



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 06:15 AM UTC

PDB ID : 9IHS / pdb_00009ihs
Title : Microbial transglutaminase mutant - D3C/G283C
Authors : Suzuki, M.; Date, M.; Kashiwagi, T.; Takahashi, K.; Nakamura, A.; Tanokura, M.; Suzuki, E.; Yokoyama, K.
Deposited on : 2024-06-18
Resolution : 2.00 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
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

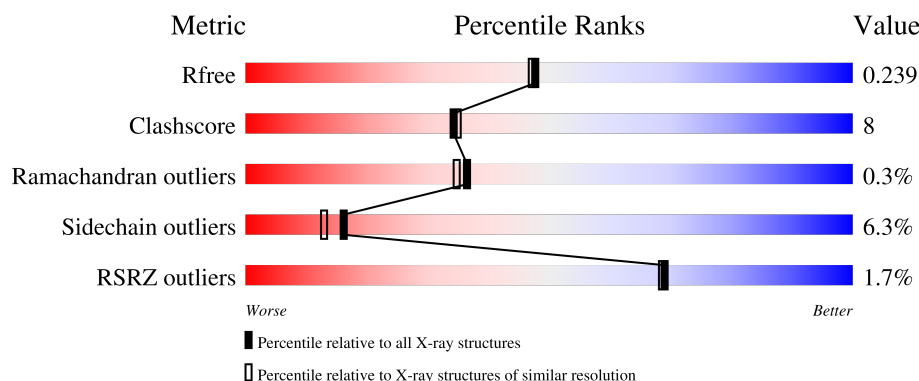
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	331	% 86% 11% .
1	B	331	83% 15% .
1	C	331	% 90% 8% .
1	D	331	5% 76% 21% .

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 11885 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 Protein-glutamine gamma-glutamyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	331	Total	C	N	O	S	0	0	0
			2678	1659	495	515	9			
1	B	331	Total	C	N	O	S	0	0	0
			2678	1659	495	515	9			
1	C	331	Total	C	N	O	S	0	1	0
			2686	1664	498	515	9			
1	D	331	Total	C	N	O	S	0	0	0
			2678	1659	495	515	9			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	3	CYS	ASP	engineered mutation	UNP P81453
A	283	CYS	GLY	engineered mutation	UNP P81453
B	3	CYS	ASP	engineered mutation	UNP P81453
B	283	CYS	GLY	engineered mutation	UNP P81453
C	3	CYS	ASP	engineered mutation	UNP P81453
C	283	CYS	GLY	engineered mutation	UNP P81453
D	3	CYS	ASP	engineered mutation	UNP P81453
D	283	CYS	GLY	engineered mutation	UNP P81453

- Molecule 2 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: $C_6H_{13}NO_4S$).

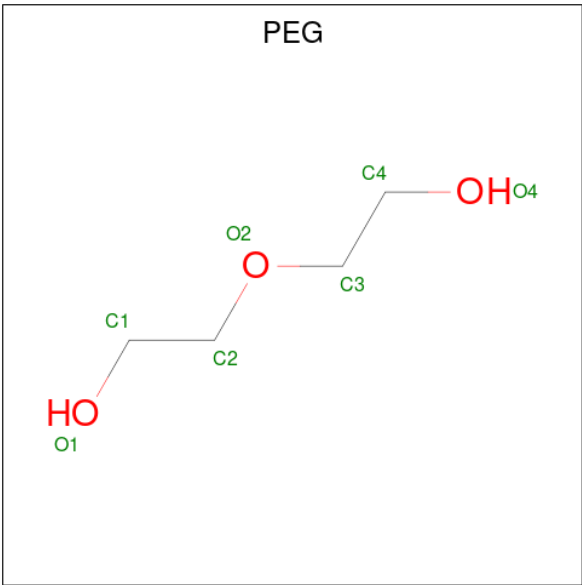


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
2	B	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
2	C	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
2	D	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Cl	0	0
			1	1		
3	B	1	Total	Cl	0	0
			1	1		
3	C	1	Total	Cl	0	0
			1	1		
3	D	1	Total	Cl	0	0
			1	1		

