WORLDWIDE wwPDB PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 31, 2021 – 09:36 PM EDT

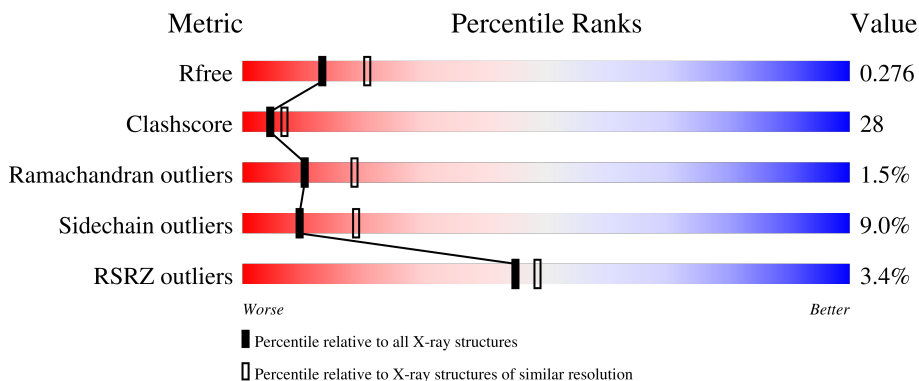|		
PDB ID	:	1UIJ
Title	:	Crystal Structure Of Soybean beta-Conglycinin Beta Homotrimer (I122M/K124W)
Authors	:	Maruyama, N.; Maruyama, Y.; Tsuruki, T.; Okuda, E.; Yoshikawa, M.; Utsumi, S.
Deposited on	:	2003-07-16
Resolution	:	2.50 Å(reported)

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.
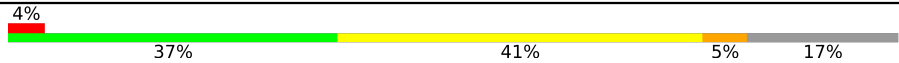
Metric	Percentile Ranks	Value
Rfree		0.276
Clashscore		28
Ramachandran outliers		1.5%
Sidechain outliers		9.0%
RSRZ outliers		3.4%

Worse   *Better*

▌ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

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 <=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	416	2% / 52% / 33% / 5% / 9%
1	B	416	2% / 47% / 36% / 5% / 11%
1	C	416	5% / 40% / 38% / 5% / 17%
1	D	416	2% / 49% / 36% / 6% / 9%
1	E	416	3% / 46% / 39% / • / 11%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	416	

2 Entry composition ⓘ

There are 2 unique types of molecules in this entry. The entry contains 18133 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 beta subunit of beta conglycinin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	377	Total 3087	C 1947	N 550	O 589	S 1	0	0	0
1	B	370	Total 3022	C 1911	N 538	O 572	S 1	0	0	0
1	C	346	Total 2824	C 1797	N 494	O 532	S 1	0	0	0
1	D	377	Total 3087	C 1947	N 550	O 589	S 1	0	0	0
1	E	370	Total 3022	C 1911	N 538	O 572	S 1	0	0	0
1	F	346	Total 2824	C 1797	N 494	O 532	S 1	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	122	MET	ILE	engineered mutation	UNP P25974
A	124	TRP	LYS	engineered mutation	UNP P25974
B	122	MET	ILE	engineered mutation	UNP P25974
B	124	TRP	LYS	engineered mutation	UNP P25974
C	122	MET	ILE	engineered mutation	UNP P25974
C	124	TRP	LYS	engineered mutation	UNP P25974
D	122	MET	ILE	engineered mutation	UNP P25974
D	124	TRP	LYS	engineered mutation	UNP P25974
E	122	MET	ILE	engineered mutation	UNP P25974
E	124	TRP	LYS	engineered mutation	UNP P25974
F	122	MET	ILE	engineered mutation	UNP P25974
F	124	TRP	LYS	engineered mutation	UNP P25974

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	62	Total 62	O 62	0	0
2	B	53	Total 53	O 53	0	0
2	C	19	Total 19	O 19	0	0
2	D	65	Total 65	O 65	0	0
2	E	47	Total 47	O 47	0	0
2	F	21	Total 21	O 21	0	0

