



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 03:02 AM GMT

PDB ID : 3M0M
Title : Crystal structure of Pseudomonas stutzeri L-rhamnose isomerase mutant S329F in complex with D-allose
Authors : Yoshida, H.; Takeda, K.; Izumori, K.; Kamitori, S.
Deposited on : 2010-03-03
Resolution : 1.45 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>

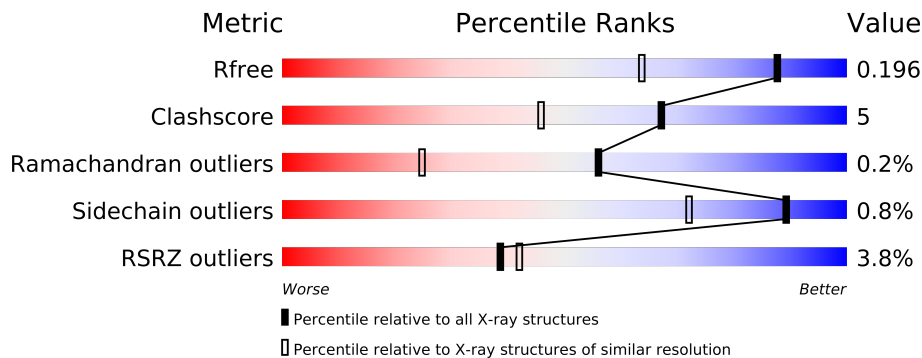
The following versions of software and data (see [references](#)) were used in the production of this report:

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 1.45 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	2476 (1.50-1.42)
Clashscore	79885	2834 (1.50-1.42)
Ramachandran outliers	78287	2769 (1.50-1.42)
Sidechain outliers	78261	2767 (1.50-1.42)
RSRZ outliers	66119	2477 (1.50-1.42)

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	438	
1	B	438	
1	C	438	
1	D	438	

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

Mol	Type	Chain	Res	Geometry	Electron density
3	AOS	A	3001	-	X
3	AOS	B	3002	-	X
3	AOS	C	3003	-	X
3	AOS	D	3004	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 14910 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 L-rhamnose isomerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	421	Total	C	N	O	S	0	0	0
			3265	2054	584	618	9			
1	B	421	Total	C	N	O	S	0	0	0
			3265	2054	584	618	9			
1	C	431	Total	C	N	O	S	0	0	0
			3326	2090	596	631	9			
1	D	419	Total	C	N	O	S	0	0	0
			3256	2048	582	617	9			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	150	ASN	ASP	ENGINEERED	UNP Q75WH8
A	329	PHE	SER	ENGINEERED	UNP Q75WH8
A	431	GLY	-	EXPRESSION TAG	UNP Q75WH8
A	432	SER	-	EXPRESSION TAG	UNP Q75WH8
A	433	HIS	-	EXPRESSION TAG	UNP Q75WH8
A	434	HIS	-	EXPRESSION TAG	UNP Q75WH8
A	435	HIS	-	EXPRESSION TAG	UNP Q75WH8
A	436	HIS	-	EXPRESSION TAG	UNP Q75WH8
A	437	HIS	-	EXPRESSION TAG	UNP Q75WH8
A	438	HIS	-	EXPRESSION TAG	UNP Q75WH8
B	150	ASN	ASP	ENGINEERED	UNP Q75WH8
B	329	PHE	SER	ENGINEERED	UNP Q75WH8
B	431	GLY	-	EXPRESSION TAG	UNP Q75WH8
B	432	SER	-	EXPRESSION TAG	UNP Q75WH8
B	433	HIS	-	EXPRESSION TAG	UNP Q75WH8
B	434	HIS	-	EXPRESSION TAG	UNP Q75WH8
B	435	HIS	-	EXPRESSION TAG	UNP Q75WH8
B	436	HIS	-	EXPRESSION TAG	UNP Q75WH8
B	437	HIS	-	EXPRESSION TAG	UNP Q75WH8
B	438	HIS	-	EXPRESSION TAG	UNP Q75WH8
C	150	ASN	ASP	ENGINEERED	UNP Q75WH8