- Molecule 4 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			7	4	3		

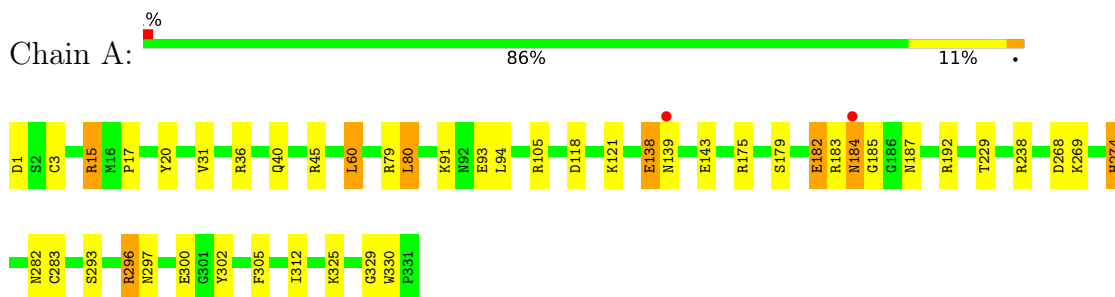
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	292	Total	O	0	0
			292	292		
5	B	306	Total	O	0	0
			306	306		
5	C	320	Total	O	0	0
			320	320		
5	D	188	Total	O	0	0
			188	188		

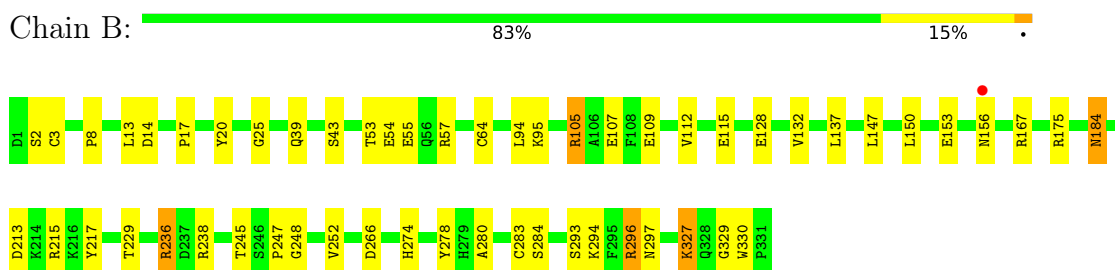
3 Residue-property plots [i](#)

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.

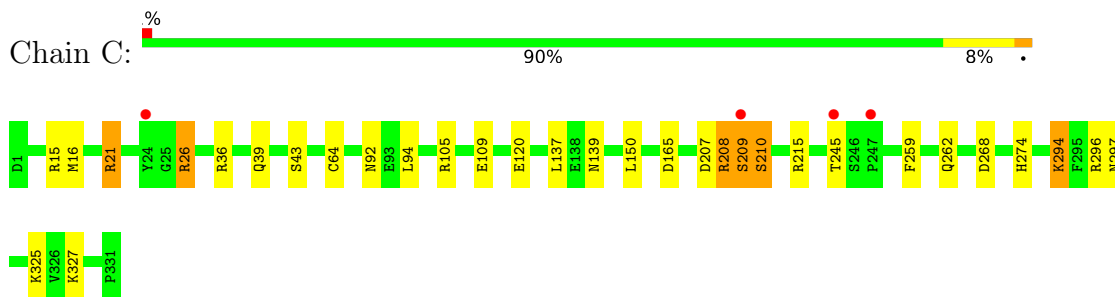
- Molecule 1: Protein-glutamine gamma-glutamyltransferase