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.
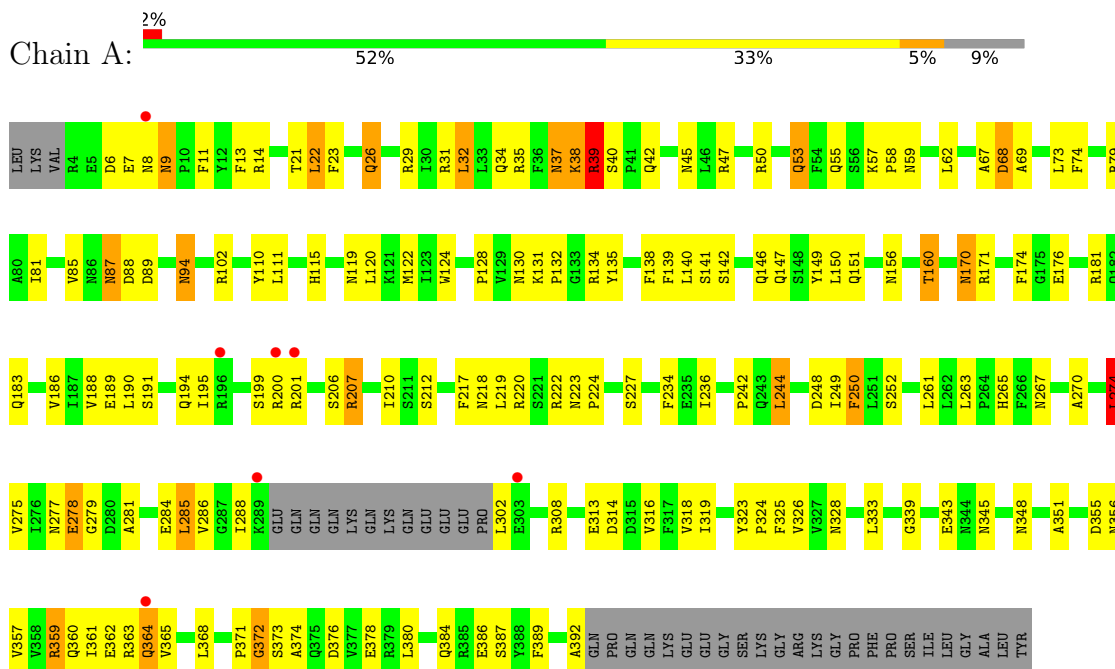
- Molecule 1: beta subunit of beta conglycinin

- Molecule 1: beta subunit of beta conglycinin

F325 N328 A329 T330 S331 N332 L333 N334 F335 N345 Q346 R347 N348 F349 L350 E353 R359 Q360 R363 Q364 V365 A369 V377 E378 R379 L380 L381 K382 K383 Q384 R385 E386 S387 Y388 F389 A392 GLN PRO GLN LYS GLU GLY SER LYS GLY ARG LYS GLY PRO

PHE PRO SER ILE GLY ALA LEU TYR

• Molecule 1: beta subunit of beta conglycinin

Chain C:

5%

40%   38%   5%   17%

LEU LYS VAL ARG GLU D6 E7 N8 N9 P10 F13 R14 S15 S16 N17 L22 F23 E24 N25 Q26 N27 G28 R29 I30 R31 L32 L33 Q34 R35 F36 N37 K38 R39 S40 R50 I51 V52 Q53 F54 Q55 S56 K57 P58 N59 T60 I61 L62 L63 P64 H65 D68 F71 L72 L73

L76 S77 G78 R79 A80 I81 L82 V85 N86 N87 D88 D89 R90 D91 N94 D99 A100 Q101 R102 I103 T108 Y109 V110 L111 V112 N113 P114 H115 D116 H117 Q118 N119 L120 K121 M122 I123 W124 L125 V129 Y135 F138 F139 L140 S141 Q146 Q147 Q151 F166 I169

N170 R171 V172 L173 F174 G175 E178 E181 E182 Q183 E184 G185 V186 I187 V188 E189 L190 SER LYS GLU ILE ARG GLN LEU SER ARG ALA LYS SER SER SER ARG LYS THR ILE SER SER GLU D191 E192 P193 F194 N195 L196 R197 S198 R199 I202 Y203 S204 N205 N206 F207

