



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 09:08 AM UTC

PDB ID : 1SY6 / pdb_00001sy6
Title : Crystal Structure of CD3gammaepsilon Heterodimer in Complex with OKT3 Fab Fragment
Authors : Kjer-Nielsen, L.; Dunstone, M.A.; Kostenko, L.; Ely, L.K.; Beddoe, T.; Misfud, N.A.; Purcell, A.W.; Brooks, A.G.; McCluskey, J.; Rossjohn, J.
Deposited on : 2004-03-31
Resolution : 2.10 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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

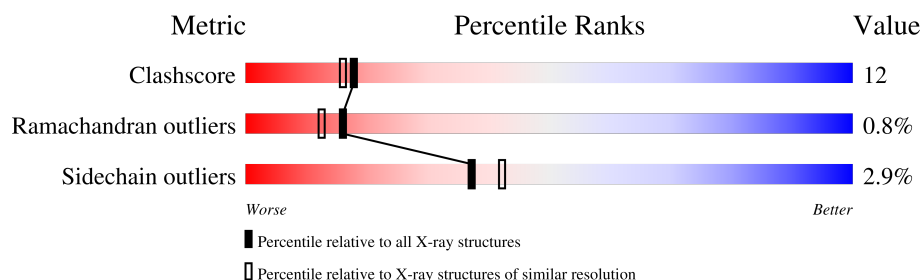
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	L	213	74% 22% .
2	H	219	76% 22% .
3	A	204	56% 24% . 18%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4651 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 OKT3 Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	213	Total	C	N	O	S	0	0	0
			1639	1015	274	340	10			

- Molecule 2 is a protein called OKT3 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	219	Total	C	N	O	S	0	0	0
			1675	1054	278	334	9			

- Molecule 3 is a protein called T-cell surface glycoprotein CD3 gamma/epsilon chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	168	Total	C	N	O	S	0	0	0
			1337	840	227	262	8			

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	82	GLY	-	SEE REMARK 999	UNP P09693
A	83	SER	-	SEE REMARK 999	UNP P09693
A	84	ALA	-	SEE REMARK 999	UNP P09693
A	85	ASP	-	SEE REMARK 999	UNP P09693
A	86	ASP	-	SEE REMARK 999	UNP P09693
A	87	ALA	-	SEE REMARK 999	UNP P09693
A	88	LYS	-	SEE REMARK 999	UNP P09693
A	89	LYS	-	SEE REMARK 999	UNP P09693
A	90	ASP	-	SEE REMARK 999	UNP P09693
A	91	ALA	-	SEE REMARK 999	UNP P09693
A	92	ALA	-	SEE REMARK 999	UNP P09693
A	93	LYS	-	SEE REMARK 999	UNP P09693
A	94	LYS	-	SEE REMARK 999	UNP P09693
A	95	ASP	-	SEE REMARK 999	UNP P09693

