



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 24, 2021 – 12:43 PM EST

PDB ID : 2PPG
Title : Crystal structure of putative isomerase from *Sinorhizobium meliloti*
Authors : Ramagopal, U.A.; Toro, R.; Dickey, M.; Logan, C.; Groshong, C.; Sauder, J.M.; Burley, S.K.; Almo, S.C.; New York SGX Research Center for Structural Genomics (NYSGXRC)
Deposited on : 2007-04-30
Resolution : 2.49 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.16
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) : 2.16

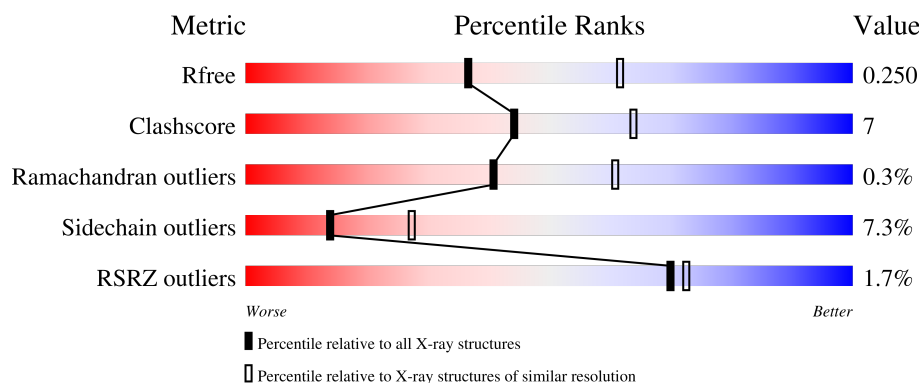
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.49 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	399	<div> <div>2%</div> <div>80%</div> <div>16%</div> <div>• •</div> </div>
1	B	399	<div> <div>2%</div> <div>74%</div> <div>17%</div> <div>• 7%</div> </div>
1	C	399	<div> <div>2%</div> <div>78%</div> <div>16%</div> <div>• •</div> </div>
1	D	399	<div> <div>2%</div> <div>77%</div> <div>17%</div> <div>• •</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 11799 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 Putative isomerase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	387	Total	C	N	O	S	Se	0	1	0
			2979	1891	533	542	4	9			
1	B	370	Total	C	N	O	S	Se	0	0	0
			2845	1807	514	511	4	9			
1	C	382	Total	C	N	O	S	Se	0	0	0
			2913	1848	523	529	4	9			
1	D	383	Total	C	N	O	S	Se	0	0	0
			2928	1856	527	532	4	9			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MSE	-	cloning artifact	UNP Q92ZS5
A	0	SER	-	cloning artifact	UNP Q92ZS5
A	1	LEU	-	cloning artifact	UNP Q92ZS5
A	79	MSE	MET	modified residue	UNP Q92ZS5
A	109	MSE	MET	modified residue	UNP Q92ZS5
A	199	MSE	MET	modified residue	UNP Q92ZS5
A	216	MSE	MET	modified residue	UNP Q92ZS5
A	232	MSE	MET	modified residue	UNP Q92ZS5
A	275	MSE	MET	modified residue	UNP Q92ZS5
A	291	MSE	MET	modified residue	UNP Q92ZS5
A	300	MSE	MET	modified residue	UNP Q92ZS5
A	359	MSE	MET	modified residue	UNP Q92ZS5
A	390	GLU	-	cloning artifact	UNP Q92ZS5
A	391	GLY	-	cloning artifact	UNP Q92ZS5
A	392	HIS	-	cloning artifact	UNP Q92ZS5
A	393	HIS	-	cloning artifact	UNP Q92ZS5
A	394	HIS	-	cloning artifact	UNP Q92ZS5
A	395	HIS	-	cloning artifact	UNP Q92ZS5
A	396	HIS	-	cloning artifact	UNP Q92ZS5
A	397	HIS	-	cloning artifact	UNP Q92ZS5
B	-1	MSE	-	cloning artifact	UNP Q92ZS5