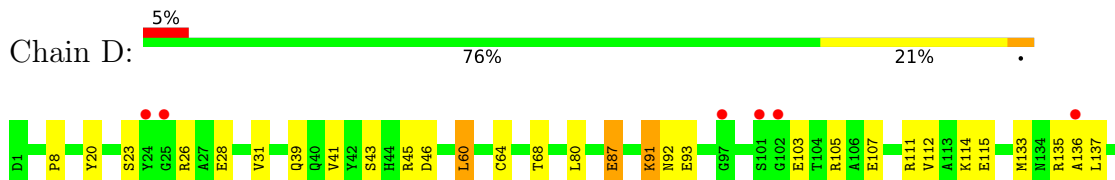
- Molecule 1: Protein-glutamine gamma-glutamyltransferase

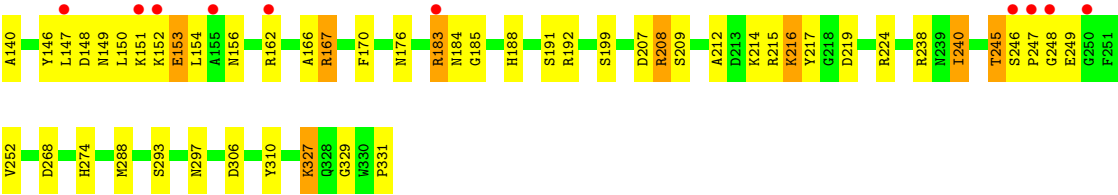


- Molecule 1: Protein-glutamine gamma-glutamyltransferase



- Molecule 1: Protein-glutamine gamma-glutamyltransferase





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	78.76Å 117.36Å 85.47Å 90.00° 113.03° 90.00°	Depositor
Resolution (Å)	47.08 – 2.00 47.08 – 2.00	Depositor EDS
% Data completeness (in resolution range)	97.2 (47.08-2.00) 97.2 (47.08-2.00)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.95 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.181 , 0.234 (Not available) , 0.239	Depositor DCC
R_{free} test set	4694 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å ²)	25.5	Xtriage
Anisotropy	0.027	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 49.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	11885	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.77% 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

5.1 Standard geometry

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

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	0.57	0/2755	1.09	2/3726 (0.1%)
1	B	0.60	0/2755	1.12	7/3726 (0.2%)
1	C	0.61	0/2766	1.05	0/3740
1	D	0.54	0/2755	1.11	3/3726 (0.1%)
All	All	0.58	0/11031	1.09	12/14918 (0.1%)

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	8	PRO	CB-CA-C	-9.82	102.16	111.39
1	B	215	ARG	CG-CD-NE	-7.51	95.47	112.00
1	D	245	THR	CB-CA-C	-6.82	100.13	110.90
1	B	105	ARG	CB-CG-CD	6.64	126.58	111.30
1	A	118	ASP	CA-CB-CG	6.38	118.98	112.60
1	A	229	THR	CA-CB-OG1	-5.92	100.72	109.60
1	B	8	PRO	N-CA-CB	5.80	106.44	103.19
1	B	266	ASP	CA-CB-CG	5.55	118.15	112.60
1	B	175	ARG	CB-CG-CD	5.48	123.91	111.30
1	B	236	ARG	CB-CG-CD	-5.33	99.05	111.30
1	D	68	THR	CA-CB-OG1	-5.25	101.73	109.60
1	B	229	THR	CA-CB-OG1	-5.20	101.80	109.60

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	2678	0	2487	43	0
1	B	2678	0	2487	38	0
1	C	2686	0	2500	33	0
1	D	2678	0	2487	58	0
2	A	12	0	13	2	0
2	B	12	0	13	1	0
2	C	12	0	13	0	0
2	D	12	0	13	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	B	7	0	10	0	0
5	A	292	0	0	8	0
5	B	306	0	0	10	0
5	C	320	0	0	9	0
5	D	188	0	0	3	0
All	All	11885	0	10023	157	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 8.

