



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 10:25 PM UTC

PDB ID : 3BUO / pdb_00003buo
Title : Crystal structure of c-Cbl-TKB domain complexed with its binding motif in EGF receptor'
Authors : Ng, C.; Jackson, R.A.; Buschdorf, J.P.; Sun, Q.; Guy, G.R.; Sivaraman, J.
Deposited on : 2008-01-03
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
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

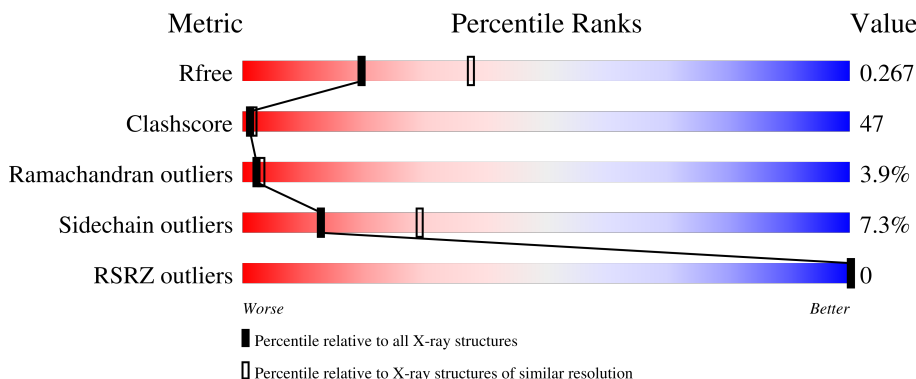
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	13	31% 23% 31% 15%
1	C	13	31% 23% 31% 15%
2	B	329	35% 50% 7% 8%
2	D	329	32% 53% 7% 8%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 5405 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 13-meric peptide from Epidermal growth factor receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	11	Total	C	N	O	P	0	0	0
			95	57	15	22	1			
1	C	11	Total	C	N	O	P	0	0	0
			95	57	15	22	1			

- Molecule 2 is a protein called E3 ubiquitin-protein ligase CBL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	304	Total	C	N	O	S	0	0	0
			2490	1612	424	441	13			
2	D	304	Total	C	N	O	S	0	0	0
			2490	1612	424	441	13			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	24	SER	GLY	cloning artifact	UNP P22681
D	24	SER	GLY	cloning artifact	UNP P22681

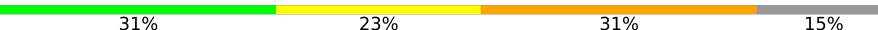
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	6	Total	O	0	0
			6	6		
3	B	111	Total	O	0	0
			111	111		
3	C	6	Total	O	0	0
			6	6		
3	D	112	Total	O	0	0
			112	112		

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: 13-meric peptide from Epidermal growth factor receptor

Chain A: 



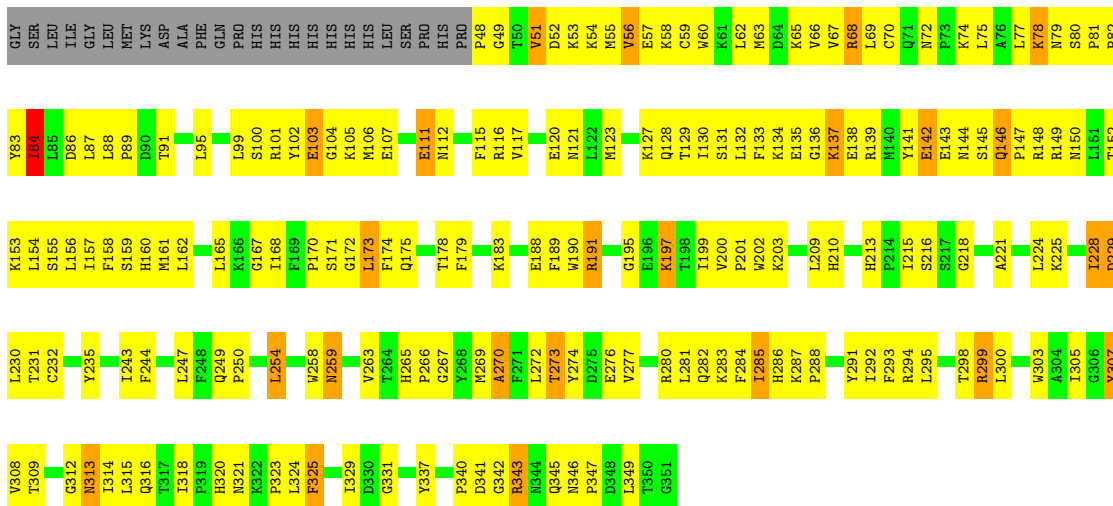
- Molecule 1: 13-meric peptide from Epidermal growth factor receptor

