



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 04:54 AM UTC

PDB ID : 1CG2 / pdb_00001cg2
Title : CARBOXYPEPTIDASE G2
Authors : Rowsell, S.; Pauptit, R.A.; Tucker, A.D.; Melton, R.G.; Blow, D.M.; Brick, P.
Deposited on : 1996-12-20
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)	:	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

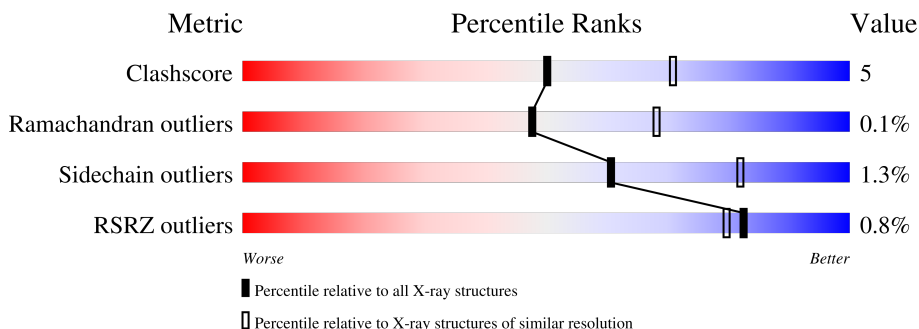
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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)
RSRZ outliers	180081	5833 (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	393	86% 13% .
1	B	393	84% 14% .
1	C	393	84% 15% ..
1	D	393	85% 13% ..

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 11466 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 CARBOXYPEPTIDASE G2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	389	Total	C	N	O	S	0	0	0
			2790	1762	475	547	6			
1	B	389	Total	C	N	O	S	0	0	0
			2779	1753	470	550	6			
1	C	389	Total	C	N	O	S	0	0	0
			2784	1757	471	550	6			
1	D	389	Total	C	N	O	S	0	0	0
			2769	1748	469	546	6			

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	4	Total	Zn	0	0
			4	4		
2	B	3	Total	Zn	0	0
			3	3		
2	C	3	Total	Zn	0	0
			3	3		
2	D	3	Total	Zn	0	0
			3	3		

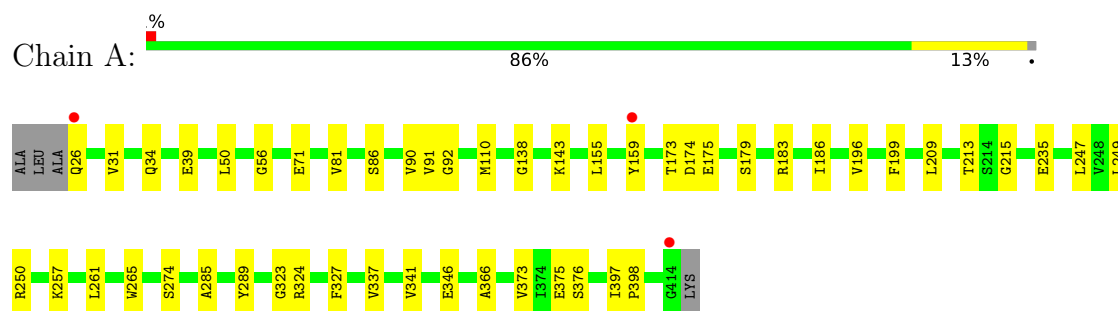
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	92	Total	O	0	0
			92	92		
3	B	88	Total	O	0	0
			88	88		
3	C	76	Total	O	0	0
			76	76		
3	D	75	Total	O	0	0
			75	75		

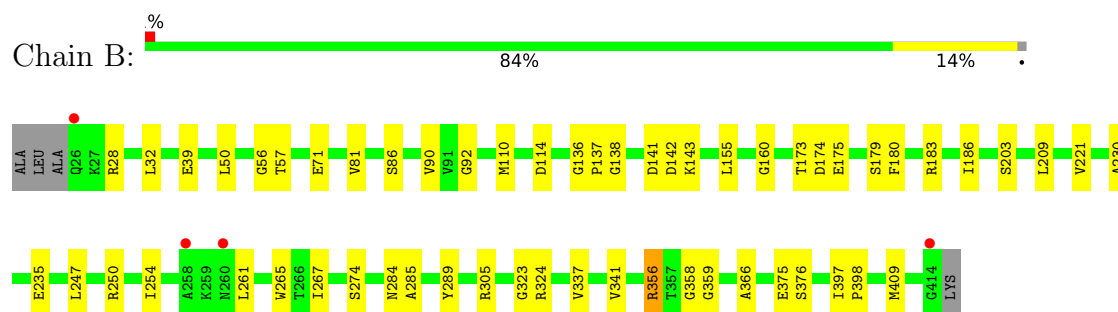
3 Residue-property plots

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 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.