F210 I213 T214 P215 E216 K217 Q220 L221 R222 F227 L228 S229 S230 V231 E235 G236 A237 L238 L239 L240 P241 H242 K246 A247 L251 V252 I253 N254 E255 G256 D257 A258 N259 I260 E261 L262 V263 K266 GLU GLN GLN GLN LYS GLN LYS GLN GLU GLU GLU P301 L302 E303

V304 Q305 R306 Y307 R308 L311 S312 E313 D314 D315 V316 I319 P320 Y323 P324 F325 V326 V327 N328 A329 T330 S331 N332 L333 N334 F335 L336 A337 N345 F349 V358 R359 E362 R363 Q364 V365 Q366 E367 L368 S373 V377 E378 R379 L380 L381 K382 K383 Q384 R385 E386 S387

Y388 F389 V390 D391 A392 GLN PRO GLN LYS GLU GLU SER LYS GLY ARG LYS GLY PRO PHE PRO SER ILE GLY ALA LEU TYR

• Molecule 1: beta subunit of beta conglycinin

Chain D:

2%

49%   36%   6%   9%

LEU LYS VAL R4 E5 D6 E7 N8 N9 P10 F11 Y12 F13 N17 S18 F19 Q20 T21 L22 F23 E24 N25 Q26 N27 G28 R29 I30 R31 L32 L33 Q34 R35 F36 N37 K38 R39 S40 P41 Q42 R50 Q53 F54 Q55 S56 K57 P58 N59 T60 I61 L62 A67 D68 A69 D70 F71 L72

L73 F74 V75 R79 A80 V85 N86 N87 D88 D89 N94 L95 Q101 R102 A105 Y110 L111 P114 H115 D116 L120 K121 M122 I123 W124 L125 P128 V129 N130 K131 R134 Y135 F138 F139 L140 Q146 Y149 L150 Q151 G152 N156 I157 T160 N170

R171 V172 L173 F174 G175 E176 R181 Q182 Q183 E184 G185 V186 I187 V188 E189 L190 S191 K192 E193 Q194 I195 R196 Q197 L198 S199 R200 R201 S206 R207 I210 S211 S212 E213 P216 F217 N218 L219 R220 S221 R222 N223 P224 I225 Y226 S227 N228 I236 T237 P238 E239 K240 N241 P242 Q243 L244

R245 I249 F250 L251 L262 L263 N267 A270 L274 V275 E278 G279 L285 V286 G287 I288 K289 GLU GLN GLN GLN LYS GLN LYS GLN GLU GLU GLU PRO L302 E303 V304 Q305 R306 Y307 R308 V316 F317 V318 I319 P320 A321 A322 Y323 N328

F252 S253 V254 E258

S331 N332 F335 L336 A337 N345 F349 L350 A351 D355 N356 V357 R358 R359 R363 Q364 V365 L368 G372 S373 A374 Q375 E378 R379 L380 L381 K382 K383 Q384 R385 E386 S387 Y388 F389 V390 D391 A392 GLN PRO GLN LYS GLU GLY SER LYS ARG LYS GLY

PRO PHE PRO SER ILE LEU GLY ALA LEU TYR

• **Molecule 1: beta subunit of beta conglycinin**

Chain E:

3%

46%　　　　　　　　　　　39%　　　•　　11%

LEU LYS VAL R4 E5 D6 E7 N8 N9 P10 F11 Y12 F13 F19 Q20 T21 L22 Q26 I30 R31 L32 L33 N37 K38 R39 N45 L46 R47 D48 Y49 R50 V52 Q53 F54 K57 P58 T60 I61 L62 D68 L73 R79 A80 I81 L82 T83 L84 V85 N86

N87 D88 D89 R90 D91 S92 Y93 N94 Q101 R102 T108 Y109 Y110 L111 V112 D116 H117 L120 K121 M122 I123 W124 V129 P132 Y135 L140 A145 Q146 S154 E159 T160 S161 F162 E165 F166 E167 E168 I169 N170 R171 V172 L173 F174 G175 GLU GLU GLU

