



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 04:43 PM UTC

PDB ID : 1P1F / pdb_00001p1f
Title : Crystal structure of apo 1L-myo-inositol 1-phosphate synthase
Authors : Jin, X.; Geiger, J.H.
Deposited on : 2003-04-12
Resolution : 2.60 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

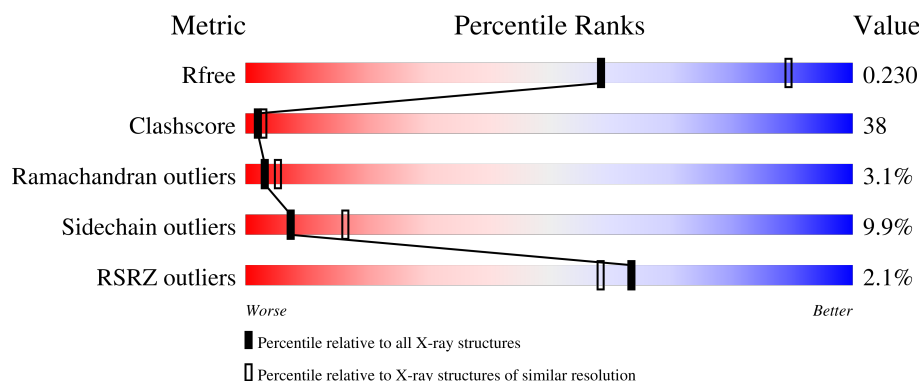
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	533	% 40% 45% 9% 6%
1	B	533	3% 36% 46% 10% 7%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 8005 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 Inositol-3-phosphate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	501	Total	C	N	O	S	0	0	0
			3953	2519	661	757	16			
1	B	496	Total	C	N	O	S	0	0	0
			3919	2500	655	748	16			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	ARG	SEE REMARK 999	UNP P11986
A	14	VAL	LEU	SEE REMARK 999	UNP P11986
A	?	-	PHE	SEE REMARK 999	UNP P11986
A	60	LEU	GLU	SEE REMARK 999	UNP P11986
A	?	-	ALA	SEE REMARK 999	UNP P11986
A	98	GLU	LYS	SEE REMARK 999	UNP P11986
A	140	ASN	LYS	SEE REMARK 999	UNP P11986
A	141	ASP	HIS	SEE REMARK 999	UNP P11986
A	201	ASN	GLN	SEE REMARK 999	UNP P11986
A	444	PRO	ALA	SEE REMARK 999	UNP P11986
B	?	-	ARG	SEE REMARK 999	UNP P11986
B	14	VAL	LEU	SEE REMARK 999	UNP P11986
B	?	-	PHE	SEE REMARK 999	UNP P11986
B	60	LEU	GLU	SEE REMARK 999	UNP P11986
B	?	-	ALA	SEE REMARK 999	UNP P11986
B	98	GLU	LYS	SEE REMARK 999	UNP P11986
B	140	ASN	LYS	SEE REMARK 999	UNP P11986
B	141	ASP	HIS	SEE REMARK 999	UNP P11986
B	201	ASN	GLN	SEE REMARK 999	UNP P11986
B	444	PRO	ALA	SEE REMARK 999	UNP P11986

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	80	Total 80	O 80	0	0
2	B	53	Total 53	O 53	0	0