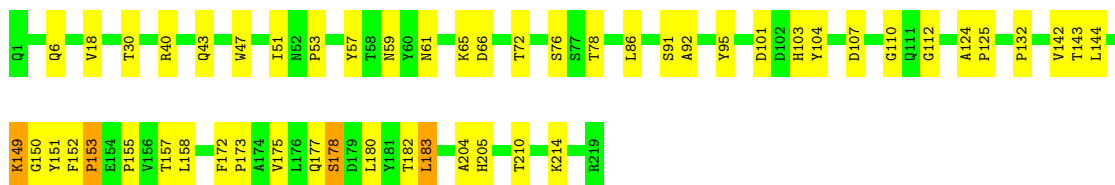
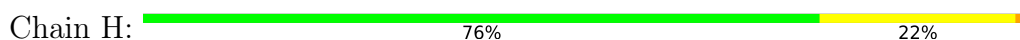
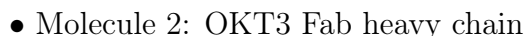
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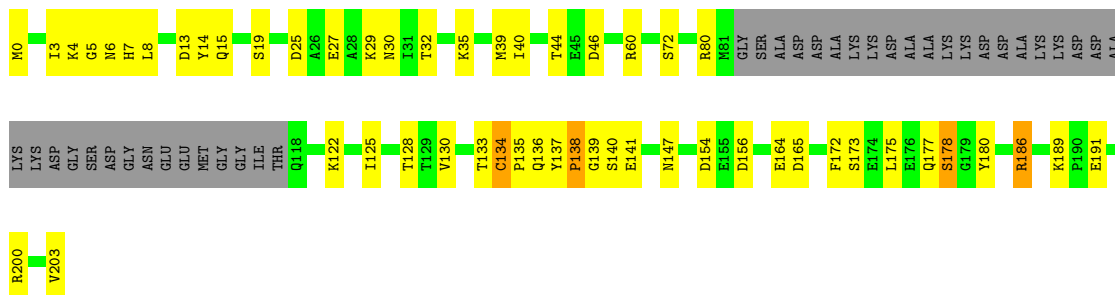
Chain	Residue	Modelled	Actual	Comment	Reference
A	96	ASP	-	SEE REMARK 999	UNP P09693
A	97	ALA	-	SEE REMARK 999	UNP P09693
A	98	LYS	-	SEE REMARK 999	UNP P09693
A	99	LYS	-	SEE REMARK 999	UNP P09693
A	100	ASP	-	SEE REMARK 999	UNP P09693
A	101	ASP	-	SEE REMARK 999	UNP P09693
A	102	ALA	-	SEE REMARK 999	UNP P09693
A	103	LYS	-	SEE REMARK 999	UNP P09693
A	104	LYS	-	SEE REMARK 999	UNP P09693
A	105	ASP	-	SEE REMARK 999	UNP P09693
A	106	GLY	-	SEE REMARK 999	UNP P09693
A	107	SER	-	SEE REMARK 999	UNP P09693

Note EDS was not executed.

- Chain L: 74% 22% .



- Molecule 3: T-cell surface glycoprotein CD3 gamma/epsilon chain



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	67.70Å 55.77Å 96.05Å 90.00° 100.85° 90.00°	Depositor
Resolution (Å)	50.00 – 2.10	Depositor
% Data completeness (in resolution range)	(Not available) (50.00-2.10)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.211 , 0.255	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4651	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

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	L	0.36	0/1678	0.91	7/2278 (0.3%)
2	H	0.35	0/1719	0.85	4/2345 (0.2%)
3	A	0.32	0/1365	0.86	5/1837 (0.3%)
All	All	0.35	0/4762	0.87	16/6460 (0.2%)

There are no bond length outliers.

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	H	61	ASN	N-CA-C	-8.18	97.70	109.96
1	L	136	ASN	N-CA-C	6.74	120.81	109.76
1	L	100	GLY	N-CA-C	6.68	120.56	112.48
1	L	98	GLY	N-CA-C	-6.27	102.99	112.89
1	L	91	SER	N-CA-C	-6.12	105.30	112.89

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	L	1639	0	1550	52	0
2	H	1675	0	1620	41	0
3	A	1337	0	1290	31	0
All	All	4651	0	4460	112	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 12.

The worst 5 of 112 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:L:19:VAL:HG21	1:L:77:MET:HE2	1.33	1.10
1:L:77:MET:HE1	1:L:103:LEU:HD21	1.37	1.06
1:L:19:VAL:HG21	1:L:77:MET:CE	2.08	0.82
2:H:125:PRO:HB3	2:H:151:TYR:HB3	1.65	0.79
1:L:188:HIS:C	1:L:189:ASN:HD22	1.95	0.74

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	L	211/213 (99%)	204 (97%)	6 (3%)	1 (0%)	24	22
2	H	217/219 (99%)	207 (95%)	9 (4%)	1 (0%)	24	22
3	A	164/204 (80%)	146 (89%)	15 (9%)	3 (2%)	6	3
All	All	592/636 (93%)	557 (94%)	30 (5%)	5 (1%)	16	12

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	178	SER
3	A	14	TYR
1	L	83	ALA
3	A	29	LYS
3	A	138	PRO

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	L	188/188 (100%)	183 (97%)	5 (3%)	39	45
2	H	189/189 (100%)	185 (98%)	4 (2%)	47	54
3	A	147/174 (84%)	141 (96%)	6 (4%)	27	29
All	All	524/551 (95%)	509 (97%)	15 (3%)	37	42

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	155	PRO
3	A	175	LEU
2	H	183	LEU
3	A	186	ARG
3	A	46	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
3	A	177	GLN
3	A	159	ASN
3	A	1	GLN
3	A	150	ASN
2	H	177	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](#)

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

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.