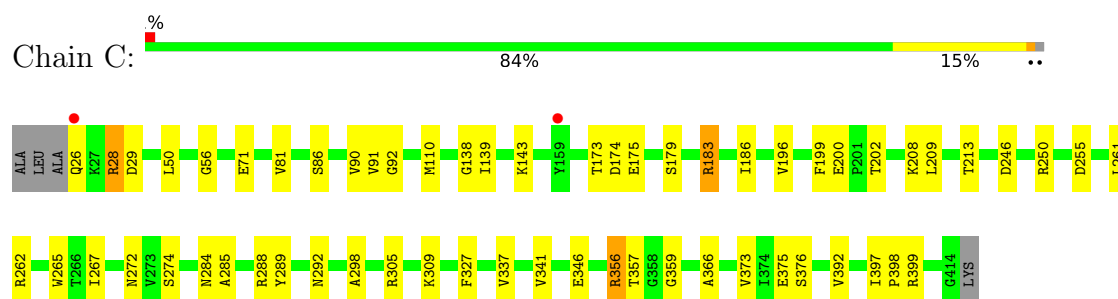
• Molecule 1: CARBOXYPEPTIDASE G2



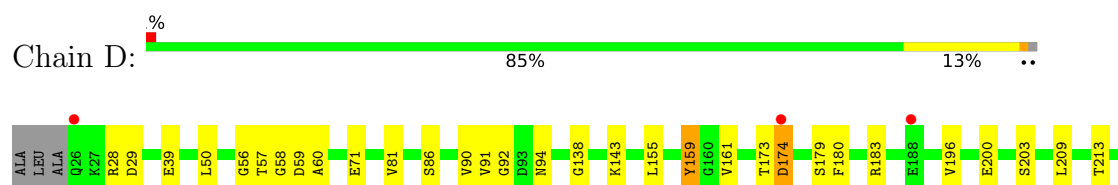
• Molecule 1: CARBOXYPEPTIDASE G2



• Molecule 1: CARBOXYPEPTIDASE G2



• Molecule 1: CARBOXYPEPTIDASE G2





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	81.26Å 105.28Å 122.19Å 90.00° 109.54° 90.00°	Depositor
Resolution (Å)	20.00 – 2.50 20.00 – 2.50	Depositor EDS
% Data completeness (in resolution range)	97.5 (20.00-2.50) 93.6 (20.00-2.50)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.11 (at 2.50Å)	Xtriage
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.196 , 0.224 0.200 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	34.5	Xtriage
Anisotropy	0.400	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 57.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.016 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	11466	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.62% 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:
ZN

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	0.55	0/2830	0.92	12/3844 (0.3%)
1	B	0.52	0/2819	0.93	12/3833 (0.3%)
1	C	0.53	0/2824	0.94	12/3840 (0.3%)
1	D	0.52	0/2809	0.92	10/3821 (0.3%)
All	All	0.53	0/11282	0.93	46/15338 (0.3%)

There are no bond length outliers.

