



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 01:51 PM UTC

PDB ID : 1N8O / pdb_00001n8o
Title : Crystal structure of a complex between bovine chymotrypsin and ecotin
Authors : Cambillau, C.; Spinelli, S.; Lauwereys, M.
Deposited on : 2002-11-21
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
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

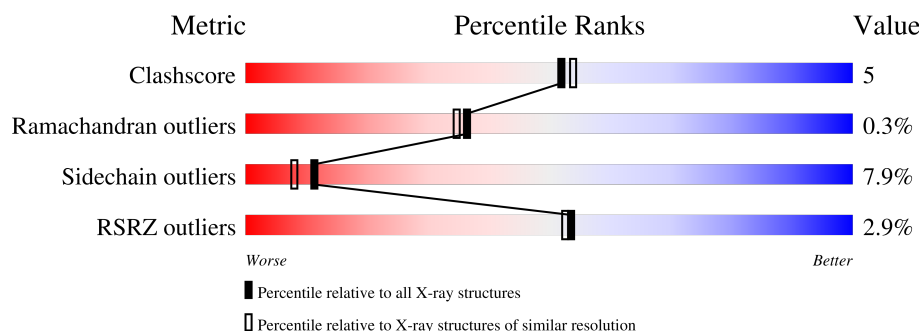
1 Overall quality at a glance

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))
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	13	
2	B	131	
3	C	97	
4	E	142	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 3009 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 Chymotrypsin A, A chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	11	Total	C	N	O	S	0	0	0
			74	48	12	13	1			

- Molecule 2 is a protein called Chymotrypsin A, b chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	131	Total	C	N	O	S	0	0	0
			980	618	162	196	4			

- Molecule 3 is a protein called Chymotrypsin A, C chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	97	Total	C	N	O	S	0	0	0
			702	436	123	136	7			

- Molecule 4 is a protein called ecotin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	136	Total	C	N	O	S	0	0	0
			1036	664	173	193	6			

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	11	Total	O	0	0
			11	11		
5	B	95	Total	O	0	0
			95	95		
5	C	45	Total	O	0	0
			45	45		
5	E	66	Total	O	0	0
			66	66		

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.

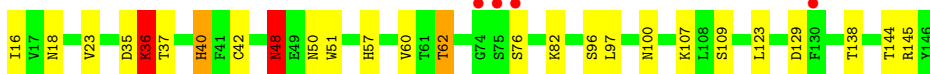
- Molecule 1: Chymotrypsin A, A chain

Chain A: 



- Molecule 2: Chymotrypsin A, b chain

Chain B: 



- Molecule 3: Chymotrypsin A, C chain

Chain C: 



- Molecule 4: ecotin

Chain E: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	95.50Å 63.80Å 79.60Å 90.00° 91.70° 90.00°	Depositor
Resolution (Å)	30.00 – 2.00 30.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	(Not available) (30.00-2.00) 42.8 (30.00-2.00)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$	-	Xtriage
Refinement program	X-PLOR	Depositor
R, R_{free}	0.205 , (Not available) 0.357 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	20.7	Xtriage
Anisotropy	0.171	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 58.1	EDS
L-test for twinning ¹	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.025 for -h,-k,l	Xtriage
F_o, F_c correlation	0.78	EDS
Total number of atoms	3009	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 100.00 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 0.0000e+00. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Theoretical 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	1.01	0/75	1.88	0/103
2	B	1.14	3/1000 (0.3%)	1.86	23/1361 (1.7%)
3	C	1.03	0/715	1.93	24/973 (2.5%)
4	E	1.00	1/1057 (0.1%)	1.79	17/1438 (1.2%)
All	All	1.06	4/2847 (0.1%)	1.85	64/3875 (1.7%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	53	HIS	CD2-NE2	-7.11	1.30	1.37
2	B	40	HIS	CB-CG	6.37	1.59	1.50
2	B	57	HIS	CD2-NE2	-6.12	1.31	1.37
2	B	40	HIS	CD2-NE2	-6.05	1.31	1.37

