



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 03:35 PM UTC

PDB ID : 1D2G / pdb_00001d2g
Title : CRYSTAL STRUCTURE OF R175K MUTANT GLYCINE N-METHYLTRANSFERASE FROM RAT LIVER
Authors : Huang, Y.; Komoto, J.; Takusagawa, F.; Konishi, K.; Takata, Y.
Deposited on : 1999-10-08
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	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

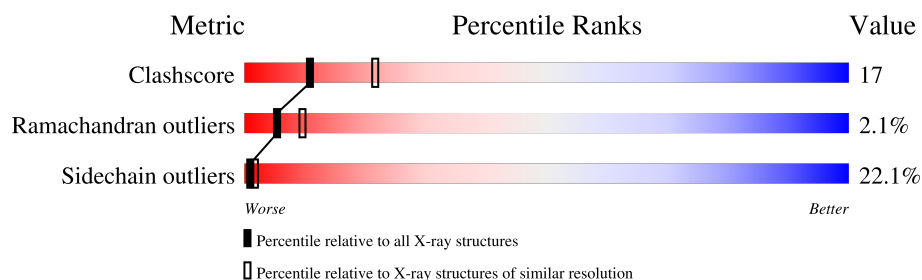
1 Overall quality at a glance

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))
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	292	 57% 31% 11% .
1	B	292	 58% 32% 9% .

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4884 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 GLYCINE N-METHYLTRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	292	Total	C	N	O	S	0	0	0
			2283	1450	397	425	11			
1	B	292	Total	C	N	O	S	0	0	0
			2283	1450	397	425	11			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	89	LYS	ARG	engineered mutation	UNP P13255
B	89	LYS	ARG	engineered mutation	UNP P13255

- Molecule 2 is water.

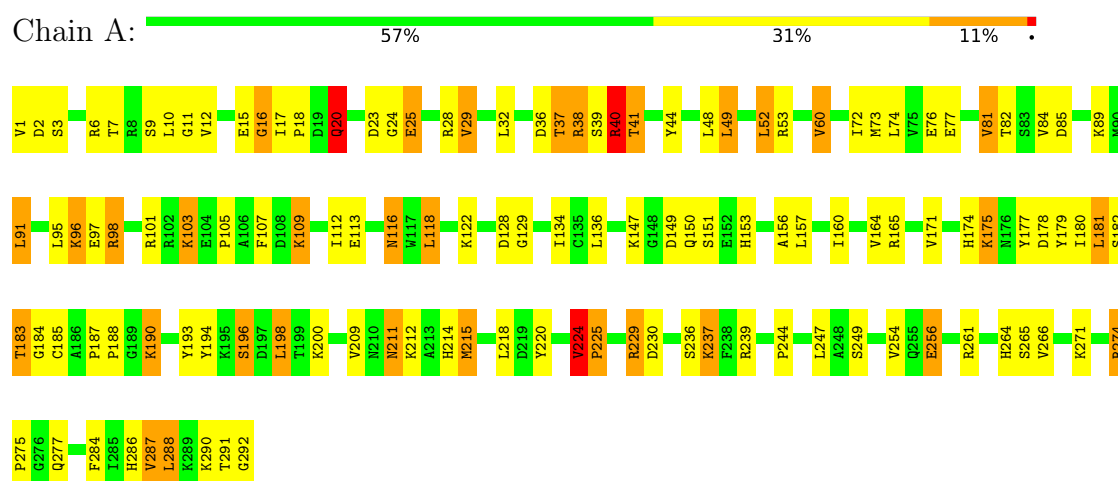
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	182	Total	O	0	0
			182	182		
2	B	136	Total	O	0	0
			136	136		