All (157) 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:C:92:ASN:HB3	5:C:745:HOH:O	1.26	1.30
1:D:327:LYS:HE2	1:D:331:PRO:OXT	1.55	1.05
1:A:184:ASN:ND2	1:A:184:ASN:H	1.64	0.94
1:B:3:CYS:CB	1:D:245:THR:HG21	1.99	0.93
1:A:184:ASN:H	1:A:184:ASN:HD22	1.18	0.88
1:A:269:LYS:HE2	1:B:115:GLU:O	1.74	0.88
1:D:238:ARG:O	1:D:240:ILE:HD13	1.73	0.87
1:A:60:LEU:HD23	1:A:60:LEU:O	1.76	0.86
1:C:21:ARG:HG2	1:C:21:ARG:HH21	1.43	0.81
1:C:165:ASP:HB3	5:C:727:HOH:O	1.79	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:60:LEU:HD23	1:A:60:LEU:C	2.06	0.80
1:C:327:LYS:HE3	5:C:734:HOH:O	1.84	0.77
1:C:26:ARG:HH22	1:C:297:ASN:HB3	1.48	0.77
1:D:166:ALA:O	5:D:501:HOH:O	2.02	0.76
1:D:167:ARG:HH11	1:D:167:ARG:HG2	1.50	0.75
1:D:188:HIS:O	5:D:502:HOH:O	2.06	0.74
1:B:3:CYS:HB3	1:D:245:THR:HG21	1.69	0.74
1:B:57:ARG:NH2	5:B:502:HOH:O	2.23	0.71
1:D:135:ARG:NH1	1:D:153:GLU:OE1	2.24	0.71
1:C:26:ARG:NH2	1:C:297:ASN:HD22	1.89	0.70
1:D:183:ARG:HB2	1:D:183:ARG:CZ	2.21	0.70
1:D:93:GLU:HG2	1:D:112:VAL:CG1	2.22	0.70
1:D:60:LEU:HD22	1:D:288:MET:HE1	1.74	0.69
1:D:93:GLU:HG2	1:D:112:VAL:HG13	1.75	0.68
1:C:94:LEU:HD21	1:C:109:GLU:HG2	1.77	0.67
1:D:31:VAL:CG2	1:D:60:LEU:HD13	2.25	0.67
1:D:293:SER:HB3	1:D:297:ASN:HB2	1.76	0.67
1:B:115:GLU:OE2	5:B:501:HOH:O	2.14	0.66
1:D:167:ARG:HH11	1:D:167:ARG:CG	2.09	0.66
1:B:3:CYS:HB2	1:D:245:THR:HG21	1.77	0.64
1:A:184:ASN:HD22	1:A:184:ASN:N	1.92	0.64
1:A:60:LEU:C	1:A:60:LEU:CD2	2.71	0.64
1:A:268:ASP:O	5:A:501:HOH:O	2.15	0.63
1:C:327:LYS:HD2	1:C:327:LYS:C	2.23	0.63
1:C:26:ARG:HH21	1:C:26:ARG:HB2	1.64	0.63
1:C:296:ARG:CZ	5:C:507:HOH:O	2.47	0.63
1:D:154:LEU:HB3	1:D:162:ARG:HB3	1.79	0.63
1:A:15:ARG:NH1	5:A:504:HOH:O	2.32	0.63
1:A:269:LYS:NZ	5:A:503:HOH:O	2.31	0.62
1:D:183:ARG:HB2	1:D:183:ARG:NH1	2.15	0.62
1:D:167:ARG:HG2	1:D:167:ARG:NH1	2.11	0.61
1:A:80:LEU:HD13	1:A:312:ILE:HB	1.83	0.60
1:C:210:SER:O	1:C:215:ARG:NH1	2.34	0.60
1:D:107:GLU:HG2	1:D:217:TYR:CG	2.36	0.60
1:A:296:ARG:NH2	5:A:501:HOH:O	2.17	0.59
1:C:120:GLU:CG	1:C:296:ARG:NH2	2.66	0.59
1:D:114:LYS:HG3	1:D:306:ASP:HB2	1.85	0.59
1:C:120:GLU:HG2	1:C:296:ARG:NH2	2.18	0.58
1:D:216:LYS:HG3	1:D:217:TYR:CD2	2.39	0.58
1:B:64:CYS:SG	5:B:735:HOH:O	2.23	0.58
1:C:296:ARG:NE	5:C:507:HOH:O	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:94:LEU:CD2	1:C:109:GLU:HG2	2.34	0.57
1:C:268:ASP:OD1	1:C:296:ARG:NH2	2.37	0.57