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Chain	Residue	Modelled	Actual	Comment	Reference
B	0	SER	-	cloning artifact	UNP Q92ZS5
B	1	LEU	-	cloning artifact	UNP Q92ZS5
B	79	MSE	MET	modified residue	UNP Q92ZS5
B	109	MSE	MET	modified residue	UNP Q92ZS5
B	199	MSE	MET	modified residue	UNP Q92ZS5
B	216	MSE	MET	modified residue	UNP Q92ZS5
B	232	MSE	MET	modified residue	UNP Q92ZS5
B	275	MSE	MET	modified residue	UNP Q92ZS5
B	291	MSE	MET	modified residue	UNP Q92ZS5
B	300	MSE	MET	modified residue	UNP Q92ZS5
B	359	MSE	MET	modified residue	UNP Q92ZS5
B	390	GLU	-	cloning artifact	UNP Q92ZS5
B	391	GLY	-	cloning artifact	UNP Q92ZS5
B	392	HIS	-	cloning artifact	UNP Q92ZS5
B	393	HIS	-	cloning artifact	UNP Q92ZS5
B	394	HIS	-	cloning artifact	UNP Q92ZS5
B	395	HIS	-	cloning artifact	UNP Q92ZS5
B	396	HIS	-	cloning artifact	UNP Q92ZS5
B	397	HIS	-	cloning artifact	UNP Q92ZS5
C	-1	MSE	-	cloning artifact	UNP Q92ZS5
C	0	SER	-	cloning artifact	UNP Q92ZS5
C	1	LEU	-	cloning artifact	UNP Q92ZS5
C	79	MSE	MET	modified residue	UNP Q92ZS5
C	109	MSE	MET	modified residue	UNP Q92ZS5
C	199	MSE	MET	modified residue	UNP Q92ZS5
C	216	MSE	MET	modified residue	UNP Q92ZS5
C	232	MSE	MET	modified residue	UNP Q92ZS5
C	275	MSE	MET	modified residue	UNP Q92ZS5
C	291	MSE	MET	modified residue	UNP Q92ZS5
C	300	MSE	MET	modified residue	UNP Q92ZS5
C	359	MSE	MET	modified residue	UNP Q92ZS5
C	390	GLU	-	cloning artifact	UNP Q92ZS5
C	391	GLY	-	cloning artifact	UNP Q92ZS5
C	392	HIS	-	cloning artifact	UNP Q92ZS5
C	393	HIS	-	cloning artifact	UNP Q92ZS5
C	394	HIS	-	cloning artifact	UNP Q92ZS5
C	395	HIS	-	cloning artifact	UNP Q92ZS5
C	396	HIS	-	cloning artifact	UNP Q92ZS5
C	397	HIS	-	cloning artifact	UNP Q92ZS5
D	-1	MSE	-	cloning artifact	UNP Q92ZS5
D	0	SER	-	cloning artifact	UNP Q92ZS5
D	1	LEU	-	cloning artifact	UNP Q92ZS5

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Chain	Residue	Modelled	Actual	Comment	Reference
D	79	MSE	MET	modified residue	UNP Q92ZS5
D	109	MSE	MET	modified residue	UNP Q92ZS5
D	199	MSE	MET	modified residue	UNP Q92ZS5
D	216	MSE	MET	modified residue	UNP Q92ZS5
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D	390	GLU	-	cloning artifact	UNP Q92ZS5
D	391	GLY	-	cloning artifact	UNP Q92ZS5
D	392	HIS	-	cloning artifact	UNP Q92ZS5
D	393	HIS	-	cloning artifact	UNP Q92ZS5
D	394	HIS	-	cloning artifact	UNP Q92ZS5
D	395	HIS	-	cloning artifact	UNP Q92ZS5
D	396	HIS	-	cloning artifact	UNP Q92ZS5
D	397	HIS	-	cloning artifact	UNP Q92ZS5