GLN ARG GLN Q183 E189 L190 S191 K192 E193 Q194 I195 R196 Q197 L198 S199 R200 R201 S205 S206 R207 K208 T209 E215 P216 F217 N218 L219 R220 S221 R222 Y226 F230 F233 F234 E235 I236 T237 P238 E239 K240 N241 P242 Q243 L244 L247 D248 I249 F250 V254 E258 G259

A260 L261 L262 L263 P264 H265 F266 N267 S268 K269 A270 L274 N277 A281 E284 L285 V286 K289 GLU GLN GLN GLN LYS GLN GLU GLU GLU PRO L302 E303 V304 Q305 R306 Y307 R308 E313 D314 D315 V316 F317 V318 I319 P320 A321 A322 F325 V326 V327 N328 S331

N332 L333 N334 F335 I340 E343 N344 N345 N348 F349 E353 N356 V357 V358 R359 Q360 R363 Q364 V365 Q366 E367 L368 Q375 D376 V377 E378 R379 L380 L381 Q384 R385 E386 S387 Y388 F389 V390 D391 A392 GLN PRO GLN LYS GLU GLU GLY SER LYS ARG LYS GLY

PRO PHE PRO SER ILE LEU GLY ALA LEU TYR

• **Molecule 1: beta subunit of beta conglycinin**

Chain F:

4%

37%　　　　　　　　41%　　　5%　　17%

LEU LYS VAL ARG GLU D6 E7 N8 N9 P10 F11 Y12 F13 R14 S15 S16 Q20 T21 L22 F23 E24 N25 Q26 N27 I30 R31 L32 L33 Q34 N37 K38 R39 N45 D48 Y49 R50 I51 V52 Q53 F54 Q55 S56 K57 P58 N59 T60 I61 L62 H65 D68 F71 L72

L73 R79 A80 I81 L82 V85 N86 N87 D88 D89 R90 N94 L95 H96 D99 A100 Q101 R102 T108 Y109 Y110 L111 V112 N113 V124 H115 D116 H117 Q118 N119 L120 K121 M122 I123 W124 L125 A126 P132 F138 F139 L140 S141 S142 T143 Q146 Q147 S148 Q151 T160

F166 E167 E168 I169 N170 R171 F174 G175 GLU GLU GLU GLN GLN ARG GLN Q183 E184 G185 V188 E189 L190 SER LYS GLU GLN ILE ARG GLN LEU SER ARG ARG ALA LYS SER SER ARG LYS THR ILE SER GLU D191 E192 N195 L196 R197 S198 R199 N200 P201 I202 N205 N206

F207 F210 F211 E212 I213 T214 P215 E216 K217 N218 P219 Q220 L221 R222 D225 I226 F227 L228 S229 S230 V231 D232 I233 N234 E235 G236 A237 L238 L239 L240 P241 H242 F243 N244 S245 K246 A247 I251 V252 I253 N254 E255 G256 D257 A258 N259 I260 E261 L262 K266 GLU GLN GLN GLN LYS GLN

LYS GLN GLU GLU GLU P301 L302 E303 R306 Y307 R308 A309 E310 L311 S312 E313 D314 D315 I319 P320 A321 A322 Y323 V326 V327 N328 A329 T330 S331 N332 L333 N334 A337 F338 G339 E343 N344 N345 R347 N348 F349 L350 A351 S352 E353 V357 V358 R359 Q360 I361 E362 R363 Q364

WORLD WIDE
PDB
PROTEIN DATA BANK

4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	130.26Å 62.58Å 159.01Å 90.00° 90.44° 90.00°	Depositor
Resolution (Å)	8.00 – 2.50 20.00 – 2.50	Depositor EDS
% Data completeness (in resolution range)	(Not available) (8.00-2.50) 93.8 (20.00-2.50)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.85 (at 2.50Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.221 , 0.273 0.224 , 0.276	Depositor DCC
R_{free} test set	4277 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å^2)	39.4	Xtriage
Anisotropy	0.638	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 61.4	EDS
L-test for twinning[2]	$< |L| > = 0.50, < L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.018 for h,-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	18133	wwPDB-VP
Average B, all atoms (Å^2)	43.0	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 43.83 % 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 1.6659e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

---

[1]Intensities estimated from amplitudes.
[2]Theoretical values of $< |L| >$, $< L^2 >$ 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 ⓘ