1:B:238:ARG:NH2	5:B:505:HOH:O	2.37	0.57
1:D:20:TYR:CE2	1:D:329:GLY:HA2	2.39	0.57
1:C:21:ARG:HG2	1:C:21:ARG:NH2	2.13	0.57
1:A:138:GLU:OE1	1:A:138:GLU:HA	2.04	0.56
1:A:187:ASN:HB2	1:A:192:ARG:NH1	2.20	0.56
1:D:207:ASP:O	1:D:215:ARG:HD3	2.05	0.56
1:B:248:GLY:HA2	1:D:252:VAL:HG12	1.87	0.55
1:B:94:LEU:HD21	1:B:109:GLU:HG2	1.88	0.55
1:D:137:LEU:HB3	1:D:146:TYR:CD1	2.42	0.55
1:B:3:CYS:HB2	1:D:245:THR:CG2	2.37	0.54
1:A:182:GLU:HB3	1:A:184:ASN:ND2	2.23	0.54
1:B:107:GLU:HG2	1:B:217:TYR:CG	2.43	0.53
1:A:20:TYR:CE2	1:A:329:GLY:HA2	2.43	0.53
1:A:293:SER:HB3	1:A:297:ASN:HB2	1.90	0.53
1:D:148:ASP:O	1:D:152:LYS:HG2	2.08	0.53
1:B:17:PRO:HG2	1:B:330:TRP:CD2	2.45	0.52
1:B:128:GLU:HB3	5:B:778:HOH:O	2.09	0.52
1:D:183:ARG:CZ	1:D:183:ARG:CB	2.87	0.52
1:A:296:ARG:NH2	1:A:296:ARG:HB2	2.26	0.51
1:B:184:ASN:ND2	1:B:184:ASN:H	2.06	0.51
1:A:79:ARG:NH1	5:A:505:HOH:O	2.34	0.51
1:B:236:ARG:HD2	5:B:695:HOH:O	2.09	0.51
1:D:140:ALA:O	1:D:191:SER:HB3	2.10	0.51
1:B:132:VAL:HG13	1:B:153:GLU:HG2	1.92	0.51
1:D:327:LYS:CE	1:D:331:PRO:OXT	2.44	0.51
1:A:15:ARG:HD2	1:A:36:ARG:HD3	1.91	0.50
1:C:137:LEU:HD11	5:C:732:HOH:O	2.09	0.50
1:D:107:GLU:HG2	1:D:217:TYR:CD2	2.47	0.49
1:C:120:GLU:HG3	1:C:296:ARG:NH2	2.27	0.49
1:A:45:ARG:HD2	5:A:692:HOH:O	2.12	0.49
1:A:302:TYR:CD2	2:A:401:MES:H61	2.47	0.49
1:A:296:ARG:HB3	1:B:296:ARG:HB2	1.95	0.48
1:A:296:ARG:HB3	1:B:296:ARG:HD3	1.94	0.48
1:D:135:ARG:HH12	1:D:153:GLU:CD	2.20	0.48
1:B:252:VAL:HG12	1:D:248:GLY:HA2	1.96	0.47
1:C:105:ARG:NH2	5:C:508:HOH:O	2.39	0.47
1:D:93:GLU:HG2	1:D:112:VAL:CG2	2.44	0.47
1:A:1:ASP:OD1	1:A:3:CYS:HB2	2.14	0.47
1:D:216:LYS:HG3	1:D:217:TYR:CE2	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:179:SER:HA	1:A:182:GLU:HG2	1.96	0.47
1:D:39:GLN:HA	1:D:43:SER:HB3	1.95	0.47
1:D:93:GLU:CG	1:D:112:VAL:CG1	2.92	0.47
1:A:17:PRO:HG2	1:A:330:TRP:CE2	2.50	0.47
1:D:214:LYS:HE3	1:D:219:ASP:OD2	2.15	0.47
1:B:14:ASP:HA	5:B:639:HOH:O	2.15	0.47
1:C:207:ASP:OD1	1:C:207:ASP:C	2.55	0.46
1:B:278:TYR:CE1	1:B:280:ALA:HB2	2.50	0.46
1:D:93:GLU:HB3	1:D:112:VAL:HG11	1.98	0.46
1:D:212:ALA:O	1:D:216:LYS:HG2	2.15	0.46
1:A:183:ARG:HA	1:A:187:ASN:ND2	2.31	0.46
1:B:245:THR:HG23	5:B:690:HOH:O	2.15	0.46
1:C:64:CYS:SG	5:C:573:HOH:O	2.45	0.46
1:B:327:LYS:HE2	5:B:694:HOH:O	2.16	0.46
1:C:207:ASP:C	1:C:209:SER:H	2.24	0.46
1:A:238:ARG:NH2	5:A:515:HOH:O	2.49	0.45
1:C:208:ARG:HA	1:C:215:ARG:HD3	1.98	0.45