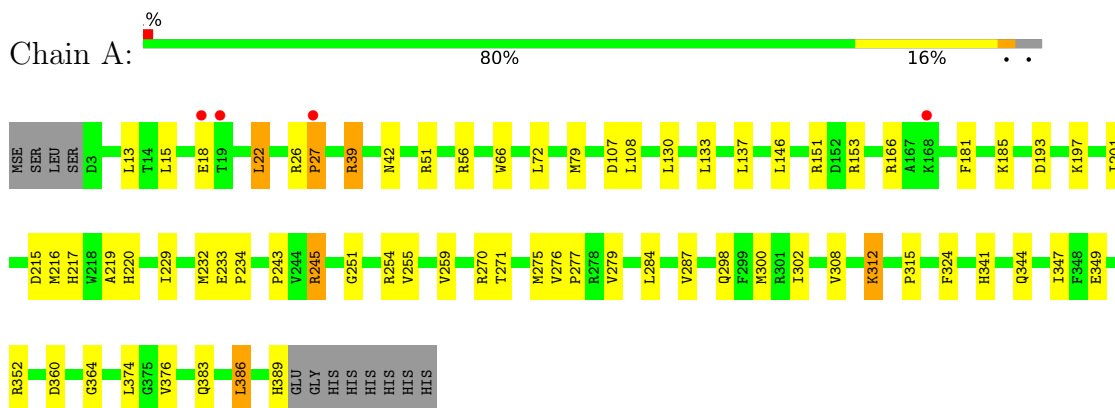
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	46	Total O 46 46	0	0
2	B	22	Total O 22 22	0	0
2	C	28	Total O 28 28	0	0
2	D	38	Total O 38 38	0	0

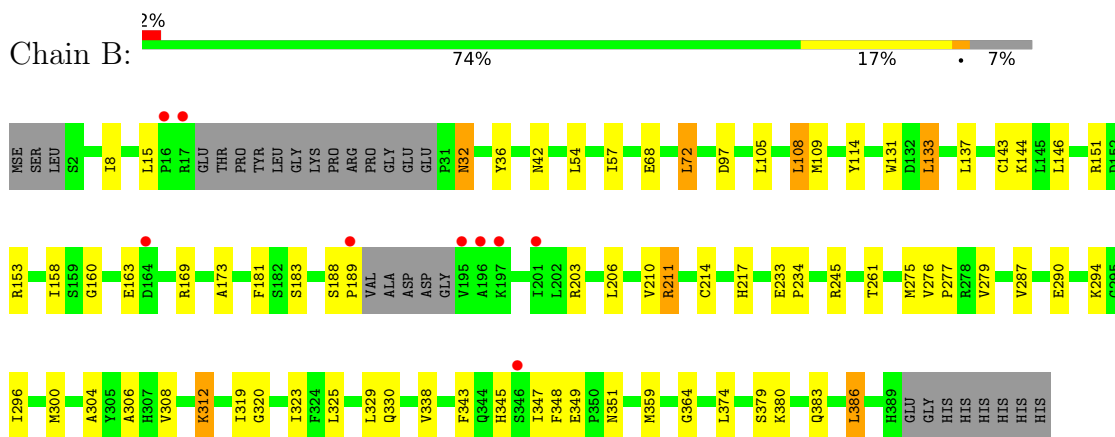
3 Residue-property plots [i](#)

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.