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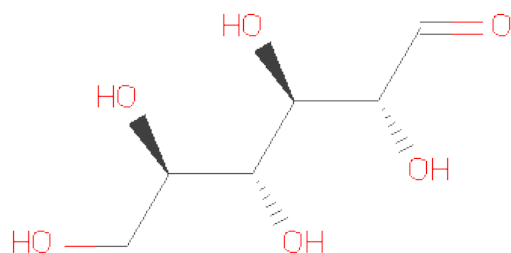
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Chain	Residue	Modelled	Actual	Comment	Reference
C	329	PHE	SER	ENGINEERED	UNP Q75WH8
C	431	GLY	-	EXPRESSION TAG	UNP Q75WH8
C	432	SER	-	EXPRESSION TAG	UNP Q75WH8
C	433	HIS	-	EXPRESSION TAG	UNP Q75WH8
C	434	HIS	-	EXPRESSION TAG	UNP Q75WH8
C	435	HIS	-	EXPRESSION TAG	UNP Q75WH8
C	436	HIS	-	EXPRESSION TAG	UNP Q75WH8
C	437	HIS	-	EXPRESSION TAG	UNP Q75WH8
C	438	HIS	-	EXPRESSION TAG	UNP Q75WH8
D	150	ASN	ASP	ENGINEERED	UNP Q75WH8
D	329	PHE	SER	ENGINEERED	UNP Q75WH8
D	431	GLY	-	EXPRESSION TAG	UNP Q75WH8
D	432	SER	-	EXPRESSION TAG	UNP Q75WH8
D	433	HIS	-	EXPRESSION TAG	UNP Q75WH8
D	434	HIS	-	EXPRESSION TAG	UNP Q75WH8
D	435	HIS	-	EXPRESSION TAG	UNP Q75WH8
D	436	HIS	-	EXPRESSION TAG	UNP Q75WH8
D	437	HIS	-	EXPRESSION TAG	UNP Q75WH8
D	438	HIS	-	EXPRESSION TAG	UNP Q75WH8

- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

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

- Molecule 3 is SUGAR (D-ALLOSE) (three-letter code: AOS) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			12	6	6		
3	B	1	Total	C	O	0	0
			12	6	6		
3	C	1	Total	C	O	0	0
			12	6	6		
3	D	1	Total	C	O	0	0
			12	6	6		

- Molecule 4 is water.

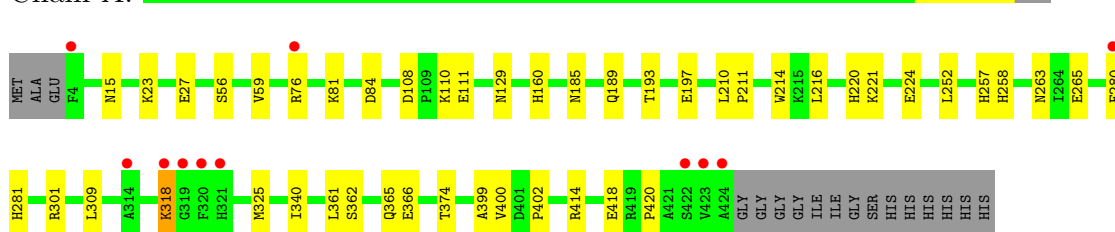
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	452	Total	O	0	0
			452	452		
4	B	448	Total	O	0	0
			448	448		
4	C	397	Total	O	0	0
			397	397		
4	D	445	Total	O	0	0
			445	445		

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.

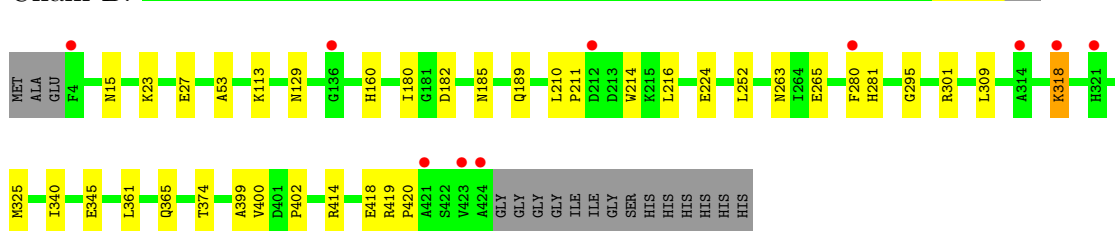
- Molecule 1: L-rhamnose isomerase

Chain A:



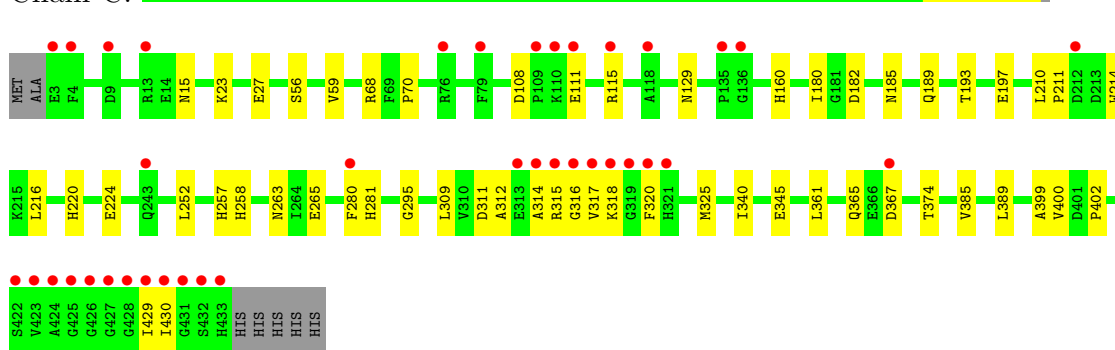
- Molecule 1: L-rhamnose isomerase

Chain B:



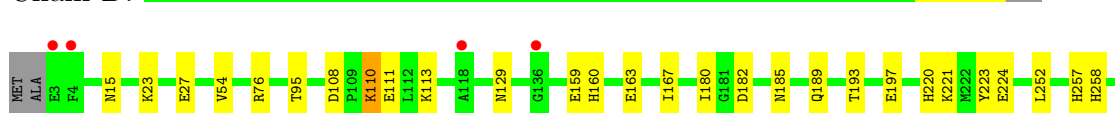
- Molecule 1: L-rhamnose isomerase

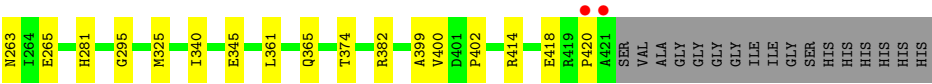
Chain C:



- Molecule 1: L-rhamnose isomerase

Chain D:





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	74.62Å 104.26Å 111.45Å 90.00° 106.20° 90.00°	Depositor
Resolution (Å)	30.10 – 1.45 30.10 – 1.45	Depositor EDS
% Data completeness (in resolution range)	95.2 (30.10-1.45) 95.4 (30.10-1.45)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.81 (at 1.45Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.177 , 0.196 0.177 , 0.196	Depositor DCC
R_{free} test set	27405 reflections (9.97%)	DCC
Wilson B-factor (Å ²)	12.1	Xtriage
Anisotropy	0.170	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 39.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 286909 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	14910	wwPDB-VP
Average B, all atoms (Å ²)	15.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.51% 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: MN, AOS

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	0.29	0/3338	0.56	0/4526
1	B	0.29	0/3338	0.54	0/4526
1	C	0.28	0/3400	0.53	0/4608
1	D	0.29	0/3329	0.54	0/4513
All	All	0.29	0/13405	0.54	0/18173

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	3265	0	3169	36	0
1	B	3265	0	3169	24	0
1	C	3326	0	3224	37	0
1	D	3256	0	3156	29	0
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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	12	0	10	1	0
3	B	12	0	10	1	0
3	C	12	0	10	2	0
3	D	12	0	10	2	0
4	A	452	0	0	3	0
4	B	448	0	0	2	0
4	C	397	0	0	0	0
4	D	445	0	0	1	0
All	All	14910	0	12758	129	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 5.