3 Residue-property plots

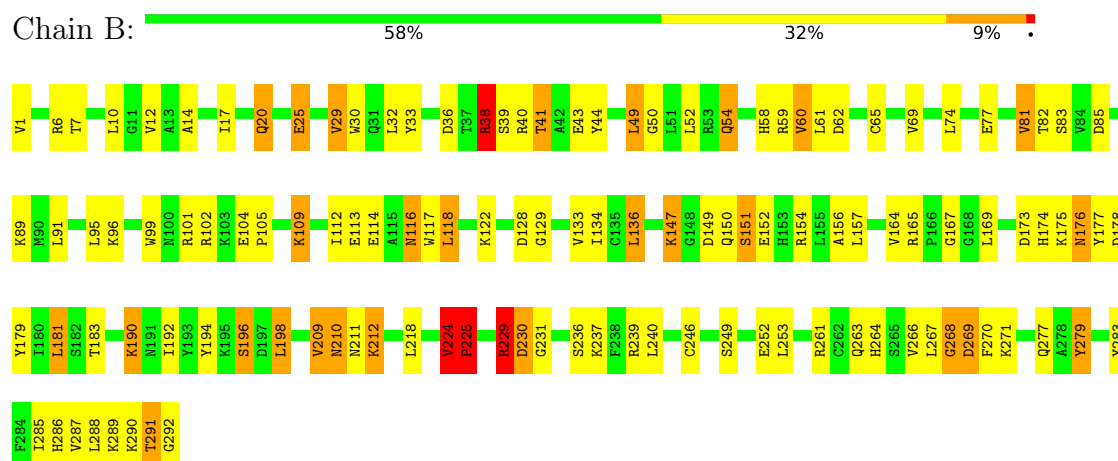
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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.

Note EDS was not executed.

• Molecule 1: GLYCINE N-METHYLTRANSFERASE



• Molecule 1: GLYCINE N-METHYLTRANSFERASE



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	86.70Å 176.00Å 45.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.50	Depositor
% Data completeness (in resolution range)	100.0 (10.00-2.50)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.194 , 0.266	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4884	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

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	0.47	0/2339	0.96	6/3171 (0.2%)
1	B	0.47	0/2339	1.01	12/3171 (0.4%)
All	All	0.47	0/4678	0.98	18/6342 (0.3%)

There are no bond length outliers.

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	224	VAL	CA-C-N	10.01	132.36	119.84
1	B	224	VAL	C-N-CA	10.01	132.36	119.84
1	A	224	VAL	CA-C-N	9.02	131.11	119.84
1	A	224	VAL	C-N-CA	9.02	131.11	119.84
1	B	81	VAL	N-CA-C	8.66	120.95	108.48
1	A	81	VAL	N-CA-C	7.96	119.94	108.48
1	B	38	ARG	N-CA-C	-6.66	106.36	114.75
1	B	20	GLN	N-CA-C	6.61	124.88	110.80
1	B	209	VAL	N-CA-C	-6.58	95.66	109.34
1	B	269	ASP	N-CA-C	-6.12	101.56	111.04
1	A	178	ASP	N-CA-C	-5.78	104.88	111.07
1	A	20	GLN	N-CA-C	5.60	122.72	110.80
1	B	268	GLY	N-CA-C	-5.23	100.78	113.18
1	B	279	TYR	N-CA-C	5.20	117.20	109.25
1	A	224	VAL	CA-C-O	5.14	122.00	119.12
1	B	167	GLY	N-CA-C	-5.05	108.73	115.40
1	B	225	PRO	N-CA-C	5.03	122.84	112.47
1	B	212	LYS	N-CA-C	5.00	117.12	109.07

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-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 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	2283	0	2243	80	0
1	B	2283	0	2243	75	0
2	A	182	0	0	2	0
2	B	136	0	0	9	0
All	All	4884	0	4486	150	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 17.