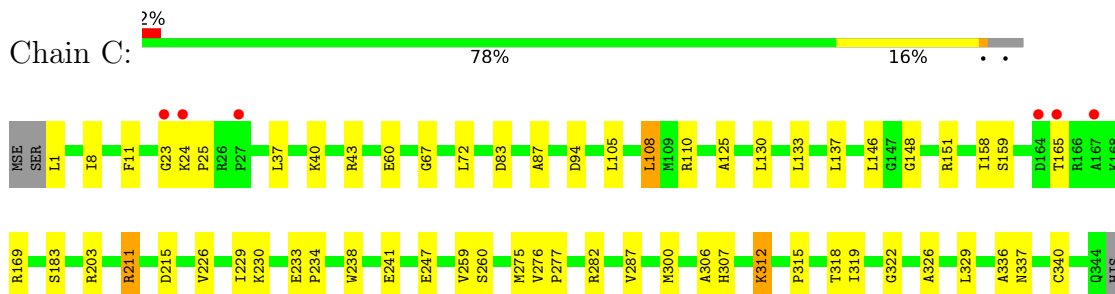
• Molecule 1: Putative isomerase



• Molecule 1: Putative isomerase

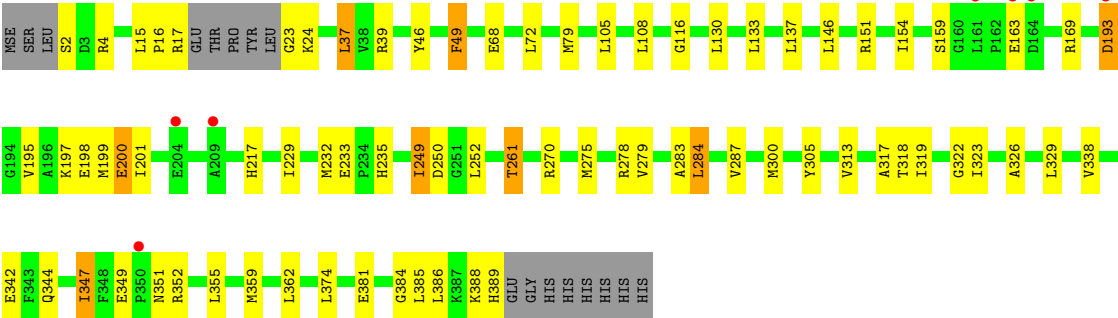
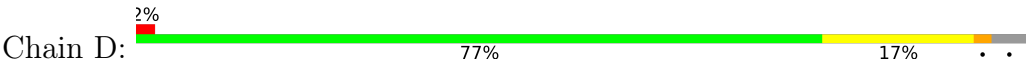


• Molecule 1: Putative isomerase





● Molecule 1: Putative isomerase



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	131.15Å 150.83Å 147.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.00 – 2.49 41.99 – 2.49	Depositor EDS
% Data completeness (in resolution range)	99.2 (42.00-2.49) 99.2 (41.99-2.49)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.49 (at 2.48Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.183 , 0.252 0.182 , 0.250	Depositor DCC
R_{free} test set	2581 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	37.3	Xtriage
Anisotropy	0.795	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 52.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	11799	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.65% 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](#)

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	0.44	0/3038	0.59	0/4109
1	B	0.42	0/2898	0.58	0/3912
1	C	0.43	0/2968	0.59	0/4013
1	D	0.41	0/2984	0.58	1/4034 (0.0%)
All	All	0.42	0/11888	0.59	1/16068 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	37	LEU	CA-CB-CG	5.71	128.44	115.30

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	2979	0	2970	36	0
1	B	2845	0	2851	46	0
1	C	2913	0	2904	37	0
1	D	2928	0	2916	40	0
2	A	46	0	0	0	0
2	B	22	0	0	2	0
2	C	28	0	0	0	0
2	D	38	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	11799	0	11641	154	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 7.