1:D:64:CYS:SG	5:D:627:HOH:O	2.43	0.45
1:D:208:ARG:NH1	1:D:240:ILE:HG13	2.32	0.45
1:A:274:HIS:CD2	1:A:274:HIS:N	2.84	0.45
1:A:300:GLU:OE1	1:B:296:ARG:NH1	2.44	0.45
1:A:305:PHE:CE2	2:A:401:MES:H62	2.52	0.45
1:C:16:MET:HE1	5:C:662:HOH:O	2.16	0.45
1:D:87:GLU:O	1:D:91:LYS:HG2	2.17	0.44
1:D:91:LYS:HG2	1:D:91:LYS:H	1.61	0.44
1:B:107:GLU:HG2	1:B:217:TYR:CD2	2.53	0.44
1:A:296:ARG:HB2	1:A:296:ARG:CZ	2.48	0.44
1:D:80:LEU:HD13	1:D:170:PHE:HA	1.98	0.44
1:A:183:ARG:HH11	1:A:183:ARG:HG3	1.83	0.44
1:D:246:SER:C	1:D:248:GLY:H	2.26	0.44
1:B:39:GLN:HA	1:B:43:SER:HB3	2.00	0.44
1:D:137:LEU:HB3	1:D:146:TYR:HD1	1.82	0.44
1:D:176:ASN:HD22	1:D:176:ASN:HA	1.49	0.43
1:A:143:GLU:OE2	1:A:175:ARG:HD3	2.18	0.43
1:B:53:THR:CG2	5:B:767:HOH:O	2.67	0.43
1:B:94:LEU:CD2	1:B:109:GLU:HG2	2.49	0.43
1:A:17:PRO:HG2	1:A:330:TRP:CD2	2.54	0.43
1:C:39:GLN:HA	1:C:43:SER:HB3	2.01	0.43
1:A:36:ARG:O	1:A:40:GLN:HG2	2.18	0.43
1:C:327:LYS:HD2	1:C:327:LYS:O	2.19	0.43
1:A:282:ASN:ND2	5:A:514:HOH:O	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:296:ARG:CB	1:B:296:ARG:HB2	2.48	0.42
1:D:216:LYS:HB3	1:D:216:LYS:HE3	1.40	0.42
1:A:182:GLU:HB2	1:A:185:GLY:H	1.85	0.42
1:B:248:GLY:CA	1:D:252:VAL:HG12	2.49	0.42
1:B:25:GLY:HA2	1:B:294:LYS:HD2	2.02	0.42
1:C:15[A]:ARG:HG3	1:C:36:ARG:HD3	2.02	0.42
1:A:31:VAL:HG23	1:A:60:LEU:HD21	2.01	0.42
1:B:293:SER:HB3	1:B:297:ASN:HB2	2.01	0.42
1:B:20:TYR:CE2	1:B:329:GLY:HA2	2.55	0.42
1:B:252:VAL:CG2	2:B:401:MES:H62	2.49	0.42
1:C:296:ARG:HE	1:D:268:ASP:CB	2.32	0.42
1:C:26:ARG:HH22	1:C:297:ASN:HD22	1.63	0.41
1:D:111:ARG:O	1:D:115:GLU:HG3	2.20	0.41
1:D:199:SER:HB2	1:D:310:TYR:CE2	2.55	0.41
1:C:259:PHE:CE1	1:C:262:GLN:HB2	2.55	0.41
1:D:185:GLY:O	1:D:192:ARG:NH2	2.53	0.41
1:D:93:GLU:CG	1:D:112:VAL:HG11	2.51	0.41
1:B:137:LEU:C	1:B:137:LEU:HD12	2.46	0.41
1:C:26:ARG:HH21	1:C:297:ASN:HD22	1.67	0.41
1:C:294:LYS:HA	1:C:294:LYS:HD2	1.82	0.41
1:D:136:ALA:HA	1:D:149:ASN:HB3	2.02	0.40
1:A:269:LYS:CE	1:B:115:GLU:O	2.58	0.40
1:A:296:ARG:NE	1:B:296:ARG:HB2	2.37	0.40
1:D:133:MET:HE3	1:D:170:PHE:CE1	2.56	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	329/331 (99%)	319 (97%)	10 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	329/331 (99%)	321 (98%)	7 (2%)	1 (0%)	36	35
1	C	330/331 (100%)	318 (96%)	10 (3%)	2 (1%)	21	17
1	D	329/331 (99%)	313 (95%)	15 (5%)	1 (0%)	36	35
All	All	1317/1324 (100%)	1271 (96%)	42 (3%)	4 (0%)	36	35