All (150) 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:41:THR:HG22	1:B:44:TYR:H	1.13	1.09
1:A:41:THR:HG22	1:A:44:TYR:H	1.22	1.01
1:A:11:GLY:H	1:A:20:GLN:HE22	1.02	0.95
1:A:29:VAL:HG11	1:A:236:SER:HB3	1.56	0.85
1:A:48:LEU:HD23	1:A:73:MET:HE1	1.58	0.83
1:A:183:THR:HG22	1:A:185:CYS:H	1.42	0.83
1:A:60:VAL:HG21	1:A:74:LEU:HD13	1.62	0.82
1:A:40:ARG:HB2	1:A:40:ARG:NH1	2.00	0.76
1:A:49:LEU:HD21	1:A:77:GLU:HG3	1.68	0.75
1:A:38:ARG:HD2	1:A:39:SER:N	2.04	0.72
1:A:215:MET:HA	1:A:244:PRO:HD3	1.73	0.71
1:A:29:VAL:CG1	1:A:236:SER:HB3	2.21	0.71
1:A:41:THR:HG22	1:A:44:TYR:N	2.03	0.71
1:B:38:ARG:HD3	1:B:39:SER:N	2.07	0.70
1:B:41:THR:HG22	1:B:44:TYR:N	1.98	0.70
1:A:49:LEU:O	1:A:53:ARG:HG3	1.92	0.69
1:B:116:ASN:HD22	1:B:118:LEU:H	1.41	0.67
1:A:174:HIS:HD2	1:A:175:LYS:O	1.78	0.67
1:B:41:THR:CG2	1:B:44:TYR:H	2.00	0.66
1:B:40:ARG:HB2	1:B:40:ARG:NH1	2.11	0.65
1:B:269:ASP:O	1:B:285:ILE:HD12	1.97	0.65
1:A:98:ARG:HD3	1:B:99:TRP:CH2	2.32	0.64
1:A:40:ARG:HH11	1:A:194:TYR:HE1	1.43	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:9:SER:O	1:A:12:VAL:HG22	1.98	0.63
1:A:11:GLY:H	1:A:20:GLN:NE2	1.85	0.63
1:B:176:ASN:C	1:B:176:ASN:HD22	2.06	0.63
1:A:150:GLN:HG2	1:A:153:HIS:CD2	2.34	0.62
1:A:36:ASP:OD1	1:A:196:SER:HB2	1.99	0.62
1:B:29:VAL:HG11	1:B:236:SER:HB3	1.82	0.62
1:B:60:VAL:HG21	1:B:74:LEU:HD13	1.81	0.62
1:A:274:ARG:NH2	1:A:277:GLN:HB2	2.14	0.62
1:A:212:LYS:O	1:A:212:LYS:HD2	2.00	0.61
1:A:6:ARG:O	1:B:239:ARG:HD3	2.00	0.61
1:A:274:ARG:O	1:A:277:GLN:HB3	2.00	0.60
1:B:14:ALA:HB3	1:B:17:ILE:HD11	1.83	0.60
1:B:129:GLY:HA3	1:B:165:ARG:HB3	1.83	0.60
1:B:36:ASP:OD1	1:B:196:SER:HB2	2.01	0.60
1:B:264:HIS:CE1	1:B:286:HIS:HD1	2.19	0.59
1:B:61:LEU:HD12	1:B:82:THR:O	2.02	0.59
1:A:40:ARG:HA	1:A:194:TYR:CD1	2.38	0.59
1:B:105:PRO:O	1:B:109:LYS:HD2	2.03	0.58
1:B:29:VAL:CG1	1:B:236:SER:HB3	2.32	0.58
1:A:24:GLY:HA3	2:B:300:HOH:O	2.02	0.58
1:B:40:ARG:HA	1:B:194:TYR:CD2	2.40	0.57
1:B:113:GLU:HG3	2:B:402:HOH:O	2.03	0.56
1:A:105:PRO:O	1:A:109:LYS:HD2	2.06	0.56
1:B:177:TYR:O	1:B:181:LEU:HB2	2.06	0.56
1:A:39:SER:O	1:A:194:TYR:HA	2.07	0.55
1:A:72:ILE:O	1:A:76:GLU:HG3	2.07	0.55