P499	V500	N501	G502	S503	N504	K505	Q506	R507	T508	A509	L510	E511	N512	F513	L514	R515	L516	L517	I518	G519	L520	P521	L526	R527	F528	E529	E530	R531	L532	L533	
V435		D438	S439	L440	L441		L445	I446		L449	L450	V451	M452	T453	E454	F455	C456	T457	R458	V459	S460	Y461	K462	K463	V464	D465	P466	VAL	GLU	ASP	ALA
GLY	TYR	ASN	LEU	SER	ALA	PRO	LYS	GLN	PHE	ARG	N299	F301	LYS	GLU	ILE	SER	LYS	SER	SER	V376	I377	D378	D379	I380	I381	T386	L387	L388	L389	L390	L391
E288	G289	V290		I293	N294	G295	S296	P297	Q298	N299	T300	F301	V302	L305	V306	Q307	L308	A309	E310	H311	E312	G313	T314	F315	I316	A317	G318	D319	D320	L321	K322
E289	G290		I294	N295	G296	S297	Q298	N299	T300	F301	V302	L305	V306	Q307	L308	A309	E310	H311	E312	G313	T314	F315	I316	A317	G318	D319	D320	L321	K322	S323	G324
E290		I295	N296	G297	S298	P299	Q299	N300	T301	V302	L305	V306	Q307	L308	A309	E310	H311	E312	G313	T314	F315	I316	A317	G318	D319	D320	L321	K322	S323	G324	Q325
E291		I296	N297	G298	S299	P300	Q301	N302	T303	V304	L305	V306	Q307	L308	A309	E310	H311	E312	G313	T314	F315	I316	A317	G318	D319	D320	L321	K322	S323	G324	T326
E292		I297	N298	G299	S300	P301	Q302	N303	T304	V305	L306	V307	Q308	L309	A310	E311	H312	E313	G314	T315	F316	I317	A318	G319	D320	L321	K322	S323	G324	K327	L328
E293		I298	N299	G300	S301	P302	Q303	N304	T305	V306	L307	V308	Q309	L310	A311	E312	H313	E314	G315	T316	F317	I318	A319	G320	D321	L322	K323	S324	G325	K328	L329
E294		I299	N300	G301	S302	P303	Q304	N305	T306	V307	L308	V309	Q310	L311	A312	E313	H314	E315	G316	T317	F318	I319	A320	G321	D322	L323	K324	S325	G326	K329	L330
E295		I300	N301	G302	S303	P304	Q305	N306	T307	V308	L309	V310	Q311	L312	A313	E314	H315	E316	G317	T318	F319	I320	A321	G322	D323	L324	K325	S326	G327	K330	L331
E296		I301	N302	G303	S304	P305	Q306	N307	T308	V309	L310	V311	Q312	L313	A314	E315	H316	E317	G318	T319	F320	I321	A322	G323	D324	L325	K326	S327	G328	K331	L332
E297		I302	N303	G304	S305	P306	Q307	N308	T309	V310	L311	V312	Q313	L314	A315	E316	H317	E318	G319	T320	F321	I322	A323	G324	D325	L326	K327	S328	G329	K332	L333
E298		I303	N304	G305	S306	P307	Q308	N309	T310	V311	L312	V313	Q314	L315	A316	E317	H318	E319	G320	T321	F322	I323	A324	G325	D326	L327	K328	S329	G330	K333	L334
E299		I304	N305	G306	S307	P308	Q309	N310	T311	V312	L313	V314	Q315	L316	A317	E318	H319	E320	G321	T322	F323	I324	A325	G326	D327	L328	K329	S330	G331	K334	L335
E300		I305	N306	G307	S308	P309	Q310	N311	T312	V313	L314	V315	Q316	L317	A318	E319	H320	E321	G322	T323	F324	I325	A326	G327	D328	L329	K330	S331	G332	K335	L336
E301		I306	N307	G308	S309	P310	Q311	N312	T313	V314	L315	V316	Q317	L318	A319	E320	H321	E322	G323	T324	F325	I326	A327	G328	D329	L330	K331	S332	G333	K336	L337
E302		I307	N308	G309	S310	P311	Q312	N313	T314	V315	L316	V317	Q318	L319	A320	E321	H322	E323	G324	T325	F326	I327	A328	G329	D330	L331	K332	S333	G334	K337	L338
E303		I308	N309	G310	S311	P312	Q313	N314	T315	V316	L317	V318	Q319	L320	A321	E322	H323	E324	G325	T326	F327	I328	A329	G330	D331	L332	K333	S334	G335	K338	L339
E304		I309	N310	G311	S312	P313	Q314	N315	T316	V317	L318	V319	Q320	L321	A322	E323	H324	E325	G326	T327	F328	I329	A330	G331	D332	L333	K334	S335	G336	K339	L340
E305		I310	N311	G312	S313	P314	Q315	N316	T317	V318	L319	V320	Q321	L322	A323	E324	H325	E326	G327	T328	F329	I330	A331	G332	D333	L334	K335	S336	G337	K340	L341
E306		I311	N312	G313	S314	P315	Q316	N317	T318	V319	L320	V321	Q322	L323	A324	E325	H326	E327	G328	T329	F330	I331	A332	G333	D334	L335	K336	S337	G338	K341	L342
E307		I312	N313	G314	S315	P316	Q317	N318	T319	V320	L321	V322	Q323	L324	A325	E326	H327	E328	G329	T330	F331	I332	A333	G334	D335	L336	K337	S338	G339	K342	L343
E308		I313	N314	G315	S316	P317	Q318	N319	T320	V321	L322	V323	Q324	L325	A326	E327	H328	E329	G330	T331	F332	I333	A334	G335	D336	L337	K338	S339	G340	K343	L344