Chain C: 



- Molecule 2: E3 ubiquitin-protein ligase CBL

Chain B: 



- Molecule 2: E3 ubiquitin-protein ligase CBL

Chain D: 

GLY	GLY	Y83	T152	I228	
SER	SER	I84	K153	D229	W303
LEU	LEU	L85	L154	D230	A304
ILE	ILE	D86	S155	T231	I305
GLY	GLY	L87	L156	C232	G306
LEU	LEU	L88	I157		Y307
MET	MET	D89	F158	Y235	V308
LYS	LYS	D90	S159		T309
ASP	ASP	T91	H160	T243	A310
ALA	ALA		M161	F244	D311
PHE	PHE	H94	L162		G312
GLN	GLN	L95		L247	N313
PRO	PRO		L165	F248	I314
HIS	HIS	L99	K166	Q249	L315
HIS	HIS	S100	G167	P250	Q316
HIS	HIS	R101	I168	W251	T317
HIS	HIS	E102	F169	S252	I318
HIS	HIS	E103	P170	S253	P319
HIS	HIS	G104	S171	L254	H320
HIS	HIS	K105	G172	L255	N321
LEU	LEU	M106	L173	R256	K322
SER	SER	E107	F174	W257	P323
PRO	PRO		Q175	W258	L324
HIS	HIS	E111		N259	F325
PRO	PRO	M112	T178		
			F179	V263	I329
P48	G49	F115		T264	D330
	W50	R116	T182	H265	G331
V51	V51	V117	K183	P266	
D52	D52		Q267		Y337
K53	K53	E120	E188	Y268	L338
K54	K54	N121	F189	W269	F339
M55	M55	L122	W190	A270	P340
V56	V56	M123	R191	F271	D341
E57	E57			L272	G342
K58	K58	K127	G195	T273	R343
C59	C59	Q128	E196	Y274	N344
W60	W60	T129	K197	D275	Q345
K61	K61	I130	T198	E276	N346
L62	L62	S131	I199	V277	P347
M63	M63	L132	V200		D348
D64	D64	F133	P201	R280	L349
K65	K65	K134	W202	L281	T350
V66	V66	E135	K203	Q282	G351
V67	V67	G136		K283	
R68	R68	K137	L209	F284	
L69	L69	E138	H210	I285	
C70	C70	R139		H286	
Q71	Q71	M140	H213	K287	
N72	N72	Y141	P214	P288	
F73	F73	E142	I215		
K74	K74	E143	S216	Y291	
L75	L75	M144	S217	I292	
A76	A76	S145	G218	F293	
L77	L77	Q146		R294	
K78	K78	P147	A221	L295	
N79	N79	R148			
S80	S80	R149	L224	T298	
P81	P81	M150	K225	R299	
P82	P82	L151		L300	

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	63.86Å 110.17Å 55.82Å 90.00° 89.94° 90.00°	Depositor
Resolution (Å)	20.00 – 2.60 20.00 – 2.60	Depositor EDS
% Data completeness (in resolution range)	51.8 (20.00-2.60) 91.5 (20.00-2.60)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.49 (at 2.61Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.231 , 0.278 0.251 , 0.267	Depositor DCC
R_{free} test set	2860 reflections (13.04%)	wwPDB-VP
Wilson B-factor (Å ²)	29.0	Xtriage
Anisotropy	0.858	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 33.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.458 for -h,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5405	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.08% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: PTR

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	0.71	0/79	1.29	1/104 (1.0%)
1	C	0.65	0/79	1.26	1/104 (1.0%)
2	B	0.66	0/2556	0.98	8/3449 (0.2%)
2	D	0.66	0/2556	0.98	7/3449 (0.2%)
All	All	0.66	0/5270	0.99	17/7106 (0.2%)

There are no bond length outliers.