All (46) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	92	GLY	N-CA-C	10.46	124.00	112.29
1	B	92	GLY	N-CA-C	8.10	124.79	112.81
1	C	92	GLY	N-CA-C	8.06	122.09	112.33
1	D	92	GLY	N-CA-C	7.83	122.55	112.68
1	D	174	ASP	N-CA-C	7.57	122.69	113.38
1	C	28	ARG	N-CA-C	7.33	121.02	110.24
1	C	174	ASP	N-CA-C	7.24	120.15	110.88
1	D	159	TYR	N-CA-C	-6.96	104.78	113.20
1	B	323	GLY	N-CA-C	-6.62	103.01	112.55
1	C	56	GLY	N-CA-C	-6.37	103.91	111.36
1	A	173	THR	N-CA-C	6.21	121.02	113.38
1	A	174	ASP	N-CA-C	6.11	119.89	111.71
1	D	323	GLY	N-CA-C	-6.10	103.95	112.13
1	D	56	GLY	N-CA-C	-6.10	104.23	111.36
1	C	309	LYS	N-CA-C	6.08	118.14	110.24
1	A	323	GLY	N-CA-C	-6.03	104.05	112.13
1	A	159	TYR	N-CA-C	-6.02	105.58	113.17
1	B	174	ASP	N-CA-C	5.94	119.67	111.71
1	B	254	ILE	N-CA-C	-5.91	104.29	112.50
1	D	274	SER	N-CA-C	5.90	119.74	112.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	209	LEU	N-CA-C	-5.84	99.88	109.40
1	C	91	VAL	N-CA-C	5.75	116.47	108.89
1	B	173	THR	N-CA-C	5.71	120.41	113.38
1	D	209	LEU	N-CA-C	-5.70	99.72	109.24
1	A	274	SER	N-CA-C	5.65	119.43	112.54
1	B	209	LEU	N-CA-C	-5.65	99.81	109.24
1	C	274	SER	N-CA-C	5.47	119.21	112.54
1	C	359	GLY	N-CA-C	5.47	118.69	111.03
1	B	56	GLY	N-CA-C	-5.46	104.97	111.36
1	B	274	SER	N-CA-C	5.38	119.10	112.54
1	C	173	THR	N-CA-C	5.37	119.84	113.28
1	A	56	GLY	N-CA-C	-5.33	105.12	111.36
1	D	91	VAL	N-CA-C	5.28	116.39	109.21
1	B	160	GLY	N-CA-C	5.27	122.05	114.10
1	B	114	ASP	N-CA-C	5.25	117.64	110.55
1	D	309	LYS	N-CA-C	5.25	117.48	110.35
1	B	28	ARG	N-CA-C	5.22	117.88	110.10
1	A	31	VAL	N-CA-C	-5.19	105.65	110.53
1	A	91	VAL	N-CA-C	5.15	115.73	109.30
1	C	199	PHE	N-CA-C	5.14	121.75	110.80
1	B	359	GLY	N-CA-C	5.12	118.50	111.54
1	A	209	LEU	N-CA-C	-5.11	100.71	109.24
1	D	254	ILE	N-CA-C	-5.07	104.95	112.04
1	A	199	PHE	N-CA-C	5.04	121.54	110.80
1	A	215	GLY	N-CA-C	-5.03	105.02	113.02
1	C	183	ARG	CB-CA-C	-5.01	102.52	110.84

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	2790	0	2701	27	0
1	B	2779	0	2671	31	0
1	C	2784	0	2681	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	2769	0	2652	30	0
2	A	4	0	0	0	0
2	B	3	0	0	0	0
2	C	3	0	0	0	0
2	D	3	0	0	0	0
3	A	92	0	0	1	0
3	B	88	0	0	0	0
3	C	76	0	0	2	0
3	D	75	0	0	0	0
All	All	11466	0	10705	116	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 5.