All (129) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:76:ARG:HD3	1:A:420:PRO:HD2	1.39	1.03
1:C:68:ARG:HH12	1:C:70:PRO:HB3	1.36	0.88
1:B:129:ASN:H	1:B:160:HIS:HE1	1.22	0.87
1:A:129:ASN:H	1:A:160:HIS:HE1	1.17	0.87
1:C:129:ASN:H	1:C:160:HIS:HE1	1.21	0.85
1:C:317:VAL:O	1:C:320:PHE:HB3	1.79	0.82
1:A:129:ASN:H	1:A:160:HIS:CE1	2.00	0.80
1:D:129:ASN:H	1:D:160:HIS:HE1	1.26	0.80
1:A:56:SER:O	1:A:59:VAL:HG12	1.85	0.76
1:C:129:ASN:H	1:C:160:HIS:CE1	2.04	0.75
1:B:129:ASN:H	1:B:160:HIS:CE1	2.06	0.73
1:D:129:ASN:H	1:D:160:HIS:CE1	2.07	0.72
1:D:163:GLU:O	1:D:167:ILE:HD13	1.90	0.72
1:A:362:SER:O	1:A:366:GLU:HG3	1.91	0.71
1:D:220:HIS:HE2	1:D:258:HIS:CE1	2.10	0.69
1:C:220:HIS:HE2	1:C:258:HIS:CE1	2.11	0.69
1:A:220:HIS:HE2	1:A:258:HIS:CE1	2.12	0.67
1:C:210:LEU:HD11	1:C:216:LEU:HB2	1.78	0.64
1:A:59:VAL:HG21	1:A:84:ASP:HB2	1.80	0.64
1:B:185:ASN:H	1:B:189:GLN:HE22	1.45	0.64
1:A:15:ASN:ND2	1:A:400:VAL:H	1.95	0.64
1:A:76:ARG:CD	1:A:420:PRO:HD2	2.24	0.63
1:C:429:ILE:HG23	1:C:430:ILE:HG23	1.80	0.62
1:C:23:LYS:O	1:C:27:GLU:HG3	1.98	0.62
1:C:185:ASN:H	1:C:189:GLN:HE22	1.45	0.62
1:B:185:ASN:H	1:B:189:GLN:NE2	1.98	0.62
1:D:220:HIS:HE2	1:D:258:HIS:HE1	1.46	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:15:ASN:HD21	1:A:400:VAL:H	1.47	0.61
1:C:68:ARG:NH1	1:C:70:PRO:HB3	2.10	0.60
1:A:185:ASN:H	1:A:189:GLN:HE22	1.47	0.60
1:B:23:LYS:O	1:B:27:GLU:HG3	2.02	0.60
1:A:220:HIS:HE2	1:A:258:HIS:HE1	1.51	0.59
1:B:15:ASN:ND2	1:B:400:VAL:H	2.01	0.58
1:D:23:LYS:O	1:D:27:GLU:HG3	2.03	0.58
1:D:15:ASN:ND2	1:D:400:VAL:H	2.02	0.58
1:B:414:ARG:O	1:B:418:GLU:HG3	2.04	0.57
1:C:312:ALA:HB1	1:C:317:VAL:HG21	1.86	0.57
1:C:185:ASN:H	1:C:189:GLN:NE2	2.03	0.57
1:D:108:ASP:OD2	1:D:111:GLU:HG3	2.04	0.57
1:A:318:LYS:O	1:A:318:LYS:HD3	2.05	0.57
1:A:185:ASN:H	1:A:189:GLN:NE2	2.02	0.57
1:B:295:GLY:HA3	1:B:345:GLU:HG2	1.86	0.56
1:C:220:HIS:HE2	1:C:258:HIS:HE1	1.53	0.56
1:D:185:ASN:H	1:D:189:GLN:NE2	2.04	0.56
1:D:185:ASN:H	1:D:189:GLN:HE22	1.52	0.56
1:B:361:LEU:O	1:B:365:GLN:HG3	2.06	0.55
1:A:280:PHE:CE2	1:A:309:LEU:HD21	2.41	0.55
1:C:312:ALA:O	1:C:317:VAL:HG22	2.06	0.55
1:B:15:ASN:HD21	1:B:399:ALA:HA	1.72	0.55
1:A:210:LEU:HD11	1:A:216:LEU:HB2	1.89	0.55
1:D:110:LYS:HD2	1:D:110:LYS:N	2.21	0.54
1:C:15:ASN:ND2	1:C:400:VAL:H	2.06	0.54
1:D:15:ASN:HD21	1:D:399:ALA:HA	1.73	0.54
1:C:15:ASN:HD21	1:C:399:ALA:HA	1.74	0.53
1:D:361:LEU:O	1:D:365:GLN:HG3	2.09	0.53
1:D:54:VAL:HG13	1:D:95:THR:HB	1.90	0.53
1:B:340:ILE:HG21	1:B:402:PRO:HB2	1.91	0.52
1:B:211:PRO:HD2	1:B:214:TRP:CG	2.44	0.52
1:C:340:ILE:HG21	1:C:402:PRO:HB2	1.92	0.51
1:B:15:ASN:HD21	1:B:400:VAL:H	1.57	0.51
1:D:193:THR:O	1:D:197:GLU:HG3	2.10	0.51
1:C:56:SER:O	1:C:59:VAL:HG22	2.11	0.51
1:A:108:ASP:HB3	1:A:111:GLU:HG3	1.91	0.50
1:D:295:GLY:HA3	1:D:345:GLU:HG2	1.94	0.50
4:A:577:HOH:O	1:D:382:ARG:HD3	2.12	0.50
1:C:295:GLY:HA3	1:C:345:GLU:HG2	1.93	0.50
1:D:15:ASN:HD21	1:D:400:VAL:H	1.59	0.49
1:B:113:LYS:HE2	4:B:1288:HOH:O	2.12	0.49
