1:C:42:ARG:HD3	1:C:333:GLY:O	2.18	0.43
1:D:42:ARG:HD3	1:D:333:GLY:O	2.18	0.43
1:D:51:PHE:CZ	1:D:85:ALA:HA	2.53	0.43
1:B:63:THR:HG21	1:D:150:VAL:HG13	2.00	0.43
1:C:260:LYS:HG2	3:C:728:HOH:O	2.18	0.43
1:D:260:LYS:HG2	3:D:761:HOH:O	2.18	0.42
1:C:349:GLU:H	1:C:349:GLU:CD	2.23	0.42
1:D:54:ASP:C	1:D:64:MET:HG2	2.40	0.42
1:A:54:ASP:C	1:A:64:MET:HG2	2.40	0.42
1:A:266:ILE:HD12	1:A:291:LEU:HD13	2.02	0.42
1:B:54:ASP:C	1:B:64:MET:HG2	2.40	0.42
1:D:349:GLU:H	1:D:349:GLU:CD	2.23	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:349:GLU:H	1:A:349:GLU:CD	2.23	0.42
1:C:51:PHE:CZ	1:C:85:ALA:HA	2.53	0.42
1:C:266:ILE:HD12	1:C:291:LEU:HD13	2.02	0.42
1:B:266:ILE:HD12	1:B:291:LEU:HD13	2.02	0.41
1:B:349:GLU:H	1:B:349:GLU:CD	2.23	0.41
1:D:266:ILE:HD12	1:D:291:LEU:HD13	2.02	0.41
1:C:54:ASP:C	1:C:64:MET:HG2	2.40	0.41
1:C:169:VAL:HG21	1:C:211:PHE:CZ	2.56	0.41
1:D:169:VAL:HG21	1:D:211:PHE:CZ	2.56	0.41
1:B:169:VAL:HG21	1:B:211:PHE:CZ	2.56	0.40
1:C:231:GLU:HA	1:C:232:PRO:HD3	1.92	0.40
1:D:73:ASP:HA	1:D:74:PRO:HD3	1.97	0.40
1:A:236:GLU:HA	1:A:237:PRO:HA	1.98	0.40
1:A:245:ASP:HB2	1:A:281:GLU:OE2	2.22	0.40

All (8) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:221:GLU:OE2	3:B:530:HOH:O[3_655]	1.66	0.54
1:C:221:GLU:OE1	3:B:530:HOH:O[3_655]	1.92	0.28
1:B:409:LYS:NZ	1:D:221:GLU:CD[3_645]	1.95	0.25
1:B:70:HIS:O	1:C:131:THR:CB[2_565]	1.96	0.24
1:C:221:GLU:CD	3:B:530:HOH:O[3_655]	1.98	0.22
1:B:70:HIS:O	1:C:131:THR:CG2[2_565]	2.06	0.14
1:B:221:GLU:CG	1:D:409:LYS:NZ[3_645]	2.08	0.12
1:C:130:LYS:O	3:B:711:HOH:O[2_564]	2.15	0.05

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	435/438 (99%)	427 (98%)	7 (2%)	1 (0%)	47	68
1	B	435/438 (99%)	427 (98%)	7 (2%)	1 (0%)	47	68
1	C	435/438 (99%)	427 (98%)	7 (2%)	1 (0%)	47	68
1	D	435/438 (99%)	427 (98%)	7 (2%)	1 (0%)	47	68
All	All	1740/1752 (99%)	1708 (98%)	28 (2%)	4 (0%)	47	68

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	236	GLU
1	B	236	GLU
1	C	236	GLU
1	D	236	GLU

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	354/370 (96%)	336 (95%)	18 (5%)	24	45
1	B	354/370 (96%)	336 (95%)	18 (5%)	24	45
1	C	354/370 (96%)	336 (95%)	18 (5%)	24	45
1	D	354/370 (96%)	336 (95%)	18 (5%)	24	45
All	All	1416/1480 (96%)	1344 (95%)	72 (5%)	24	45

All (72) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	19	ASN
1	A	29	GLU
1	A	42	ARG
1	A	58	GLN
1	A	129	LEU
1	A	150	VAL
1	A	158	ASN

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Mol	Chain	Res	Type
1	A	198	ASN
1	A	212	LEU
1	A	258	LEU
1	A	269	ASN
1	A	282	LEU
1	A	283	ARG
1	A	316	MET
1	A	319	LEU
1	A	383	GLU
1	A	413	GLU
1	A	427	LEU
1	B	19	ASN
1	B	29	GLU
1	B	42	ARG
1	B	58	GLN
1	B	129	LEU
1	B	150	VAL
1	B	158	ASN
1	B	198	ASN
1	B	212	LEU
1	B	258	LEU
1	B	269	ASN
1	B	282	LEU
1	B	283	ARG
1	B	316	MET
1	B	319	LEU
1	B	383	GLU
1	B	413	GLU
1	B	427	LEU
1	C	19	ASN
1	C	29	GLU
1	C	42	ARG
1	C	58	GLN
1	C	129	LEU
1	C	150	VAL
1	C	158	ASN
1	C	198	ASN
1	C	212	LEU
1	C	258	LEU
1	C	269	ASN
1	C	282	LEU
1	C	283	ARG