All (64) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	232	THR	N-CA-CB	-9.40	95.74	110.22
2	B	62	THR	N-CA-CB	-8.73	96.28	110.42
2	B	36	LYS	CB-CG-CD	8.63	131.15	111.30
3	C	151	THR	CA-CB-OG1	-8.28	97.18	109.60
3	C	151	THR	CA-C-O	-8.11	109.05	120.16
3	C	151	THR	CA-CB-CG2	7.93	123.98	110.50
2	B	36	LYS	CA-CB-CG	-7.73	98.63	114.10
2	B	100	ASN	OD1-CG-ND2	-7.61	114.99	122.60
2	B	18	ASN	OD1-CG-ND2	-7.59	115.01	122.60
2	B	35	ASP	CA-CB-CG	7.58	120.18	112.60
4	E	48	VAL	N-CA-CB	-7.35	98.34	111.93
3	C	167	ASN	OD1-CG-ND2	-7.35	115.25	122.60
4	E	21	LYS	CB-CG-CD	-7.11	94.96	111.30
4	E	77	VAL	N-CA-CB	-7.06	104.58	111.57
4	E	54	ARG	CD-NE-CZ	6.79	133.91	124.40
4	E	128	ARG	NE-CZ-NH2	6.75	125.28	119.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	215	TRP	CG-CD2-CE3	6.73	140.63	133.90
4	E	53	HIS	CB-CG-CD2	-6.65	122.55	131.20
2	B	48	ASN	OD1-CG-ND2	-6.55	116.05	122.60
3	C	175	LYS	N-CA-C	-6.54	104.56	112.54
3	C	167	ASN	CB-CG-ND2	6.43	126.04	116.40
3	C	199	LEU	N-CA-C	-6.29	97.02	108.02
2	B	36	LYS	CG-CD-CE	6.15	125.44	111.30
3	C	192	MET	CA-C-N	6.11	132.41	122.69
3	C	192	MET	C-N-CA	6.11	132.41	122.69
3	C	232	THR	CB-CA-C	6.08	121.89	110.63
3	C	165	ASN	OD1-CG-ND2	-6.07	116.53	122.60
2	B	37	THR	N-CA-C	-6.05	105.90	113.28
4	E	49	ASP	CA-CB-CG	6.02	118.62	112.60
2	B	107	LYS	CA-CB-CG	-5.98	102.15	114.10
4	E	7	LEU	N-CA-C	5.91	117.72	111.28
4	E	98	THR	N-CA-CB	-5.83	101.52	110.85
4	E	128	ARG	CB-CG-CD	-5.79	97.98	111.30
3	C	224	THR	CA-C-N	5.76	125.67	119.85
3	C	224	THR	C-N-CA	5.76	125.67	119.85
3	C	239	GLN	OE1-CD-NE2	-5.70	116.90	122.60
2	B	62	THR	CB-CA-C	5.61	120.76	110.11
3	C	149	ALA	N-CA-C	-5.57	95.40	111.00
2	B	23	VAL	N-CA-C	-5.51	103.55	108.95
2	B	82	LYS	CG-CD-CE	-5.50	98.66	111.30
2	B	18	ASN	CB-CG-ND2	5.47	124.60	116.40
2	B	76	SER	N-CA-C	-5.46	105.93	112.59
3	C	232	THR	OG1-CB-CG2	5.46	120.22	109.30
3	C	153	ASP	CA-CB-CG	5.39	117.99	112.60
4	E	115	ILE	N-CA-C	-5.35	100.88	108.58
3	C	215	TRP	CE2-CD2-CG	-5.33	100.81	107.20
4	E	66	GLY	N-CA-C	-5.33	108.29	115.21
2	B	57	HIS	CA-CB-CG	5.28	119.08	113.80
3	C	178	ASP	CA-CB-CG	5.22	117.83	112.60
4	E	98	THR	CA-CB-OG1	-5.22	101.78	109.60
2	B	48	ASN	CA-CB-CG	5.21	117.81	112.60
2	B	40	HIS	CA-CB-CG	5.18	118.98	113.80
2	B	57	HIS	CB-CG-CD2	-5.18	124.47	131.20
4	E	61	ASN	OD1-CG-ND2	-5.17	117.43	122.60
2	B	138	THR	CA-CB-CG2	5.11	119.18	110.50
4	E	128	ARG	NE-CZ-NH1	-5.10	116.40	121.50
3	C	215	TRP	CB-CG-CD1	-5.10	119.26	126.90
2	B	48	ASN	CB-CG-ND2	5.09	124.03	116.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	139	ALA	N-CA-C	-5.08	104.16	110.41
2	B	145	ARG	CD-NE-CZ	5.08	131.51	124.40
4	E	54	ARG	NE-CZ-NH2	5.06	123.75	119.20
2	B	138	THR	CA-CB-OG1	-5.02	102.07	109.60
3	C	216	GLY	CA-C-N	5.02	128.23	121.05
3	C	216	GLY	C-N-CA	5.02	128.23	121.05