1:D:257:HIS:HE1	3:D:3004:AOS:H2	1.78	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:414:ARG:O	1:D:418:GLU:HG3	2.13	0.49
1:C:317:VAL:HG23	1:C:317:VAL:O	2.13	0.48
1:C:311:ASP:O	1:C:315:ARG:HG2	2.13	0.48
1:A:263:ASN:OD1	1:A:265:GLU:HG2	2.14	0.48
1:C:108:ASP:OD2	1:C:111:GLU:HG3	2.14	0.48
1:A:361:LEU:O	1:A:365:GLN:HG3	2.14	0.48
1:D:221:LYS:HA	1:D:257:HIS:HB3	1.96	0.48
1:C:318:LYS:C	1:C:320:PHE:H	2.16	0.47
1:A:211:PRO:HD2	1:A:214:TRP:CG	2.49	0.47
1:C:193:THR:O	1:C:197:GLU:HG3	2.14	0.47
1:B:53:ALA:HB3	1:B:325:MET:HG2	1.96	0.47
1:C:211:PRO:HD2	1:C:214:TRP:CG	2.50	0.47
1:A:252:LEU:HD21	1:A:281:HIS:CG	2.50	0.47
1:A:108:ASP:OD2	1:A:110:LYS:HB2	2.14	0.47
1:D:180:ILE:HD12	1:D:182:ASP:CG	2.36	0.46
1:A:340:ILE:HG21	1:A:402:PRO:HB2	1.97	0.46
1:A:257:HIS:HE1	3:A:3001:AOS:H2	1.81	0.46
1:D:159:GLU:O	1:D:163:GLU:HG3	2.16	0.46
1:A:280:PHE:CZ	1:A:309:LEU:HD21	2.52	0.45
1:A:15:ASN:HD21	1:A:399:ALA:HA	1.82	0.45
1:A:108:ASP:OD2	1:A:111:GLU:HG3	2.16	0.45
1:C:252:LEU:HD21	1:C:281:HIS:CG	2.52	0.45
1:C:15:ASN:HD21	1:C:400:VAL:H	1.63	0.45
1:B:340:ILE:CG2	1:B:402:PRO:HB2	2.47	0.45
1:A:110:LYS:HE2	4:A:1706:HOH:O	2.17	0.45
1:D:340:ILE:HG21	1:D:402:PRO:HB2	1.98	0.45
3:B:3002:AOS:H1	3:B:3002:AOS:H4	1.79	0.45
1:A:414:ARG:O	1:A:418:GLU:HG3	2.17	0.45
3:C:3003:AOS:H1	3:C:3003:AOS:H4	1.75	0.45
1:C:361:LEU:O	1:C:365:GLN:HG3	2.17	0.44
1:D:263:ASN:OD1	1:D:265:GLU:HG2	2.18	0.44
1:A:23:LYS:O	1:A:27:GLU:HG3	2.18	0.44
1:C:340:ILE:CG2	1:C:402:PRO:HB2	2.48	0.44
1:A:221:LYS:HA	1:A:257:HIS:HB3	1.99	0.44
1:B:280:PHE:CE2	1:B:309:LEU:HD21	2.54	0.43
1:B:252:LEU:HD21	1:B:281:HIS:CG	2.54	0.43
1:C:257:HIS:HE1	3:C:3003:AOS:H2	1.84	0.43
1:C:385:VAL:O	1:C:389:LEU:HD13	2.18	0.43
1:B:419:ARG:HA	1:B:420:PRO:HD3	1.87	0.43
1:C:263:ASN:OD1	1:C:265:GLU:HG2	2.19	0.42
1:C:317:VAL:O	1:C:320:PHE:CB	2.59	0.42
1:D:221:LYS:HE2	1:D:223:TYR:O	2.19	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:252:LEU:HD21	1:D:281:HIS:CG	2.53	0.42
1:A:193:THR:O	1:A:197:GLU:HG3	2.19	0.42
1:C:314:ALA:C	1:C:316:GLY:H	2.21	0.42
1:B:210:LEU:HD11	1:B:216:LEU:HB2	2.00	0.42
1:A:59:VAL:HG21	1:A:84:ASP:CB	2.47	0.42
1:B:263:ASN:OD1	1:B:265:GLU:HG2	2.20	0.42
1:C:280:PHE:CE2	1:C:309:LEU:HD21	2.55	0.42
1:C:115:ARG:HA	1:C:115:ARG:HD2	1.90	0.41
1:A:59:VAL:CG1	1:A:81:LYS:HG2	2.50	0.41
1:B:301:ARG:HD3	4:B:518:HOH:O	2.20	0.41
1:D:113:LYS:HE2	4:D:970:HOH:O	2.20	0.41
1:D:76:ARG:HD3	1:D:420:PRO:CD	2.51	0.41
1:B:318:LYS:O	1:B:318:LYS:HD3	2.21	0.41
1:A:129:ASN:N	1:A:160:HIS:HE1	1.99	0.41
1:A:301:ARG:HD3	4:A:685:HOH:O	2.20	0.41
1:B:180:ILE:HD12	1:B:182:ASP:CG	2.41	0.41
1:C:180:ILE:HD12	1:C:182:ASP:CG	2.41	0.40
3:D:3004:AOS:H4	3:D:3004:AOS:H1	1.84	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	419/438 (96%)	410 (98%)	8 (2%)	1 (0%)	56	25
1	B	419/438 (96%)	409 (98%)	9 (2%)	1 (0%)	56	25
1	C	429/438 (98%)	415 (97%)	13 (3%)	1 (0%)	56	25
1	D	417/438 (95%)	408 (98%)	8 (2%)	1 (0%)	56	25
All	All	1684/1752 (96%)	1642 (98%)	38 (2%)	4 (0%)	56	25