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Mol	Chain	Res	Type
1	C	316	MET
1	C	319	LEU
1	C	383	GLU
1	C	413	GLU
1	C	427	LEU
1	D	19	ASN
1	D	29	GLU
1	D	42	ARG
1	D	58	GLN
1	D	129	LEU
1	D	150	VAL
1	D	158	ASN
1	D	198	ASN
1	D	212	LEU
1	D	258	LEU
1	D	269	ASN
1	D	282	LEU
1	D	283	ARG
1	D	316	MET
1	D	319	LEU
1	D	383	GLU
1	D	413	GLU
1	D	427	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (48) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	19	ASN
1	A	65	GLN
1	A	69	ASN
1	A	115	ASN
1	A	158	ASN
1	A	183	ASN
1	A	198	ASN
1	A	241	GLN
1	A	279	GLN
1	A	419	ASN
1	A	424	GLN
1	A	432	ASN
1	B	19	ASN
1	B	65	GLN
1	B	69	ASN

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Mol	Chain	Res	Type
1	B	115	ASN
1	B	158	ASN
1	B	183	ASN
1	B	198	ASN
1	B	241	GLN
1	B	279	GLN
1	B	419	ASN
1	B	424	GLN
1	B	432	ASN
1	C	19	ASN
1	C	65	GLN
1	C	69	ASN
1	C	115	ASN
1	C	158	ASN
1	C	183	ASN
1	C	198	ASN
1	C	241	GLN
1	C	279	GLN
1	C	419	ASN
1	C	424	GLN
1	C	432	ASN
1	D	19	ASN
1	D	65	GLN
1	D	69	ASN
1	D	115	ASN
1	D	158	ASN
1	D	183	ASN
1	D	198	ASN
1	D	241	GLN
1	D	279	GLN
1	D	419	ASN
1	D	424	GLN
1	D	432	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 8 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	437/438 (99%)	-0.83	3 (0%) 87 89	10, 17, 36, 56	0
1	B	437/438 (99%)	-0.72	10 (2%) 60 63	10, 17, 36, 56	0
1	C	437/438 (99%)	-0.74	10 (2%) 60 63	10, 17, 36, 56	0
1	D	437/438 (99%)	-0.74	10 (2%) 60 63	10, 17, 36, 56	0
All	All	1748/1752 (99%)	-0.76	33 (1%) 66 69	10, 17, 36, 56	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	70	HIS	8.3
1	C	131	THR	5.1
1	B	69	ASN	4.9
1	B	72	THR	4.6
1	D	69	ASN	4.3
1	C	415	SER	3.9
1	D	413	GLU	3.9
1	D	70	HIS	3.8
1	A	1	ASN	3.7
1	D	1	ASN	3.5
1	B	415	SER	3.3
1	D	72	THR	3.1
1	C	69	ASN	3.0
1	C	6	ASN	3.0
1	A	415	SER	2.9
1	A	416	GLN	2.8
1	C	1	ASN	2.7
1	B	1	ASN	2.7
1	D	416	GLN	2.7
1	C	113	GLU	2.7
1	D	113	GLU	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	71	TYR	2.6
1	C	70	HIS	2.5
1	C	316	MET	2.5
1	D	6	ASN	2.5
1	D	415	SER	2.4
1	C	127	ASP	2.3
1	D	437	ALA	2.2
1	B	413	GLU	2.2
1	B	316	MET	2.1
1	C	416	GLN	2.1
1	B	67	PRO	2.0
1	B	409	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 monosaccharides 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
2	CO	C	491	1/1	0.98	0.03	33,33,33,33	0
2	CO	D	491	1/1	0.98	0.04	33,33,33,33	0
2	CO	B	492	1/1	0.99	0.03	15,15,15,15	0
2	CO	A	491	1/1	0.99	0.02	33,33,33,33	0
2	CO	A	492	1/1	0.99	0.02	15,15,15,15	0
2	CO	D	492	1/1	0.99	0.03	15,15,15,15	0
2	CO	B	491	1/1	1.00	0.02	33,33,33,33	0
2	CO	C	492	1/1	1.00	0.02	15,15,15,15	0

6.5 Other polymers [i](#)

There are no such residues in this entry.