All (116) 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:230:ALA:HB3	1:C:288:ARG:NH1	1.96	0.80
1:D:356:ARG:HH11	1:D:356:ARG:HB3	1.47	0.79
1:B:110:MET:HE1	1:B:366:ALA:HB2	1.69	0.75
1:D:174:ASP:CB	1:D:179:SER:HA	2.16	0.75
1:C:110:MET:HE1	1:C:366:ALA:HB2	1.67	0.74
1:C:356:ARG:HH11	1:C:356:ARG:HB3	1.53	0.74
1:B:356:ARG:HB3	1:B:356:ARG:NH1	2.06	0.71
1:C:202:THR:HG21	1:C:208:LYS:H	1.55	0.69
1:A:110:MET:HE1	1:A:366:ALA:HB2	1.75	0.69
1:D:174:ASP:HB2	1:D:179:SER:HA	1.75	0.67
1:D:356:ARG:HB3	1:D:356:ARG:NH1	2.08	0.66
1:D:174:ASP:HB3	1:D:179:SER:HA	1.79	0.65
1:D:250:ARG:HD2	1:D:305:ARG:O	1.97	0.64
1:C:246:ASP:O	1:C:250:ARG:HB2	1.99	0.62
1:B:71:GLU:HG3	1:B:81:VAL:HG11	1.82	0.61
1:D:50:LEU:HB3	1:D:143:LYS:HD2	1.82	0.60
1:C:71:GLU:HG3	1:C:81:VAL:HG11	1.82	0.60
1:A:71:GLU:HG3	1:A:81:VAL:HG11	1.83	0.60
1:A:86:SER:HB3	1:A:90:VAL:HB	1.84	0.59
1:B:221:VAL:HG11	1:B:247:LEU:HD21	1.86	0.58
1:C:196:VAL:HB	1:C:373:VAL:HG22	1.85	0.57
1:A:138:GLY:O	1:A:143:LYS:HG2	2.04	0.57
1:C:86:SER:HB3	1:C:90:VAL:HB	1.85	0.57
1:C:138:GLY:O	1:C:143:LYS:HG2	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:110:MET:CE	1:C:186:ILE:HG23	2.35	0.55
1:D:71:GLU:HG3	1:D:81:VAL:HG11	1.89	0.55
1:A:39:GLU:HG2	1:A:155:LEU:HD21	1.89	0.54
1:B:250:ARG:HD2	1:B:305:ARG:O	2.09	0.53
1:A:26:GLN:HA	1:A:346:GLU:OE2	2.09	0.52
1:D:138:GLY:O	1:D:143:LYS:HG2	2.09	0.52
1:A:249:LEU:HD12	1:D:249:LEU:HD12	1.91	0.52
1:B:230:ALA:HB3	1:C:288:ARG:HH11	1.72	0.52
1:A:50:LEU:HB3	1:A:143:LYS:HD2	1.92	0.52
1:B:39:GLU:HG3	1:B:155:LEU:HD21	1.90	0.51
1:B:230:ALA:HB3	1:C:288:ARG:HH12	1.75	0.51
1:A:257:LYS:HE2	1:D:235:GLU:HG2	1.92	0.51
1:D:397:ILE:HB	1:D:398:PRO:HD3	1.93	0.51
1:B:110:MET:CE	1:B:186:ILE:HG23	2.41	0.51
1:C:179:SER:O	1:C:183:ARG:HG3	2.11	0.51
1:C:50:LEU:HB3	1:C:143:LYS:HD2	1.93	0.49
1:B:180:PHE:CE1	1:B:183:ARG:NH2	2.81	0.49
1:A:397:ILE:HB	1:A:398:PRO:HD3	1.94	0.49
1:B:221:VAL:HG11	1:B:247:LEU:CD2	2.42	0.49
1:B:397:ILE:HB	1:B:398:PRO:HD3	1.94	0.49
1:D:196:VAL:HB	1:D:373:VAL:HG22	1.96	0.48
1:A:26:GLN:O	1:A:26:GLN:HG2	2.13	0.48
1:C:397:ILE:HB	1:C:398:PRO:HD3	1.96	0.48
1:B:235:GLU:H	1:B:235:GLU:CD	2.19	0.48
1:C:265:TRP:CE3	1:C:285:ALA:HB2	2.49	0.48
1:A:39:GLU:CG	1:A:155:LEU:HD21	2.43	0.48
1:A:324:ARG:NH1	3:A:553:HOH:O	2.45	0.48
1:B:337:VAL:O	1:B:341:VAL:HG23	2.13	0.47
1:A:34:GLN:NE2	1:A:34:GLN:HA	2.28	0.47
1:D:261:LEU:HD12	1:D:289:TYR:HB3	1.95	0.47
1:C:110:MET:HE1	1:C:186:ILE:HG23	1.95	0.47
1:C:261:LEU:HD12	1:C:289:TYR:HB3	1.97	0.47
1:C:202:THR:HG23	3:C:566:HOH:O	2.14	0.47
1:C:337:VAL:O	1:C:341:VAL:HG23	2.14	0.47
1:A:257:LYS:HB2	1:A:257:LYS:HE3	1.61	0.46
1:B:356:ARG:HB3	1:B:356:ARG:CZ	2.45	0.46
1:B:180:PHE:CD1	1:B:183:ARG:NH2	2.84	0.46