1:B:58:HIS:HB3	2:B:332:HOH:O	2.07	0.55
1:A:40:ARG:HB2	1:A:40:ARG:CZ	2.36	0.54
1:B:209:VAL:O	1:B:210:ASN:C	2.50	0.54
1:B:277:GLN:NE2	1:B:279:TYR:HB3	2.22	0.54
1:B:49:LEU:HD21	1:B:77:GLU:HG3	1.90	0.54
1:B:229:ARG:O	1:B:231:GLY:N	2.39	0.53
1:B:40:ARG:HB2	1:B:40:ARG:CZ	2.39	0.53
1:B:291:THR:HG22	1:B:292:GLY:N	2.22	0.53
1:A:40:ARG:HD3	1:A:194:TYR:CE1	2.44	0.53
1:A:36:ASP:CG	1:A:36:ASP:O	2.53	0.52
1:B:36:ASP:CG	1:B:198:LEU:HB2	2.35	0.52
1:A:164:VAL:O	1:A:290:LYS:HD3	2.09	0.52
1:B:253:LEU:HD23	2:B:393:HOH:O	2.10	0.52
1:B:174:HIS:HD2	1:B:175:LYS:O	1.92	0.51
1:A:32:LEU:HG	1:A:198:LEU:HD21	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:147:LYS:HB3	1:B:149:ASP:OD2	2.11	0.51
1:A:96:LYS:HE2	1:B:114:GLU:OE2	2.12	0.50
1:A:134:ILE:HB	1:A:136:LEU:CD2	2.42	0.50
1:B:40:ARG:HB3	2:B:357:HOH:O	2.12	0.49
1:B:32:LEU:HG	1:B:198:LEU:HD21	1.95	0.49
1:B:173:ASP:OD1	1:B:173:ASP:C	2.54	0.49
1:A:177:TYR:O	1:A:181:LEU:HB2	2.12	0.49
1:A:156:ALA:O	1:A:160:ILE:HG13	2.13	0.49
1:B:25:GLU:O	1:B:29:VAL:HG22	2.13	0.49
1:A:38:ARG:HD2	1:A:39:SER:H	1.77	0.48
1:B:30:TRP:O	1:B:33:TYR:HB3	2.13	0.48
1:B:152:GLU:HB2	2:B:304:HOH:O	2.14	0.47
1:A:40:ARG:HB2	1:A:40:ARG:HH11	1.75	0.47
1:B:122:LYS:HA	1:B:122:LYS:HD2	1.77	0.47
1:B:50:GLY:O	1:B:54:GLN:HB3	2.15	0.47
1:A:98:ARG:NH1	1:A:112:ILE:H	2.12	0.47
1:A:209:VAL:HG23	1:A:214:HIS:HB2	1.97	0.47
1:B:40:ARG:HG2	1:B:44:TYR:HD2	1.80	0.47
1:A:84:VAL:HA	1:A:113:GLU:O	2.15	0.47
1:A:103:LYS:HB2	2:A:307:HOH:O	2.14	0.46
1:B:116:ASN:HD21	1:B:118:LEU:HD22	1.81	0.46
1:B:105:PRO:HD2	2:B:397:HOH:O	2.15	0.46
1:A:129:GLY:HA3	1:A:165:ARG:HB3	1.98	0.46
1:B:176:ASN:C	1:B:176:ASN:ND2	2.73	0.46
1:B:210:ASN:HB2	2:B:396:HOH:O	2.16	0.46
1:A:224:VAL:HA	1:A:225:PRO:HD2	1.59	0.46
1:A:247:LEU:HD22	1:A:284:PHE:CE2	2.51	0.46
1:A:190:LYS:HA	1:A:190:LYS:HD2	1.53	0.45
1:B:190:LYS:HD2	1:B:190:LYS:HA	1.61	0.45
1:B:149:ASP:C	1:B:151:SER:H	2.24	0.45
1:B:65:CYS:HB3	1:B:85:ASP:HB2	1.99	0.45
1:B:179:TYR:O	1:B:183:THR:HB	2.17	0.45
1:B:43:GLU:H	1:B:43:GLU:CD	2.24	0.45
1:B:229:ARG:HB3	1:B:230:ASP:H	1.46	0.45
1:B:134:ILE:HB	1:B:136:LEU:HD22	1.97	0.45
1:A:37:THR:HG22	1:A:194:TYR:HB2	1.99	0.44