All (154) 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:A:216:MSE:HE2	1:A:232:MSE:HE1	1.29	1.14
1:D:329:LEU:HD12	1:D:359:MSE:HE2	1.33	1.09
1:C:329:LEU:HD12	1:C:359:MSE:HE2	1.12	1.08
1:D:326:ALA:HA	1:D:359:MSE:HE1	1.26	1.08
1:C:326:ALA:HA	1:C:359:MSE:HE1	1.26	1.07
1:B:325:LEU:HG	1:B:359:MSE:HE1	1.33	1.06
1:D:49:PHE:HD2	1:D:49:PHE:H	1.14	0.91
1:B:348:PHE:HE1	1:B:359:MSE:HE2	1.36	0.91
1:C:329:LEU:HD12	1:C:359:MSE:CE	2.00	0.90
1:D:326:ALA:CA	1:D:359:MSE:HE1	2.08	0.82
1:D:326:ALA:HA	1:D:359:MSE:CE	2.11	0.80
1:B:319:ILE:HA	1:B:347:ILE:HG21	1.65	0.79
1:C:329:LEU:CD1	1:C:359:MSE:HE2	2.05	0.76
1:B:348:PHE:CE1	1:B:359:MSE:HE2	2.23	0.74
1:A:383:GLN:HA	1:A:386:LEU:HD22	1.71	0.72
1:B:325:LEU:CG	1:B:359:MSE:HE1	2.16	0.71
1:B:183:SER:OG	1:B:211:ARG:NH1	2.26	0.68
1:B:8:ILE:HG12	1:B:57:ILE:HG12	1.76	0.67
1:A:107:ASP:OD2	1:C:43:ARG:NH2	2.26	0.66
1:C:322:GLY:HA3	1:C:355:LEU:HD11	1.77	0.65
1:D:329:LEU:CD1	1:D:359:MSE:HE2	2.20	0.63
1:A:216:MSE:HE1	1:A:229:ILE:HG12	1.81	0.63
1:D:349:GLU:OE2	1:D:352:ARG:NH1	2.32	0.62
1:C:215:ASP:HA	1:C:241:GLU:HB3	1.83	0.61
1:B:320:GLY:O	1:B:351:ASN:ND2	2.33	0.60
1:B:189:PRO:HG2	1:B:217:HIS:HB2	1.83	0.60
1:D:193:ASP:N	1:D:193:ASP:OD2	2.33	0.60
1:A:26:ARG:HB3	1:A:27:PRO:HD2	1.83	0.59
1:B:383:GLN:HA	1:B:386:LEU:HD22	1.84	0.59
1:C:247:GLU:H	1:C:247:GLU:CD	2.07	0.58
1:A:193:ASP:HB3	1:A:197:LYS:HD2	1.85	0.57
1:C:183:SER:OG	1:C:211:ARG:NH1	2.38	0.57
1:B:133:LEU:O	1:B:137:LEU:HB2	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:24:LYS:N	1:C:25:PRO:HD3	2.19	0.57
1:D:163:GLU:HB2	1:D:169:ARG:HG2	1.86	0.57
1:D:322:GLY:HA3	1:D:355:LEU:HD11	1.86	0.56
1:D:49:PHE:CD2	1:D:49:PHE:N	2.66	0.56
1:B:144:LYS:NZ	1:C:94:ASP:OD2	2.35	0.56
1:B:290:GLU:H	1:B:294:LYS:NZ	2.04	0.55
1:A:79:MSE:SE	1:A:389:HIS:HB2	2.57	0.54
1:A:216:MSE:HE2	1:A:232:MSE:CE	2.19	0.54
1:D:197:LYS:HA	1:D:200:GLU:HB3	1.90	0.54
1:D:23:GLY:HA2	1:D:24:LYS:CB	2.38	0.54
1:A:276:VAL:HB	1:A:277:PRO:HD3	1.90	0.54
1:C:326:ALA:CA	1:C:359:MSE:HE1	2.18	0.54
1:B:32:ASN:ND2	1:B:36:TYR:H	2.06	0.54
1:A:352:ARG:NH2	1:A:360:ASP:OD1	2.41	0.53
1:B:143:CYS:HB3	1:B:330:GLN:O	2.08	0.53
1:D:344:GLN:HB2	1:D:347:ILE:HG12	1.90	0.53
1:A:271:THR:HA	1:A:298:GLN:HG3	1.90	0.53
1:D:163:GLU:HB2	1:D:169:ARG:CG	2.38	0.53
1:D:68:GLU:HB2	1:D:323:ILE:HB	1.91	0.52
1:A:166:ARG:HG2	1:A:201:ILE:HG21	1.90	0.52