1:B:230:ALA:CB	1:C:288:ARG:HH11	2.28	0.46
1:D:86:SER:HB3	1:D:90:VAL:HB	1.96	0.46
1:B:50:LEU:HB3	1:B:143:LYS:HD2	1.98	0.46
1:B:138:GLY:O	1:B:143:LYS:HG2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:26:GLN:HA	1:C:346:GLU:OE2	2.16	0.45
1:B:267:ILE:HB	1:B:284:ASN:HB2	1.98	0.45
1:C:292:ASN:HB3	3:C:574:HOH:O	2.16	0.45
1:A:196:VAL:HB	1:A:373:VAL:HG22	1.99	0.45
1:D:39:GLU:HG2	1:D:155:LEU:HD21	1.99	0.45
1:A:110:MET:HE1	1:A:186:ILE:HG23	1.99	0.44
1:B:261:LEU:HD12	1:B:289:TYR:HB3	1.98	0.44
1:D:58:GLY:O	1:D:60:ALA:N	2.50	0.44
1:B:39:GLU:CG	1:B:155:LEU:HD21	2.47	0.44
1:A:265:TRP:CE3	1:A:285:ALA:HB2	2.53	0.44
1:D:39:GLU:CG	1:D:155:LEU:HD21	2.48	0.44
1:A:213:THR:OG1	1:A:327:PHE:HB3	2.18	0.44
1:A:175:GLU:HA	1:A:179:SER:OG	2.17	0.44
1:C:213:THR:OG1	1:C:327:PHE:HB3	2.18	0.44
1:C:375:GLU:HG3	1:C:376:SER:N	2.32	0.44
1:A:26:GLN:HG3	1:A:346:GLU:OE2	2.18	0.43
1:A:261:LEU:HD12	1:A:289:TYR:HB3	1.99	0.43
1:B:86:SER:HB3	1:B:90:VAL:HB	2.01	0.43
1:D:247:LEU:C	1:D:247:LEU:HD23	2.44	0.43
1:A:179:SER:OG	1:A:324:ARG:NH2	2.52	0.43
1:A:110:MET:CE	1:A:186:ILE:HG23	2.49	0.43
1:A:337:VAL:O	1:A:341:VAL:HG23	2.19	0.43
1:C:200:GLU:O	1:C:376:SER:HA	2.17	0.43
1:D:28:ARG:HG2	1:D:29:ASP:N	2.32	0.43
1:D:200:GLU:O	1:D:376:SER:HA	2.19	0.43
1:A:247:LEU:HA	1:A:250:ARG:HG2	2.01	0.43
1:B:175:GLU:HA	1:B:179:SER:OG	2.19	0.42
1:D:265:TRP:CE3	1:D:285:ALA:HB2	2.54	0.42
1:C:175:GLU:HA	1:C:179:SER:OG	2.19	0.42
1:C:267:ILE:HB	1:C:284:ASN:HB2	2.02	0.42
1:C:202:THR:CG2	1:C:208:LYS:H	2.28	0.42
1:B:32:LEU:HD22	1:B:409:MET:HE1	2.02	0.42
1:D:94:ASN:HD21	1:D:173:THR:H	1.68	0.42
1:B:141:ASP:HA	1:B:142:ASP:HA	1.79	0.42
1:B:110:MET:HE2	1:B:186:ILE:HG23	2.02	0.41
1:A:375:GLU:HG3	1:A:376:SER:N	2.34	0.41
1:C:139:ILE:HG23	1:C:392:VAL:HG13	2.02	0.41
1:D:180:PHE:CE1	1:D:183:ARG:NH2	2.89	0.41
1:B:265:TRP:CE3	1:B:285:ALA:HB2	2.55	0.41
1:C:356:ARG:HB3	1:C:356:ARG:NH1	2.28	0.41
1:C:28:ARG:HG2	1:C:29:ASP:N	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:375:GLU:HG3	1:D:376:SER:N	2.35	0.41
1:D:337:VAL:O	1:D:341:VAL:HG23	2.20	0.41
1:B:136:GLY:HA2	1:B:137:PRO:HD3	1.95	0.41
1:D:267:ILE:HB	1:D:284:ASN:HB2	2.03	0.41
1:C:255:ASP:OD1	1:C:262:ARG:HA	2.20	0.41
1:D:261:LEU:HD21	1:D:298:ALA:HB2	2.02	0.41
1:C:261:LEU:HD21	1:C:298:ALA:HB2	2.03	0.41
1:D:159:TYR:HB3	1:D:161:VAL:HG23	2.03	0.41
1:B:375:GLU:HG3	1:B:376:SER:N	2.37	0.40
1:D:213:THR:OG1	1:D:327:PHE:HB3	2.21	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	387/393 (98%)	374 (97%)	13 (3%)	0	100	100
1	B	387/393 (98%)	376 (97%)	10 (3%)	1 (0%)	36	55
1	C	387/393 (98%)	375 (97%)	12 (3%)	0	100	100
1	D	387/393 (98%)	371 (96%)	15 (4%)	1 (0%)	36	55
All	All	1548/1572 (98%)	1496 (97%)	50 (3%)	2 (0%)	48	68