1:B:192:ILE:HG12	1:B:283:TYR:CD1	2.52	0.44
1:B:192:ILE:HD12	1:B:270:PHE:CZ	2.53	0.44
1:A:179:TYR:O	1:A:183:THR:HB	2.17	0.44
1:A:85:ASP:HB3	1:A:91:LEU:HD13	1.99	0.44
1:A:36:ASP:HB2	1:A:198:LEU:HD22	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:101:ARG:CZ	1:A:107:PHE:CZ	3.01	0.44
1:A:116:ASN:HD22	1:A:118:LEU:H	1.66	0.44
1:B:176:ASN:HD21	1:B:178:ASP:HB2	1.83	0.43
1:A:25:GLU:O	1:A:29:VAL:HG22	2.17	0.43
1:A:52:LEU:HD12	1:A:52:LEU:HA	1.90	0.43
1:A:287:VAL:C	1:A:288:LEU:HD23	2.43	0.43
1:B:174:HIS:CE1	1:B:286:HIS:NE2	2.87	0.43
1:A:39:SER:HB3	2:A:408:HOH:O	2.17	0.43
1:A:264:HIS:CE1	1:A:286:HIS:ND1	2.87	0.43
1:B:246:CYS:HB2	2:B:360:HOH:O	2.18	0.43
1:B:176:ASN:ND2	1:B:179:TYR:H	2.17	0.43
1:A:136:LEU:HD11	1:A:171:VAL:HG12	2.01	0.42
1:A:11:GLY:N	1:A:20:GLN:HE22	1.87	0.42
1:B:133:VAL:CG2	1:B:164:VAL:HG22	2.48	0.42
1:A:174:HIS:CE1	1:A:286:HIS:HE2	2.37	0.42
1:A:122:LYS:HA	1:A:122:LYS:HD2	1.71	0.42
1:A:149:ASP:C	1:A:151:SER:H	2.27	0.42
1:B:38:ARG:HD3	1:B:38:ARG:C	2.44	0.42
1:B:101:ARG:HB3	1:B:104:GLU:OE2	2.19	0.42
1:B:117:TRP:HB3	1:B:156:ALA:HB1	2.02	0.42
1:A:183:THR:CG2	1:A:185:CYS:H	2.23	0.42
1:A:220:TYR:O	1:A:237:LYS:HB3	2.19	0.42
1:B:263:GLN:HB2	1:B:289:LYS:HB3	2.02	0.42
1:B:38:ARG:HA	1:B:69:VAL:HG21	2.02	0.41
1:A:256:GLU:O	1:A:256:GLU:HG2	2.19	0.41
1:A:261:ARG:CD	1:A:292:GLY:HA3	2.50	0.41
1:B:149:ASP:OD2	1:B:149:ASP:N	2.53	0.41
1:A:16:GLY:HA3	1:B:117:TRP:CH2	2.56	0.41
1:A:134:ILE:HB	1:A:136:LEU:HD22	2.02	0.41
1:A:212:LYS:HD2	1:A:212:LYS:C	2.46	0.41
1:A:220:TYR:O	1:A:237:LYS:HA	2.19	0.41
1:B:62:ASP:HA	1:B:134:ILE:HG13	2.01	0.41
1:A:180:ILE:O	1:A:184:GLY:N	2.51	0.41
1:A:211:ASN:HD22	1:A:211:ASN:HA	1.71	0.41
1:A:239:ARG:HD3	1:B:6:ARG:O	2.21	0.41
1:B:150:GLN:O	1:B:154:ARG:HG3	2.21	0.41
1:B:224:VAL:O	1:B:224:VAL:HG22	2.20	0.41
1:A:187:PRO:HA	1:A:188:PRO:HD3	1.84	0.41
1:A:288:LEU:HD23	1:A:288:LEU:N	2.35	0.41
1:A:275:PRO:C	1:A:277:GLN:H	2.28	0.40
1:A:49:LEU:HD12	1:A:49:LEU:HA	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:40:ARG:HG2	1:B:44:TYR:CD2	2.56	0.40
1:A:17:ILE:HA	1:A:18:PRO:HD3	1.96	0.40
1:B:83:SER:O	1:B:112:ILE:HA	2.21	0.40
1:B:224:VAL:HA	1:B:225:PRO:HD2	1.60	0.40