1:B:109:MSE:HE3	1:B:114:TYR:CD2	2.43	0.52
1:D:79:MSE:SE	1:D:389:HIS:HB2	2.60	0.52
1:A:271:THR:HA	1:A:298:GLN:CG	2.39	0.52
1:D:198:GLU:O	1:D:201:ILE:HG22	2.10	0.52
1:D:275:MSE:SE	1:D:287:VAL:HG11	2.60	0.51
1:B:329:LEU:HD11	1:B:359:MSE:HE3	1.93	0.51
1:C:359:MSE:HE3	1:C:369:PRO:HG3	1.92	0.51
1:A:315:PRO:HB2	1:A:341:HIS:CD2	2.47	0.50
1:C:83:ASP:OD2	1:C:389:HIS:ND1	2.19	0.50
1:B:276:VAL:HB	1:B:277:PRO:HD3	1.94	0.49
1:C:146:LEU:HD22	1:C:300:MSE:HG3	1.94	0.49
1:C:23:GLY:CA	1:C:24:LYS:CB	2.89	0.49
1:D:317:ALA:HB1	1:D:347:ILE:HD13	1.94	0.49
1:A:22:LEU:HD22	1:A:39:ARG:HD3	1.95	0.49
1:B:290:GLU:H	1:B:294:LYS:HZ2	1.59	0.49
1:D:252:LEU:HG	1:D:283:ALA:HB1	1.95	0.48
1:B:68:GLU:HB2	1:B:323:ILE:HB	1.95	0.48
1:D:2:SER:OG	1:D:4:ARG:NH2	2.46	0.48
1:B:304:ALA:O	1:B:308:VAL:HG23	2.13	0.48
1:B:173:ALA:HB1	1:B:206:LEU:HD11	1.95	0.48
1:D:278:ARG:HB3	1:D:284:LEU:CD2	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:181:PHE:CD1	1:A:364:GLY:HA2	2.48	0.48
1:D:249:ILE:HG12	1:D:249:ILE:H	1.50	0.48
1:B:181:PHE:CD1	1:B:364:GLY:HA2	2.48	0.47
1:D:159:SER:HB2	1:D:342:GLU:HG3	1.95	0.47
1:D:146:LEU:HD22	1:D:300:MSE:HG3	1.97	0.47
1:A:233:GLU:N	1:A:234:PRO:HD2	2.29	0.47
1:B:275:MSE:HE1	1:B:306:ALA:HB2	1.96	0.47
1:C:383:GLN:HA	1:C:386:LEU:HD22	1.96	0.47
1:D:116:GLY:HA2	1:D:270:ARG:HG3	1.97	0.47
1:A:216:MSE:CE	1:A:232:MSE:HE1	2.22	0.46
1:A:13:LEU:O	1:A:51:ARG:HA	2.15	0.46
1:B:158:ILE:HD13	1:B:343:PHE:HD2	1.79	0.46
1:C:233:GLU:N	1:C:234:PRO:HD2	2.31	0.45
1:B:105:LEU:HA	1:B:108:LEU:HD22	1.98	0.45
1:B:163:GLU:HB2	1:B:169:ARG:HG2	1.98	0.45
1:A:185:LYS:HE3	1:A:215:ASP:HB2	1.98	0.45
1:C:226:VAL:O	1:C:230:LYS:HG3	2.16	0.45
1:D:199:MSE:HE3	1:D:235:HIS:HB2	1.97	0.45
1:A:275:MSE:SE	1:A:302:ILE:HG23	2.66	0.45
1:B:151:ARG:HH12	1:B:338:VAL:HB	1.82	0.45
1:B:54:LEU:HG	1:B:68:GLU:HG3	1.99	0.45
1:A:146:LEU:HB3	1:A:300:MSE:HE2	1.98	0.45
1:A:245:ARG:HG2	1:C:110:ARG:NH2	2.32	0.45
1:A:308:VAL:HG11	1:D:305:TYR:CE1	2.52	0.45
1:B:203:ARG:NH1	1:B:210:VAL:O	2.39	0.44
1:C:312:LYS:HD2	1:C:312:LYS:HA	1.66	0.44
1:A:151:ARG:HG2	1:A:153:ARG:O	2.17	0.44
1:C:8:ILE:HD12	1:C:87:ALA:HA	1.99	0.44
1:B:188:SER:HB3	1:B:214:CYS:SG	2.57	0.44
1:C:276:VAL:HB	1:C:277:PRO:HD3	2.00	0.44
1:B:379:SER:O	1:B:383:GLN:HG3	2.18	0.43
1:D:151:ARG:HD2	1:D:154:ILE:HD13	2.00	0.43
1:A:270:ARG:O	1:A:298:GLN:HG2	2.18	0.43