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	59	ASP
1	B	358	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	263/298 (88%)	261 (99%)	2 (1%)	73	88
1	B	262/298 (88%)	258 (98%)	4 (2%)	57	80
1	C	263/298 (88%)	258 (98%)	5 (2%)	50	76
1	D	258/298 (87%)	255 (99%)	3 (1%)	63	83
All	All	1046/1192 (88%)	1032 (99%)	14 (1%)	61	82

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	183	ARG
1	A	235	GLU
1	B	57	THR
1	B	203	SER
1	B	324	ARG
1	B	356	ARG
1	C	272	ASN
1	C	305	ARG
1	C	356	ARG
1	C	357	THR
1	C	399	ARG
1	D	57	THR
1	D	203	SER
1	D	235	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	34	GLN
1	A	146	ASN
1	A	220	GLN
1	A	284	ASN
1	A	307	GLN

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Mol	Chain	Res	Type
1	B	146	ASN
1	B	220	GLN
1	B	284	ASN
1	B	307	GLN
1	C	187	GLN
1	C	220	GLN
1	C	272	ASN
1	C	284	ASN
1	C	307	GLN
1	D	94	ASN
1	D	146	ASN
1	D	220	GLN
1	D	284	ASN
1	D	307	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 13 ligands modelled in this entry, 13 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	389/393 (98%)	-0.22	3 (0%) 82 80	17, 33, 45, 59	0
1	B	389/393 (98%)	-0.19	4 (1%) 79 76	17, 35, 48, 66	0
1	C	389/393 (98%)	-0.12	2 (0%) 87 85	20, 37, 52, 70	0
1	D	389/393 (98%)	-0.03	3 (0%) 82 80	20, 38, 54, 63	0
All	All	1556/1572 (98%)	-0.14	12 (0%) 82 80	17, 36, 51, 70	0

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	159	TYR	3.2
1	B	26	GLN	3.1
1	C	26	GLN	3.0
1	D	174	ASP	2.6
1	D	26	GLN	2.6
1	B	258	ALA	2.5
1	C	159	TYR	2.5
1	A	26	GLN	2.4
1	B	260	ASN	2.2
1	A	414	GLY	2.1
1	D	188	GLU	2.1
1	B	414	GLY	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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	ZN	A	503	1/1	0.97	0.03	28,28,28,28	0
2	ZN	A	502	1/1	0.99	0.02	43,43,43,43	0
2	ZN	B	502	1/1	0.99	0.03	43,43,43,43	0
2	ZN	D	502	1/1	0.99	0.02	35,35,35,35	0
2	ZN	B	500	1/1	1.00	0.02	24,24,24,24	0
2	ZN	B	501	1/1	1.00	0.01	21,21,21,21	0
2	ZN	A	500	1/1	1.00	0.02	22,22,22,22	0
2	ZN	C	500	1/1	1.00	0.02	28,28,28,28	0
2	ZN	C	501	1/1	1.00	0.02	28,28,28,28	0
2	ZN	C	502	1/1	1.00	0.03	36,36,36,36	0
2	ZN	D	500	1/1	1.00	0.01	27,27,27,27	0
2	ZN	D	501	1/1	1.00	0.02	29,29,29,29	0
2	ZN	A	501	1/1	1.00	0.01	19,19,19,19	0

6.5 Other polymers

There are no such residues in this entry.