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	218	GLY	N-CA-C	-7.13	105.82	114.66
2	B	218	GLY	N-CA-C	-7.06	105.90	114.66
2	B	213	HIS	CA-C-N	6.63	128.13	119.84
2	B	213	HIS	C-N-CA	6.63	128.13	119.84
2	B	228	ILE	N-CA-C	6.55	117.17	110.82

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	95	0	80	16	0
1	C	95	0	80	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	2490	0	2499	237	0
2	D	2490	0	2499	239	0
3	A	6	0	0	0	0
3	B	111	0	0	16	0
3	C	6	0	0	1	0
3	D	112	0	0	18	0
All	All	5405	0	5158	490	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 47.

The worst 5 of 490 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:D:82:PRO:HG3	2:D:156:LEU:HD12	1.33	1.09
2:D:277:VAL:HG13	2:D:292:ILE:HD11	1.37	1.05
2:B:82:PRO:HG3	2:B:156:LEU:HD12	1.33	1.04
2:B:282:GLN:HE22	2:B:285:ILE:HD12	1.23	1.00
2:D:282:GLN:HE22	2:D:285:ILE:HD12	1.22	1.00

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	8/13 (62%)	4 (50%)	2 (25%)	2 (25%)	0	0
1	C	8/13 (62%)	4 (50%)	2 (25%)	2 (25%)	0	0
2	B	302/329 (92%)	248 (82%)	44 (15%)	10 (3%)	3	5
2	D	302/329 (92%)	248 (82%)	44 (15%)	10 (3%)	3	5
All	All	620/684 (91%)	504 (81%)	92 (15%)	24 (4%)	2	3

5 of 24 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	103	GLU
2	B	270	ALA
2	B	285	ILE
2	D	103	GLU
2	D	270	ALA

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	10/11 (91%)	9 (90%)	1 (10%)	7	16
1	C	10/11 (91%)	9 (90%)	1 (10%)	7	16
2	B	271/293 (92%)	251 (93%)	20 (7%)	13	29
2	D	271/293 (92%)	252 (93%)	19 (7%)	14	31
All	All	562/608 (92%)	521 (93%)	41 (7%)	13	29

5 of 41 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	84	ILE
2	D	259	ASN
2	D	111	GLU
2	D	191	ARG
2	D	299	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	175	GLN
2	D	259	ASN
2	D	345	GLN
2	D	213	HIS
2	D	282	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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	$\# Z > 2$
1	PTR	A	1069	1	15,16,17	1.43	3 (20%)	17,22,24	1.00	0
1	PTR	C	1069	1	15,16,17	1.41	3 (20%)	17,22,24	1.01	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
1	PTR	A	1069	1	-	1/10/11/13	0/1/1/1
1	PTR	C	1069	1	-	1/10/11/13	0/1/1/1

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1069	PTR	P-OH	2.61	1.64	1.59
1	C	1069	PTR	P-OH	2.56	1.64	1.59
1	A	1069	PTR	CE1-CD1	2.29	1.42	1.38
1	C	1069	PTR	CE1-CD1	2.17	1.42	1.38
1	A	1069	PTR	CD2-CG	2.05	1.43	1.38

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	1069	PTR	O-C-CA-CB
1	C	1069	PTR	O-C-CA-CB

There are no ring outliers.

No monomer is involved in short contacts.

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	10/13 (76%)	-1.53	0 100 100	22, 32, 48, 51	0
1	C	10/13 (76%)	-1.51	0 100 100	22, 32, 48, 51	0
2	B	304/329 (92%)	-1.62	0 100 100	16, 32, 52, 71	0
2	D	304/329 (92%)	-1.63	0 100 100	16, 32, 52, 71	0
All	All	628/684 (91%)	-1.62	0 100 100	16, 32, 52, 71	0

There are no RSRZ outliers to report.

6.2 Non-standard residues in protein, DNA, RNA chains [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(Å ²)	Q<0.9
1	PTR	A	1069	16/17	1.00	0.02	27,28,29,30	0
1	PTR	C	1069	16/17	1.00	0.03	27,28,29,30	0

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.