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	208	ARG
1	C	210	SER
1	B	247	PRO
1	D	247	PRO

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	280/280 (100%)	264 (94%)	16 (6%)	18	15
1	B	280/280 (100%)	262 (94%)	18 (6%)	16	12
1	C	281/280 (100%)	272 (97%)	9 (3%)	34	35
1	D	280/280 (100%)	252 (90%)	28 (10%)	7	4
All	All	1121/1120 (100%)	1050 (94%)	71 (6%)	16	13

All (71) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	ARG
1	A	60	LEU
1	A	80	LEU
1	A	91	LYS
1	A	93	GLU
1	A	94	LEU
1	A	105	ARG

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Mol	Chain	Res	Type
1	A	121	LYS
1	A	138	GLU
1	A	139	ASN
1	A	182	GLU
1	A	184	ASN
1	A	274	HIS
1	A	283	CYS
1	A	296	ARG
1	A	325	LYS
1	B	2	SER
1	B	13	LEU
1	B	54	GLU
1	B	55	GLU
1	B	95	LYS
1	B	105	ARG
1	B	112	VAL
1	B	147	LEU
1	B	150	LEU
1	B	156	ASN
1	B	167	ARG
1	B	184	ASN
1	B	213	ASP
1	B	274	HIS
1	B	283	CYS
1	B	284	SER
1	B	296	ARG
1	B	327	LYS
1	C	21	ARG
1	C	26	ARG
1	C	139	ASN
1	C	150	LEU
1	C	209	SER
1	C	245	THR
1	C	274	HIS
1	C	294	LYS
1	C	325	LYS
1	D	23	SER
1	D	26	ARG
1	D	28	GLU
1	D	41	VAL
1	D	45	ARG
1	D	46	ASP