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	74	0	81	1	0
2	B	980	0	951	12	1
3	C	702	0	698	13	21
4	E	1036	0	1002	9	22
5	A	11	0	0	0	0
5	B	95	0	0	3	0
5	C	45	0	0	3	0
5	E	66	0	0	0	0
All	All	3009	0	2732	28	22

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 (28) 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)
2:B:48:ASN:HD22	2:B:50:ASN:H	1.28	0.82
3:C:192:MET:HE3	4:E:84:MET:SD	2.34	0.67
2:B:36:LYS:HG2	5:B:232:HOH:O	2.00	0.61
2:B:36:LYS:O	2:B:36:LYS:HD3	2.04	0.58
2:B:40:HIS:H	3:C:149:ALA:HB2	1.72	0.55
4:E:59:LEU:HB2	4:E:101:LEU:HD22	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:48:ASN:HD21	2:B:51:TRP:HD1	1.58	0.52
3:C:232:THR:HB	5:C:250:HOH:O	2.10	0.52
5:B:148:HOH:O	3:C:197:GLY:HA3	2.12	0.50
2:B:48:ASN:HD22	2:B:50:ASN:N	2.04	0.47
2:B:48:ASN:ND2	2:B:50:ASN:H	2.02	0.47
3:C:165:ASN:ND2	3:C:230:ARG:HH11	2.12	0.47
3:C:149:ALA:N	3:C:150:ASN:OD1	2.47	0.47
2:B:16:ILE:HG21	3:C:158:ALA:HB2	1.97	0.45
3:C:178:ASP:HB3	5:C:285:HOH:O	2.17	0.45
1:A:10:LEU:HD13	3:C:157:GLN:NE2	2.31	0.45
2:B:60:VAL:HG23	5:B:157:HOH:O	2.16	0.44
4:E:57:GLY:HA3	4:E:74:PHE:CZ	2.52	0.44
3:C:150:ASN:OD1	4:E:86:ALA:HB1	2.19	0.43
4:E:25:ILE:HB	4:E:115:ILE:HB	2.00	0.43
3:C:232:THR:HG21	5:C:259:HOH:O	2.18	0.42
4:E:15:GLN:HA	4:E:22:ARG:HH11	1.84	0.42
2:B:16:ILE:O	2:B:144:THR:HA	2.20	0.42
2:B:40:HIS:HB3	3:C:149:ALA:HA	2.02	0.41
3:C:212:ILE:HD13	3:C:212:ILE:HG21	1.83	0.41
4:E:47:GLU:HA	4:E:93:GLU:O	2.21	0.41
2:B:42:CYS:SG	4:E:85:MET:HG2	2.60	0.41
4:E:22:ARG:HG3	4:E:118:TYR:CZ	2.56	0.41