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	224	GLU
1	B	224	GLU
1	C	224	GLU
1	D	224	GLU

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	330/341 (97%)	327 (99%)	3 (1%)	87	68
1	B	330/341 (97%)	328 (99%)	2 (1%)	92	79
1	C	335/341 (98%)	332 (99%)	3 (1%)	87	68
1	D	329/341 (96%)	326 (99%)	3 (1%)	87	68
All	All	1324/1364 (97%)	1313 (99%)	11 (1%)	89	72

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

Mol	Chain	Res	Type
1	A	318	LYS
1	A	325	MET
1	A	374	THR
1	B	318	LYS
1	B	374	THR
1	C	325	MET
1	C	367	ASP
1	C	374	THR
1	D	110	LYS
1	D	325	MET
1	D	374	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	15	ASN
1	A	150	ASN
1	A	160	HIS

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Mol	Chain	Res	Type
1	A	189	GLN
1	A	258	HIS
1	A	344	ASN
1	B	15	ASN
1	B	160	HIS
1	B	189	GLN
1	B	243	GLN
1	B	321	HIS
1	B	344	ASN
1	C	15	ASN
1	C	160	HIS
1	C	189	GLN
1	C	258	HIS
1	C	344	ASN
1	D	15	ASN
1	D	160	HIS
1	D	189	GLN
1	D	258	HIS
1	D	324	HIS
1	D	344	ASN

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 12 ligands modelled in this entry, 8 are monoatomic - leaving 4 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	$\# Z > 2$
3	AOS	A	3001	2	11,11,11	0.53	0	14,14,14	0.84	1 (7%)
3	AOS	B	3002	2	11,11,11	0.51	0	14,14,14	0.78	1 (7%)
3	AOS	C	3003	2	11,11,11	0.51	0	14,14,14	0.74	1 (7%)
3	AOS	D	3004	2	11,11,11	0.54	0	14,14,14	0.96	1 (7%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	AOS	A	3001	2	-	0/15/16/16	0/0/0/0
3	AOS	B	3002	2	-	0/15/16/16	0/0/0/0
3	AOS	C	3003	2	-	0/15/16/16	0/0/0/0
3	AOS	D	3004	2	-	0/15/16/16	0/0/0/0