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Mol	Chain	Res	Type
1	D	60	LEU
1	D	87	GLU
1	D	91	LYS
1	D	92	ASN
1	D	103	GLU
1	D	105	ARG
1	D	147	LEU
1	D	150	LEU
1	D	151	LYS
1	D	153	GLU
1	D	156	ASN
1	D	167	ARG
1	D	183	ARG
1	D	184	ASN
1	D	208	ARG
1	D	209	SER
1	D	216	LYS
1	D	224	ARG
1	D	240	ILE
1	D	249	GLU
1	D	274	HIS
1	D	327	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	184	ASN
1	A	187	ASN
1	A	282	ASN
1	B	44	HIS
1	B	184	ASN
1	C	78	ASN
1	C	96	ASN
1	C	297	ASN
1	D	156	ASN
1	D	176	ASN
1	D	282	ASN

5.3.3 RNA ⓘ

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 4 are monoatomic - leaving 5 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	MES	D	401	-	12,12,12	0.65	0	15,16,16	0.76	0
4	PEG	B	402	-	6,6,6	0.24	0	5,5,5	0.20	0
2	MES	C	401	-	12,12,12	0.81	0	15,16,16	1.49	3 (20%)
2	MES	B	401	-	12,12,12	0.66	0	15,16,16	0.57	0
2	MES	A	401	-	12,12,12	0.68	0	15,16,16	0.54	0

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	MES	D	401	-	-	2/6/14/14	0/1/1/1
4	PEG	B	402	-	-	1/4/4/4	-
2	MES	C	401	-	-	1/6/14/14	0/1/1/1
2	MES	B	401	-	-	1/6/14/14	0/1/1/1
2	MES	A	401	-	-	0/6/14/14	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	401	MES	C5-N4-C3	3.28	115.90	108.84
2	C	401	MES	C2-C3-N4	3.01	114.69	110.12
2	C	401	MES	C6-C5-N4	2.59	114.05	110.12

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	401	MES	C8-C7-N4-C5
2	D	401	MES	C8-C7-N4-C3
2	D	401	MES	C8-C7-N4-C5
2	B	401	MES	N4-C7-C8-S
4	B	402	PEG	C4-C3-O2-C2

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	401	MES	1	0
2	A	401	MES	2	0

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	331/331 (100%)	-0.23	2 (0%) 85 85	16, 26, 47, 77	0
1	B	331/331 (100%)	-0.34	1 (0%) 90 89	14, 23, 42, 64	0
1	C	331/331 (100%)	-0.33	4 (1%) 76 76	13, 23, 44, 67	1 (0%)
1	D	331/331 (100%)	0.33	16 (4%) 35 34	20, 35, 62, 94	0
All	All	1324/1324 (100%)	-0.14	23 (1%) 69 68	13, 27, 52, 94	1 (0%)

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	247	PRO	4.5
1	D	155	ALA	4.2
1	D	248	GLY	3.5
1	D	151	LYS	2.9
1	C	209	SER	2.7
1	D	247	PRO	2.7
1	A	139	ASN	2.5
1	D	101	SER	2.5
1	D	25	GLY	2.5
1	D	24	TYR	2.4
1	D	136	ALA	2.4
1	A	184	ASN	2.3
1	D	152	LYS	2.3
1	D	246	SER	2.2
1	D	102	GLY	2.1
1	D	147	LEU	2.1
1	D	97	GLY	2.1
1	D	162	ARG	2.1
1	B	156	ASN	2.1
1	D	183	ARG	2.1
1	D	250	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	24	TYR	2.0
1	C	245	THR	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 oligosaccharides 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($\text{\AA}^2$)	Q<0.9
2	MES	B	401	12/12	0.79	0.15	40,51,68,69	0
2	MES	A	401	12/12	0.80	0.15	41,46,72,75	0
2	MES	D	401	12/12	0.85	0.13	42,47,58,59	0
4	PEG	B	402	7/7	0.85	0.14	41,46,54,54	0
3	CL	B	403	1/1	0.95	0.10	32,32,32,32	0
2	MES	C	401	12/12	0.97	0.06	25,27,32,34	0
3	CL	A	402	1/1	0.97	0.10	39,39,39,39	0
3	CL	D	402	1/1	0.99	0.04	27,27,27,27	0
3	CL	C	402	1/1	0.99	0.04	21,21,21,21	0

6.5 Other polymers [i](#)

There are no such residues in this entry.