All (22) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:166:THR:CG2	4:E:34:SER:OG[2_656]	0.57	1.63
3:C:166:THR:N	4:E:32:ASP:OD1[2_656]	0.65	1.55
3:C:166:THR:CA	4:E:32:ASP:OD1[2_656]	1.00	1.20
3:C:166:THR:CG2	4:E:34:SER:CB[2_656]	1.04	1.16
3:C:166:THR:CB	4:E:34:SER:OG[2_656]	1.15	1.05
3:C:166:THR:CA	4:E:32:ASP:CG[2_656]	1.39	0.81
3:C:165:ASN:CB	4:E:31:GLU:O[2_656]	1.52	0.68
3:C:166:THR:N	4:E:32:ASP:CG[2_656]	1.54	0.66
3:C:166:THR:OG1	4:E:34:SER:N[2_656]	1.64	0.56
3:C:166:THR:CA	4:E:32:ASP:OD2[2_656]	1.67	0.53
3:C:166:THR:CB	4:E:32:ASP:OD1[2_656]	1.84	0.36
2:B:129:ASP:OD2	4:E:112:LYS:NZ[2_656]	1.87	0.33
3:C:165:ASN:C	4:E:32:ASP:OD1[2_656]	1.87	0.33

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:166:THR:CB	4:E:34:SER:CB[2_656]	1.94	0.26
3:C:165:ASN:C	4:E:32:ASP:CG[2_656]	2.00	0.20
3:C:166:THR:CG2	4:E:34:SER:CA[2_656]	2.00	0.20
3:C:166:THR:CA	4:E:34:SER:OG[2_656]	2.04	0.16
3:C:178:ASP:OD2	4:E:31:GLU:N[2_656]	2.10	0.10
3:C:166:THR:OG1	4:E:32:ASP:C[2_656]	2.11	0.09
3:C:166:THR:OG1	4:E:32:ASP:OD1[2_656]	2.15	0.05
3:C:166:THR:OG1	4:E:32:ASP:O[2_656]	2.16	0.04
3:C:165:ASN:CG	4:E:31:GLU:O[2_656]	2.19	0.01

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	9/13 (69%)	9 (100%)	0	0	100	100
2	B	129/131 (98%)	124 (96%)	5 (4%)	0	100	100
3	C	95/97 (98%)	92 (97%)	2 (2%)	1 (1%)	11	7
4	E	132/142 (93%)	126 (96%)	6 (4%)	0	100	100
All	All	365/383 (95%)	351 (96%)	13 (4%)	1 (0%)	36	35

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	151	THR

5.3.2 Protein sidechains [i](#)

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	9/10 (90%)	9 (100%)	0	100	100
2	B	109/109 (100%)	102 (94%)	7 (6%)	16	12
3	C	77/77 (100%)	72 (94%)	5 (6%)	15	12
4	E	107/125 (86%)	95 (89%)	12 (11%)	6	3
All	All	302/321 (94%)	278 (92%)	24 (8%)	11	8

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	36	LYS
2	B	48	ASN
2	B	62	THR
2	B	96	SER
2	B	97	LEU
2	B	109	SER
2	B	123	LEU
3	C	165	ASN
3	C	192	MET
3	C	203	LYS
3	C	232	THR
3	C	234	LEU
4	E	7	LEU
4	E	15	GLN
4	E	48	VAL
4	E	55	LEU
4	E	76	LYS
4	E	77	VAL
4	E	79	SER
4	E	98	THR
4	E	108	ARG
4	E	113	LEU
4	E	121	ASP
4	E	135	LYS

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

Mol	Chain	Res	Type
2	B	48	ASN
3	C	165	ASN

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Mol	Chain	Res	Type
3	C	167	ASN
4	E	23	GLN
4	E	30	GLN
4	E	138	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 oligosaccharides 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 [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	11/13 (84%)	0.01	0 100 100	15, 20, 36, 55	0
2	B	131/131 (100%)	-0.41	4 (3%) 51 50	6, 17, 44, 64	0
3	C	97/97 (100%)	-0.19	2 (2%) 63 63	9, 20, 44, 71	0
4	E	136/142 (95%)	0.36	5 (3%) 45 44	15, 37, 64, 76	0
All	All	375/383 (97%)	-0.06	11 (2%) 53 52	6, 25, 58, 76	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	75	SER	3.1
3	C	149	ALA	2.6
4	E	79	SER	2.5
2	B	74	GLY	2.5
4	E	5	GLN	2.3
2	B	76	SER	2.1
4	E	78	SER	2.1
2	B	130	PHE	2.1
4	E	89	ASP	2.0
3	C	150	ASN	2.0
4	E	29	PRO	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.