E309		I314	N315	G316	S317	P318	Q319	N320	T321	V322	L323	V324	Q325	L326	A327	E328	H329	E330	G331	T332	F333	I334	A335	G336	D337	L338	K339	S340	G341	K344	L345
E310		I315	N316	G317	S318	P319	Q320	N321	T322	V323	L324	V325	Q326	L327	A328	E329	H330	E331	G332	T333	F334	I335	A336	G337	D338	L339	K340	S341	G342	K345	L346
E311		I316	N317	G318	S319	P320	Q321	N322	T323	V324	L325	V326	Q327	L328	A329	E330	H331	E332	G333	T334	F335	I336	A337	G338	D339	L340	K341	S342	G343	K346	L347
E312		I317	N318	G319	S320	P321	Q322	N323	T324	V325	L326	V327	Q328	L329	A330	E331	H332	E333	G334	T335	F336	I337	A338	G339	D340	L341	K342	S343	G344	K347	L348
E313		I318	N319	G320	S321	P322	Q323	N324	T325	V326	L327	V328	Q329	L330	A331	E332	H333	E334	G335	T336	F337	I338	A339	G340	D341	L342	K343	S344	G345	K348	L349
E314		I319	N320	G321	S322	P323	Q324	N325	T326	V327	L328	V329	Q330	L331	A332	E333	H334	E335	G336	T337	F338	I339	A340	G341	D342	L343	K344	S345	G346	K349	L350
E315		I320	N321	G322	S323	P324	Q325	N326	T327	V328	L329	V330	Q331	L332	A333	E334	H335	E336	G337	T338	F339	I340	A341	G342	D343	L344	K345	S346	G347	K350	L351
E316		I321	N322	G323	S324	P325	Q326	N327	T328	V329	L330	V331	Q332	L333	A334	E335	H336	E337	G338	T339	F340	I341	A342	G343	D344	L345	K346	S347	G348	K351	L352
E317		I322	N323	G324	S325	P326	Q327	N328	T329	V330	L331	V332	Q333	L334	A335	E336	H337	E338	G339	T340	F341	I342	A343	G344	D345	L346	K347	S348	G349	K352	L353
E318		I323	N324	G325	S326	P327	Q328	N329	T330	V331	L332	V333	Q334	L335	A336	E337	H338	E339	G340	T341	F342	I343	A344	G345	D346	L347	K348	S349	G350	K353	L354
E319		I324	N325	G326	S327	P328	Q329	N330	T331	V332	L333	V334	Q335	L336	A337	E338	H339	E340	G341	T342	F343	I344	A345	G346	D347	L348	K349	S350	G351	K354	L355
E320		I325	N326	G327	S328	P329	Q330	N331	T332	V333	L334	V335	Q336	L337	A338	E339	H340	E341	G342	T343	F344	I345	A346	G347	D348	L349	K350	S351	G352	K355	L356
E321		I326	N327	G328	S329	P330	Q331	N332	T333	V334	L335	V336	Q337	L338	A339	E340	H341	E342	G343	T344	F345	I346	A347	G348	D349	L350	K351	S352	G353	K356	L357
E322		I327	N328	G329	S330	P331	Q332	N333	T334	V335	L336	V337	Q338	L339	A340	E341	H342	E343	G344	T345	F346	I347	A348	G349	D350	L351	K352	S353	G354	K357	L358
E323		I328	N329	G330	S331	P332	Q333	N334	T335	V336	L337	V338	Q339	L340	A341	E342	H343	E344	G345	T346	F347	I348	A349	G350	D351	L352	K353	S354	G355	K358	L359
E324		I329	N330	G331	S332	P333	Q334	N335	T336	V337	L338	V339	Q340	L341	A342	E343	H344	E345	G346	T347	F348	I349	A350	G351	D352	L353	K354	S355	G356	K359	L360
E325		I330	N331	G332	S333	P334	Q335	N336	T337	V338	L339	V340	Q341	L342	A343	E344	H345	E346	G347	T348	F349	I350	A351	G352	D353	L354	K355	S356	G357	K360	L361
E326		I331	N332	G333	S334	P335	Q336	N337	T338	V339	L340	V341	Q342	L343	A344	E345	H346	E347	G348	T349	F350	I351	A352	G353	D354	L355	K356	S357	G358	K361	L362
E327		I332	N333	G334	S335	P336	Q337	N338	T339	V340	L341	V342	Q343	L344	A345	E346	H347	E348	G349	T350	F351	I352	A353	G354	D355	L356	K357	S358	G359	K362	L363
E328		I333	N334	G335	S336	P337	Q338	N339	T340	V341	L342	V343	Q344	L345	A346	E347	H348	E349	G350	T351	F352	I353	A354	G355	D356	L357	K358	S359	G360	K363	L364
E329		I334	N335	G336	S337	P338	Q339	N340	T341	V342	L343	V344	Q345	L346	A347	E348	H349	E350	G351	T352	F353	I354	A355	G356	D357	L358	K359	S360	G361	K364	L365
E330		I335	N336	G337	S338	P339	Q340	N341	T342	V343	L344	V345	Q346	L347	A348	E349	H350	E351	G352	T353	F354	I355	A356	G357	D358	L359	K360	S361	G362	K365	L366
E331		I336	N337	G338	S339	P340	Q341	N342	T343	V344	L345	V346	Q347	L348	A349	E350	H351	E352	G353	T354	F355	I356	A357	G358	D359	L360	K361	S362	G363	K366	L367
E332		I337	N338	G339	S340	P341	Q342	N343	T344																						