1:B:188:SER:OG	1:B:189:PRO:HD3	2.17	0.43
1:D:381:GLU:O	1:D:384:GLY:N	2.51	0.43
1:B:97:ASP:HA	1:C:148:GLY:HA3	2.01	0.43
1:D:229:ILE:HA	1:D:232:MSE:HE3	2.01	0.43
1:B:163:GLU:HB2	1:B:169:ARG:CG	2.49	0.43
1:B:319:ILE:HA	1:B:347:ILE:CG2	2.40	0.43
1:D:233:GLU:OE2	1:D:261:THR:HG22	2.18	0.43
1:B:32:ASN:HD21	1:B:36:TYR:H	1.66	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:200:GLU:HG3	1:D:201:ILE:N	2.34	0.42
1:A:251:GLY:O	1:A:255:VAL:HG23	2.19	0.42
1:C:307:HIS:HD2	1:C:336:ALA:HB3	1.84	0.42
1:C:337:ASN:N	1:C:337:ASN:OD1	2.52	0.42
1:D:313:VAL:O	1:D:338:VAL:HA	2.19	0.42
1:A:344:GLN:HB3	1:A:347:ILE:HD12	2.02	0.42
1:C:307:HIS:CD2	1:C:336:ALA:HB3	2.54	0.42
1:A:18:GLU:H	1:A:18:GLU:CD	2.22	0.42
1:A:56:ARG:HB2	1:A:66:TRP:CZ3	2.55	0.42
1:A:229:ILE:HA	1:A:232:MSE:HE3	2.01	0.42
1:A:255:VAL:O	1:A:259:VAL:HG22	2.19	0.42
1:B:345:HIS:CD2	1:B:345:HIS:H	2.37	0.42
1:A:220:HIS:HB2	1:A:243:PRO:O	2.20	0.41
1:C:203:ARG:HD3	1:C:203:ARG:HA	1.87	0.41
1:A:42:ASN:HD22	1:A:217:HIS:HD2	1.68	0.41
1:A:284:LEU:N	1:A:284:LEU:HD23	2.35	0.41
1:A:312:LYS:HA	1:A:312:LYS:HD2	1.81	0.41
1:C:105:LEU:HA	1:C:108:LEU:HD22	2.02	0.41
1:C:67:GLY:HA3	1:C:125:ALA:O	2.21	0.41
1:C:183:SER:HB3	1:C:238:TRP:CZ3	2.56	0.41
1:B:146:LEU:HD13	1:B:300:MSE:SE	2.71	0.41
1:B:233:GLU:N	1:B:234:PRO:CD	2.84	0.41
1:D:39:ARG:HD2	1:D:46:TYR:CE2	2.56	0.41
1:B:72:LEU:HD13	2:B:400:HOH:O	2.20	0.41
1:C:275:MSE:HE1	1:C:306:ALA:HB2	2.02	0.41
1:C:11:PHE:CD1	1:C:386:LEU:HB3	2.56	0.41
1:D:105:LEU:HA	1:D:105:LEU:HD23	1.85	0.41
1:D:116:GLY:CA	1:D:270:ARG:HG3	2.51	0.41
1:D:278:ARG:HB3	1:D:284:LEU:HD22	2.02	0.41
1:C:24:LYS:H	1:C:25:PRO:HD3	1.85	0.41
1:B:131:TRP:CD1	1:B:296:ILE:HB	2.56	0.41
1:C:229:ILE:HG21	1:C:259:VAL:HG21	2.02	0.40
1:C:315:PRO:HD2	1:C:340:CYS:O	2.20	0.40
1:C:165:THR:O	1:C:169:ARG:HG3	2.21	0.40
1:B:151:ARG:NH1	1:B:338:VAL:HB	2.36	0.40
1:B:245:ARG:NH1	2:B:398:HOH:O	2.37	0.40
1:B:312:LYS:HD2	1:B:312:LYS:HA	1.83	0.40
1:D:159:SER:OG	1:D:342:GLU:OE2	2.34	0.40
1:B:181:PHE:CE1	1:B:364:GLY:HA2	2.57	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	386/399 (97%)	366 (95%)	18 (5%)	2 (0%)	29	48
1	B	364/399 (91%)	343 (94%)	20 (6%)	1 (0%)	41	61
1	C	378/399 (95%)	361 (96%)	17 (4%)	0	100	100
1	D	379/399 (95%)	365 (96%)	13 (3%)	1 (0%)	41	61
All	All	1507/1596 (94%)	1435 (95%)	68 (4%)	4 (0%)	41	61