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	0.39	0/3150	0.68	1/4260 (0.0%)
1	B	0.40	0/3084	0.67	1/4171 (0.0%)
1	C	0.34	0/2886	0.61	0/3910
1	D	0.39	0/3150	0.68	1/4260 (0.0%)
1	E	0.39	0/3084	0.65	0/4171
1	F	0.35	0/2886	0.62	1/3910 (0.0%)
All	All	0.38	0/18240	0.66	4/24682 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	274	LEU	CA-CB-CG	6.46	130.16	115.30
1	F	251	LEU	CA-CB-CG	5.72	128.46	115.30
1	D	274	LEU	CA-CB-CG	5.45	127.84	115.30
1	A	274	LEU	CA-CB-CG	5.34	127.59	115.30

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	3087	0	3004	150	0
1	B	3022	0	2950	157	0
1	C	2824	0	2739	202	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	3087	0	3004	163	0
1	E	3022	0	2950	176	0
1	F	2824	0	2739	210	0
2	A	62	0	0	3	0
2	B	53	0	0	3	0
2	C	19	0	0	0	0
2	D	65	0	0	4	0
2	E	47	0	0	5	0
2	F	21	0	0	2	0
All	All	18133	0	17386	1002	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 28.

The worst 5 of 1002 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:59:ASN:HD22	1:B:195:ILE:HD12	1.03	1.07
1:E:90:ARG:HH11	1:F:362:GLU:HG2	1.19	1.05
1:E:59:ASN:HD22	1:E:195:ILE:HD12	1.20	1.05
1:A:26:GLN:H	1:A:26:GLN:HE21	1.04	1.03
1:A:183:GLN:HG2	1:A:188:VAL:HG11	1.42	1.01

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	373/416 (90%)	348 (93%)	21 (6%)	4 (1%)	14	26
1	B	364/416 (88%)	343 (94%)	14 (4%)	7 (2%)	8	13

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	338/416 (81%)	306 (90%)	25 (7%)	7 (2%)	7	11
1	D	373/416 (90%)	342 (92%)	27 (7%)	4 (1%)	14	26
1	E	364/416 (88%)	340 (93%)	20 (6%)	4 (1%)	14	26
1	F	338/416 (81%)	295 (87%)	37 (11%)	6 (2%)	8	14
All	All	2150/2496 (86%)	1974 (92%)	144 (7%)	32 (2%)	10	18

5 of 32 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	6	ASP
1	C	7	GLU
1	D	6	ASP
1	E	6	ASP
1	E	201	ARG

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	341/375 (91%)	309 (91%)	32 (9%)	8	17
1	B	334/375 (89%)	301 (90%)	33 (10%)	8	15
1	C	311/375 (83%)	287 (92%)	24 (8%)	13	25
1	D	341/375 (91%)	304 (89%)	37 (11%)	6	12
1	E	334/375 (89%)	307 (92%)	27 (8%)	11	23
1	F	311/375 (83%)	287 (92%)	24 (8%)	13	25
All	All	1972/2250 (88%)	1795 (91%)	177 (9%)	9	19

5 of 177 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	254	VAL
1	E	244	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	275	VAL
1	E	22	LEU
1	E	328	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 175 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	345	ASN
1	E	334	ASN
1	D	384	GLN
1	E	94	ASN
1	F	9	ASN

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 monosaccharides 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 ⓘ

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	377/416 (90%)	-0.16	7 (1%)	66	69	18, 34, 67, 82	0
1	B	370/416 (88%)	-0.02	10 (2%)	54	58	14, 36, 62, 76	0
1	C	346/416 (83%)	0.39	19 (5%)	25	26	25, 54, 74, 85	0
1	D	377/416 (90%)	-0.14	7 (1%)	66	69	17, 32, 67, 80	0
1	E	370/416 (88%)	0.04	14 (3%)	40	43	15, 39, 69, 78	0
1	F	346/416 (83%)	0.36	18 (5%)	27	29	28, 53, 75, 84	0
All	All	2186/2496 (87%)	0.07	75 (3%)	45	48	14, 40, 70, 85	0

The worst 5 of 75 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	117	HIS	5.3
1	C	26	GLN	4.5
1	F	301	PRO	4.4
1	E	207	ARG	4.3
1	D	200	ARG	4.1

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.