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	153.54Å 97.06Å 122.06Å 90.00° 125.72° 90.00°	Depositor
Resolution (Å)	10.00 – 2.60 10.00 – 2.60	Depositor EDS
% Data completeness (in resolution range)	(Not available) (10.00-2.60) 89.4 (10.00-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.47 (at 2.61Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.190 , 0.278 0.227 , 0.230	Depositor DCC
R_{free} test set	2231 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	38.3	Xtriage
Anisotropy	0.558	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 73.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	8005	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.15% 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 [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	0.46	0/4030	1.00	16/5465 (0.3%)
1	B	0.71	1/3995 (0.0%)	1.07	29/5417 (0.5%)
All	All	0.60	1/8025 (0.0%)	1.04	45/10882 (0.4%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	463	LYS	C-N	34.26	1.80	1.33

The worst 5 of 45 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	463	LYS	CA-C-N	-15.98	93.20	121.97
1	B	463	LYS	C-N-CA	-15.98	93.20	121.97
1	B	463	LYS	O-C-N	10.27	136.34	122.57
1	A	377	ILE	N-CA-C	-9.24	103.39	112.17
1	A	331	VAL	N-CA-C	-9.16	104.39	111.62

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	3953	0	3964	292	0
1	B	3919	0	3933	334	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	80	0	0	8	0
2	B	53	0	0	7	0
All	All	8005	0	7897	600	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 38.

The worst 5 of 600 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:55:VAL:HG23	1:B:464:VAL:CG2	1.28	1.61
1:B:55:VAL:CG2	1:B:464:VAL:CG2	1.96	1.42
1:B:463:LYS:C	1:B:464:VAL:N	1.80	1.39
1:B:55:VAL:CG2	1:B:464:VAL:HG21	1.54	1.36
1:B:293:ILE:HA	1:B:317:ALA:HB2	1.33	1.10

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	497/533 (93%)	427 (86%)	55 (11%)	15 (3%)	3	6
1	B	490/533 (92%)	409 (84%)	65 (13%)	16 (3%)	3	5
All	All	987/1066 (93%)	836 (85%)	120 (12%)	31 (3%)	3	5

5 of 31 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	122	GLU
1	A	191	ILE

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Mol	Chain	Res	Type
1	B	193	ALA
1	B	210	ASN
1	B	311	HIS

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	443/471 (94%)	399 (90%)	44 (10%)	7	16
1	B	440/471 (93%)	397 (90%)	43 (10%)	7	17
All	All	883/942 (94%)	796 (90%)	87 (10%)	7	16

5 of 87 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	194	ASN
1	B	328	LEU
1	B	196	ASP
1	B	246	ASN
1	B	380	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 57 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	476	ASN
1	B	498	HIS
1	B	140	ASN
1	B	433	HIS
1	B	299	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](#)

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	B	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	463:LYS	C	464:VAL	N	1.80

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	501/533 (93%)	-0.19	5 (0%) 79 76	13, 43, 77, 80	0
1	B	496/533 (93%)	-0.08	16 (3%) 50 44	17, 44, 80, 80	0
All	All	997/1066 (93%)	-0.13	21 (2%) 63 58	13, 43, 79, 80	0

The worst 5 of 21 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	464	VAL	4.4
1	B	193	ALA	3.5
1	B	465	ASP	3.3
1	A	404	TYR	3.3
1	B	192	ALA	3.2

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.