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	219	ALA
1	D	16	PRO
1	A	27	PRO
1	B	160	GLY

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	300/301 (100%)	282 (94%)	18 (6%)	19	37
1	B	287/301 (95%)	271 (94%)	16 (6%)	21	40
1	C	291/301 (97%)	267 (92%)	24 (8%)	11	22
1	D	294/301 (98%)	267 (91%)	27 (9%)	9	18
All	All	1172/1204 (97%)	1087 (93%)	85 (7%)	14	27

All (85) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	LEU
1	A	22	LEU
1	A	39	ARG
1	A	72	LEU
1	A	108	LEU
1	A	130	LEU
1	A	133	LEU
1	A	137	LEU
1	A	245	ARG
1	A	254	ARG
1	A	279	VAL
1	A	287	VAL
1	A	312	LYS
1	A	324	PHE
1	A	349	GLU
1	A	374	LEU
1	A	376	VAL
1	A	386	LEU
1	B	15	LEU
1	B	32	ASN
1	B	42	ASN
1	B	72	LEU
1	B	108	LEU
1	B	133	LEU
1	B	153	ARG
1	B	211	ARG
1	B	261	THR
1	B	279	VAL
1	B	287	VAL
1	B	312	LYS
1	B	349	GLU
1	B	374	LEU
1	B	380	LYS
1	B	386	LEU
1	C	1	LEU
1	C	37	LEU
1	C	40	LYS
1	C	60	GLU
1	C	72	LEU
1	C	108	LEU
1	C	130	LEU
1	C	133	LEU

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Mol	Chain	Res	Type
1	C	137	LEU
1	C	151	ARG
1	C	158	ILE
1	C	159	SER
1	C	211	ARG
1	C	260	SER
1	C	282	ARG
1	C	287	VAL
1	C	312	LYS
1	C	318	THR
1	C	319	ILE
1	C	355	LEU
1	C	362	LEU
1	C	374	LEU
1	C	386	LEU
1	C	388	LYS
1	D	15	LEU
1	D	17	ARG
1	D	37	LEU
1	D	49	PHE
1	D	72	LEU
1	D	108	LEU
1	D	130	LEU
1	D	133	LEU
1	D	137	LEU
1	D	193	ASP
1	D	195	VAL
1	D	200	GLU
1	D	217	HIS
1	D	249	ILE
1	D	250	ASP
1	D	261	THR
1	D	279	VAL
1	D	284	LEU
1	D	318	THR
1	D	319	ILE
1	D	347	ILE
1	D	351	ASN
1	D	362	LEU
1	D	374	LEU
1	D	385	LEU
1	D	386	LEU

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Mol	Chain	Res	Type
1	D	388	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	217	HIS
1	B	32	ASN
1	B	42	ASN
1	B	61	ASN
1	C	220	HIS
1	D	351	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](#)

There are no ligands in this entry.

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	378/399 (94%)	-0.38	4 (1%) 80 82	21, 34, 61, 89	0
1	B	361/399 (90%)	-0.06	9 (2%) 57 61	22, 40, 75, 86	0
1	C	373/399 (93%)	-0.23	6 (1%) 72 74	25, 38, 64, 81	0
1	D	374/399 (93%)	-0.21	7 (1%) 66 69	25, 39, 77, 98	0
All	All	1486/1596 (93%)	-0.22	26 (1%) 70 72	21, 38, 73, 98	0

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	350	PRO	5.3
1	C	27	PRO	4.7
1	B	201	ILE	3.7
1	D	164	ASP	3.5
1	C	167	ALA	3.3
1	D	163	GLU	3.3
1	B	164	ASP	2.9
1	B	17	ARG	2.8
1	A	27	PRO	2.8
1	B	195	VAL	2.7
1	D	204	GLU	2.6
1	B	189	PRO	2.6
1	C	165	THR	2.6
1	D	209	ALA	2.5
1	B	16	PRO	2.5
1	A	19	THR	2.4
1	B	197	LYS	2.3
1	C	24	LYS	2.2
1	C	23	GLY	2.2
1	B	196	ALA	2.1
1	D	161	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	346	SER	2.1
1	A	168	LYS	2.1
1	A	18	GLU	2.1
1	C	164	ASP	2.1
1	D	193	ASP	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.