There are no symmetry-related clashes.

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	290/292 (99%)	262 (90%)	22 (8%)	6 (2%)	5	9
1	B	290/292 (99%)	272 (94%)	12 (4%)	6 (2%)	5	9
All	All	580/584 (99%)	534 (92%)	34 (6%)	12 (2%)	5	9

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	15	GLU
1	A	229	ARG
1	A	230	ASP
1	B	210	ASN
1	B	229	ARG
1	B	230	ASP
1	A	225	PRO
1	B	225	PRO
1	B	290	LYS
1	A	40	ARG
1	A	16	GLY
1	B	268	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	242/242 (100%)	185 (76%)	57 (24%)	1	1
1	B	242/242 (100%)	192 (79%)	50 (21%)	1	2
All	All	484/484 (100%)	377 (78%)	107 (22%)	1	2

All (107) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	VAL
1	A	2	ASP
1	A	3	SER
1	A	7	THR
1	A	10	LEU
1	A	20	GLN
1	A	23	ASP
1	A	25	GLU
1	A	28	ARG
1	A	29	VAL
1	A	37	THR
1	A	38	ARG
1	A	40	ARG
1	A	41	THR
1	A	49	LEU
1	A	52	LEU
1	A	60	VAL
1	A	81	VAL
1	A	82	THR
1	A	89	LYS
1	A	91	LEU
1	A	95	LEU
1	A	96	LYS
1	A	97	GLU
1	A	98	ARG
1	A	103	LYS
1	A	109	LYS

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Mol	Chain	Res	Type
1	A	116	ASN
1	A	118	LEU
1	A	128	ASP
1	A	147	LYS
1	A	157	LEU
1	A	175	LYS
1	A	181	LEU
1	A	182	SER
1	A	183	THR
1	A	190	LYS
1	A	193	TYR
1	A	196	SER
1	A	198	LEU
1	A	200	LYS
1	A	211	ASN
1	A	215	MET
1	A	218	LEU
1	A	224	VAL
1	A	229	ARG
1	A	237	LYS
1	A	249	SER
1	A	254	VAL
1	A	256	GLU
1	A	265	SER
1	A	266	VAL
1	A	271	LYS
1	A	274	ARG
1	A	287	VAL
1	A	288	LEU
1	A	291	THR
1	B	1	VAL
1	B	7	THR
1	B	10	LEU
1	B	12	VAL
1	B	20	GLN
1	B	25	GLU
1	B	29	VAL
1	B	38	ARG
1	B	41	THR
1	B	49	LEU
1	B	52	LEU
1	B	54	GLN

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Mol	Chain	Res	Type
1	B	59	ARG
1	B	60	VAL
1	B	81	VAL
1	B	89	LYS
1	B	91	LEU
1	B	95	LEU
1	B	96	LYS
1	B	102	ARG
1	B	109	LYS
1	B	116	ASN
1	B	118	LEU
1	B	128	ASP
1	B	136	LEU
1	B	147	LYS
1	B	151	SER
1	B	157	LEU
1	B	169	LEU
1	B	176	ASN
1	B	181	LEU
1	B	190	LYS
1	B	196	SER
1	B	198	LEU
1	B	211	ASN
1	B	212	LYS
1	B	218	LEU
1	B	224	VAL
1	B	229	ARG
1	B	237	LYS
1	B	240	LEU
1	B	249	SER
1	B	252	GLU
1	B	261	ARG
1	B	266	VAL
1	B	267	LEU
1	B	271	LYS
1	B	287	VAL
1	B	288	LEU
1	B	291	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	20	GLN
1	A	116	ASN
1	A	150	GLN
1	A	153	HIS
1	A	159	ASN
1	A	174	HIS
1	A	176	ASN
1	A	191	ASN
1	A	211	ASN
1	A	245	HIS
1	A	263	GLN
1	A	264	HIS
1	B	116	ASN
1	B	153	HIS
1	B	159	ASN
1	B	174	HIS
1	B	176	ASN
1	B	211	ASN
1	B	245	HIS
1	B	264	HIS

5.3.3 RNA ⓘ

There are no RNA molecules 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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.