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	3001	AOS	O1-C1-C2	-2.17	118.94	125.31
3	D	3004	AOS	O1-C1-C2	-2.15	118.99	125.31
3	B	3002	AOS	O1-C1-C2	-2.08	119.19	125.31
3	C	3003	AOS	O1-C1-C2	-2.03	119.35	125.31

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	421/438 (96%)	0.10	11 (2%) 53 58	8, 13, 23, 40	0
1	B	421/438 (96%)	0.08	10 (2%) 56 62	8, 13, 24, 36	0
1	C	431/438 (98%)	0.49	38 (8%) 10 11	8, 16, 31, 45	0
1	D	419/438 (95%)	0.07	6 (1%) 72 78	7, 13, 23, 43	0
All	All	1692/1752 (96%)	0.19	65 (3%) 38 42	7, 13, 26, 45	0

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	317	VAL	9.1
1	C	319	GLY	8.5
1	C	428	GLY	6.5
1	C	318	LYS	6.1
1	C	432	SER	6.1
1	D	3	GLU	5.4
1	C	433	HIS	5.3
1	C	316	GLY	5.2
1	D	421	ALA	5.0
1	C	3	GLU	4.7
1	A	318	LYS	4.5
1	C	430	ILE	4.5
1	C	320	PHE	4.5
1	C	136	GLY	4.4
1	B	423	VAL	4.4
1	C	4	PHE	4.3
1	C	426	GLY	4.3
1	C	427	GLY	4.2
1	C	424	ALA	4.2
1	D	4	PHE	4.2
1	B	4	PHE	4.0

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Mol	Chain	Res	Type	RSRZ
1	C	321	HIS	4.0
1	A	424	ALA	3.7
1	C	135	PRO	3.6
1	A	423	VAL	3.5
1	B	424	ALA	3.4
1	C	110	LYS	3.4
1	A	320	PHE	3.4
1	C	431	GLY	3.4
1	A	422	SER	3.3
1	C	423	VAL	3.3
1	C	76	ARG	3.2
1	A	280	PHE	3.2
1	C	315	ARG	3.1
1	A	4	PHE	3.1
1	A	321	HIS	3.1
1	B	136	GLY	3.0
1	C	314	ALA	2.9
1	C	422	SER	2.9
1	C	425	GLY	2.8
1	A	76	ARG	2.8
1	B	318	LYS	2.8
1	D	136	GLY	2.7
1	B	280	PHE	2.7
1	C	79	PHE	2.6
1	D	420	PRO	2.5
1	C	367	ASP	2.5
1	C	115	ARG	2.4
1	B	321	HIS	2.4
1	A	319	GLY	2.4
1	C	280	PHE	2.4
1	C	109	PRO	2.3
1	C	118	ALA	2.3
1	B	421	ALA	2.3
1	C	429	ILE	2.3
1	C	243	GLN	2.3
1	C	212	ASP	2.2
1	C	9	ASP	2.2
1	C	111	GLU	2.1
1	C	13	ARG	2.1
1	A	314	ALA	2.0
1	C	313	GLU	2.0
1	B	212	ASP	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	314	ALA	2.0
1	D	118	ALA	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
3	AOS	B	3002	12/12	0.13	5.39	12,16,19,21	0
3	AOS	C	3003	12/12	0.13	2.27	16,20,22,23	0
3	AOS	D	3004	12/12	0.13	2.10	13,15,16,17	0
3	AOS	A	3001	12/12	0.12	2.02	12,15,19,20	0
2	MN	D	507	1/1	0.05	-2.18	11,11,11,11	0
2	MN	B	503	1/1	0.05	-2.90	12,12,12,12	0
2	MN	C	505	1/1	0.04	-3.11	15,15,15,15	0
2	MN	C	506	1/1	0.03	-3.19	12,12,12,12	0
2	MN	A	501	1/1	0.04	-3.25	12,12,12,12	0
2	MN	A	502	1/1	0.02	-4.01	10,10,10,10	0
2	MN	D	508	1/1	0.03	-4.21	9,9,9,9	0
2	MN	B	504	1/1	0.02	-8.01	10,10,10,10	0

6.5 Other polymers ⓘ

There are no such residues in this entry.